

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
6 September 2002 (06.09.2002)

PCT

(10) International Publication Number
WO 02/068677 A2

(51) International Patent Classification⁷:

C12Q

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TI, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(21) International Application Number:

PCT/US02/06001

(22) International Filing Date: 14 January 2002 (14.01.2002)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

| | | |
|------------|-------------------------------|----|
| 60/272,206 | 27 February 2001 (27.02.2001) | US |
| 60/281,149 | 2 April 2001 (02.04.2001) | US |
| 60/284,555 | 17 April 2001 (17.04.2001) | US |

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TI, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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Declaration under Rule 4.17:

— *of inventorship (Rule 4.17(iv)) for US only*

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 02/068677 A2

(54) Title: NOVEL METHODS OF DIAGNOSIS OF METASTATIC COLORECTAL CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC COLORECTAL CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of metastatic colorectal cancer. Also described herein are methods that can be used to identify modulators of metastatic colorectal cancer.

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NOVEL METHODS OF DIAGNOSIS OF METASTATIC COLORECTAL CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC COLORECTAL CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is related to USSN 60/272,206, filed February 27, 2001, USSN 60/281,149, filed April 2, 2001, and USSN 60/284,555, filed April 17, 2001, all of which are herein incorporated by reference in their entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in metastatic colorectal cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of metastatic colorectal cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit metastatic colorectal cancer.

BACKGROUND OF THE INVENTION

Cancer of the colon and/or rectum (referred to as "colorectal cancer") are significant in Western populations and particularly in the United States. Cancers of the colon and rectum occur in both men and women most commonly after the age of 50. These develop as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- β signaling pathway. For a review, see *Molecular Biology of Colorectal Cancer*, pp. 238-299, in *Curr. Probl. Cancer*, Sept/Oct 1997; see also Williams, *Colorectal Cancer*

(1996); Kinsella & Schofield, *Colorectal Cancer: A Scientific Perspective* (1993); *Colorectal Cancer: Molecular Mechanisms, Premalignant State and its Prevention* (Schmiegel & Scholmerich eds., 2000); *Colorectal Cancer: New Aspects of Molecular Biology and Their Clinical Applications* (Hanski et al., eds 2000); McArdle et al.; *Colorectal Cancer* (2000); Wanebo, *Colorectal Cancer* (1993); Levin, *The American Cancer Society: Colorectal Cancer* (1999); *Treatment of Hepatic Metastases of Colorectal Cancer* (Nordlinger & Jaeck eds., 1993); *Management of Colorectal Cancer* (Dunitz et al., eds. 1998); *Cancer: Principles and Practice of Oncology* (Devita et al., eds. 2001); *Surgical Oncology: Contemporary Principles and Practice* (Kirby et al., eds. 2001); Offit, *Clinical Cancer Genetics: Risk Counseling and Management* (1997); *Radioimmunotherapy of Cancer* (Abrams & Fritzberg eds. 2000); Fleming, *AJCC Cancer Staging Handbook* (1998); *Textbook of Radiation Oncology* (Leibel & Phillips eds. 2000); and *Clinical Oncology* (Abeloff et al., eds. 2000).

Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, metastasis of the tumor to the lumen, and metastasis of tumor cells to regional lymph nodes are important prognostic factors (see, e.g., *PET in Oncology: Basics and Clinical Application* (Ruhlmann et al. eds. 1999). For example, five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast majority of colorectal cancers but not in normal tissues. Liefers et al., *New England J. of Med.* 339(4):223 (1998). In addition, colorectal cancers often metastasize to the liver. However, the lack of information about the gene expression exhibited by these cancers limits the ability to effectively diagnose and treat the disease.

Thus, methods for diagnosis and prognosis of metastatic colorectal cancer and effective treatment of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of metastatic colorectal cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, colorectal cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in metastatic colorectal disease and other metastatic cancers.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in metastatic colorectal cancer cells. Such genes and the proteins they

encode are useful for diagnostic and prognostic purposes, and also as targets for screening for therapeutic compounds that modulate metastatic colorectal cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include, early detection of colon cancers, monitoring and early detection of relapse following treatment of colon cancers, monitoring response to therapy of colon cancers, determining prognosis of colon cancers, directing therapy of colon cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous colon adenomas. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a metastatic colorectal cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat metastatic colorectal cancer. In another embodiment, the patient is suspected of having metastatic colorectal cancer.

In one embodiment, the patient is a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides methods of detecting polypeptide encoded by a metastatic colorectal cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with an antibody that specifically binds a polypeptide encoded by a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26., thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated transcript to a level of the metastatic colorectal cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, wherein the polypeptide specifically binds to the metastatic colorectal cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated antibody to a level of the metastatic colorectal cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated polypeptide to a level of the metastatic

colorectal cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a metastatic colorectal cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to metastatic colorectal cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates a metastatic colorectal cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a metastatic colorectal cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a metastatic colorectal cancer-associated cell to treat colorectal cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having colorectal cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of colorectal cancer.

In one embodiment, the control is a mammal with colorectal cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In another aspect, the present invention provides a method for treating a mammal having colorectal cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having colorectal cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of colon and/or rectal cancer (e.g., colorectal cancer), including metastatic colorectal cancers, as well as methods for screening for compositions which modulate colorectal cancer. By "metastatic colorectal cancer" herein is meant a colon and/or rectal tumor or cancer that is classified as Dukes stage C or D (see, e.g., Cohen *et al.*, *Cancer of the Colon*, in *Cancer: Principles and Practice of Oncology*, pp. 1144-1197 (Devita *et al.*, eds., 5th ed. 1997); see also *Harrison's Principles of Internal Medicine*, pp. 1289-129 (Wilson *et al.*, eds., 12th ed., 1991). "Treatment, monitoring, detection or modulation of metastatic colorectal cancer" includes treatment, monitoring, detection, or modulation of metastatic colorectal disease in those patients who have metastatic colorectal

disease (Dukes stage C or D). In Dukes stage A, the tumor has penetrated into, but not through, the bowel wall. In Dukes stage B, the tumor has penetrated through the bowel wall but there is not yet any lymph involvement. In Dukes stage C, the cancer involves regional lymph nodes. In Dukes stage D, there is distant metastasis, e.g., liver, lung, etc.

Tables 1-26 provide UniGene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in metastasizing colorectal cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the UniGene cluster. In Tables 1-26, the ratio provided represents primary tumor samples from known Dukes B stage survivors vs. liver metastasis samples from patients with metastatic colorectal cancer. In these samples, the identified genes are underexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio provided represents liver metastasis samples from patients with known metastatic colorectal cancer vs. known primary tumor samples from Dukes B stage survivors. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio provided represents primary tumor samples from known Dukes B stage survivors vs. liver metastasis samples from patients with metastatic colorectal cancer. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less. Survivors are subjects who have been disease free for five years or longer.

In Tables 1-26, the ratio provided represents liver metastasis samples from patients with known metastatic disease vs. tissue samples from normal colon tissue. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio represents liver metastasis samples from patients with known metastatic disease vs. tissue samples from normal colon tissue. In these samples, the identified genes are underexpressed in the metastatic samples, as the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

One of skill will recognize that although the sequences identified in Tables 1-26 exhibited increased or decreased expression in metastasizing colorectal cancer samples, the sequences of the invention, and their encoded proteins, can be used to diagnose, treat or prevent cancers in patients with Dukes stage A or B colorectal cancers. Alteration of gene

expression for a gene in Tables 1-26 may be more likely or less likely to indicate that the subject will progress to metastatic disease. The sequences can also be used to diagnose, treat or prevent precancerous or benign conditions such as precancerous colon adenomas.

Alteration of gene expression for a gene in Tables 1-26 may or may not indicate that the subject is more likely to progress to cancer or to metastatic disease. Thus, although the specification focuses primarily on metastasizing colorectal cancer, the methods described below can also be applied to non-metastasizing colorectal cancers (e.g., Dukes stages A and B) and precancerous or benign conditions (e.g., precancerous adenomas) as well.

Definitions

The term "metastatic colorectal cancer protein" or "metastatic colorectal cancer polynucleotide" or "metastatic colorectal cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "metastatic colorectal cancer polypeptide" and a "metastatic colorectal cancer polynucleotide," include both naturally occurring or recombinant.

A "full length" metastatic colorectal cancer protein or nucleic acid refers to a metastatic colorectal cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type metastatic colorectal cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a metastatic colorectal cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions

and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short

words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5877 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules

or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.*, the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine,

norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins (1984)*).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g., Alberts et al., Molecular Biology of the Cell (3rd ed., 1994)* and *Cantor & Schimmel, Biophysical Chemistry Part I: The Conformation of Biological Macromolecules (1980)*. “Primary structure” refers to the amino acid sequence of a particular peptide. “Secondary structure” refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. “Tertiary structure” refers to the complete three dimensional structure of a polypeptide monomer. “Quaternary structure” refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

“Nucleic acid” or “oligonucleotide” or “polynucleotide” or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui &

Cook, eds.. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins

or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g.,

recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence,

wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification,

although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and *Current Protocols in Molecular Biology*, ed. Ausubel, *et al.*

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a metastatic colorectal cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the metastatic colorectal cancer protein or nucleic acid, e.g., an enzymatic, functional, physical, or chemical effect, such as the ability to decrease metastatic colorectal cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic colorectal cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a metastatic colorectal cancer protein sequence, e.g., functional, enzymatic, physical and

chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the metastatic colorectal cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on metastatic colorectal cancer can also be performed using metastatic colorectal cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic colorectal cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for metastatic colorectal cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of metastatic colorectal cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of metastatic colorectal cancer polynucleotide and polypeptide sequences of the invention. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of metastatic colorectal cancer proteins of the invention, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate metastatic colorectal cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of metastatic colorectal cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the metastatic colorectal cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then

determining the functional effects on activity, as described above. Activators and inhibitors of metastatic colorectal cancer can also be identified by incubating metastatic colorectal cancer cells with the test compound and determining increases or decreases in the expression of 1 or more metastatic colorectal cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more metastatic colorectal cancer proteins, such as colorectal cancer proteins encoded by the sequences set out in Tables 1-26.

Samples or assays comprising metastatic colorectal cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a metastatic colorectal cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney, *Culture of Animal Cells a Manual of Basic Technique* pp. 231-241 (3rd ed. 1994).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed. 1994)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen.

The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, *Fundamental Immunology*.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab')_2$, a dimer of Fab which itself is a light chain joined to $V_H\text{-}C_{H1}$ by a disulfide bond. The $F(ab')_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab')_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see *Fundamental Immunology* (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty *et al.*, *Nature* 348:552-554 (1990))

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al.*, *Immunology Today* 4:72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce

antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty *et al.*, *Nature* 348:552-554 (1990); Marks *et al.*, *Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of metastatic colorectal cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different metastatic colorectal cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in metastatic colorectal cancer versus non-metastatic colorectal cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate metastatic colorectal cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of metastatic colorectal cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a

particular expression profile; e.g., screening can be done for drugs that suppress the metastatic colorectal cancer expression profile. This may be done by making biochips comprising sets of the important metastatic colorectal cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the metastatic colorectal cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the metastatic colorectal cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the metastatic colorectal cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in metastatic colorectal cancer, herein termed "metastatic colorectal cancer sequences." As outlined below, metastatic colorectal cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in metastatic colorectal cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the metastatic colorectal cancer sequences are from humans; however, as will be appreciated by those in the art, metastatic colorectal cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other metastatic colorectal cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Metastatic colorectal cancer sequences from other organisms may be obtained using the techniques outlined below.

Metastatic colorectal cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, metastatic colorectal cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the metastatic colorectal cancer sequences can be generated.

A metastatic colorectal cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the metastatic colorectal cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid

or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying metastatic colorectal cancer-associated sequences, the metastatic colorectal cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue, or tumor tissue samples from patients who have been diagnosed with Dukes stage A or B cancer but have survived vs. metastatic tissue. Other suitable tissue comparisons include comparing metastatic colorectal cancer samples with metastatic cancer samples from other cancers, such as lung, breast, other gastrointestinal cancers, prostate, ovarian, etc. Samples of, e.g., Dukes stage B survivor tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal colon, but also including, and not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the metastatic colorectal cancer screen that are expressed in significant amounts in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, metastatic colorectal cancer sequences are those that are up-regulated in metastatic colorectal cancer; that is, the expression of these genes is higher in the metastatic tissue as compared to non-metastatic cancerous tissue or normal colon tissue (see, e.g., Tables 1-26). "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. All UniGene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, metastatic colorectal cancer sequences are those that are down-regulated in the metastatic colorectal cancer; that is, the expression of these genes is lower in metastatic tissue as compared to non-metastatic cancerous tissue or normal colon tissue (see, e.g., Tables 1-26). "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

Informatics

The ability to identify genes that are over or under expressed in metastatic colorectal cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with metastatic colorectal cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson, *Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing metastatic colorectal cancer, i.e., the identification of metastatic colorectal cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount *et al.*, *Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxevanis & Ouellette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological*

Science and Medicine (1999); *Introduction to Computational Molecular Biology* (Setubal et al., eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000); *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* (Higgins & Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for metastatic colorectal cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The

comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example,

a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of metastatic colorectal cancer-associated proteins

Metastatic colorectal cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the metastatic colorectal cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus and/or in the organelles. Proteins containing one or more transmembrane domains that exclusively reside in organelles are also considered intracellular proteins. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (*see, e.g., Molecular Biology of the Cell* (Alberts, ed., 3rd ed., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein

interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g., Bateman et al., Nuc. Acids Res.* 28:263-266 (2000); Sonnhammer et al., *Proteins* 28:405-420 (1997); Bateman et al., *Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer et al., *Nuc. Acids Res.* 26:320-322 (1998)).

In another embodiment, the metastatic colorectal cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive

hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Metastatic colorectal cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the metastatic colorectal cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they often serve to transmit signals to various other cell types. The secreted protein may

function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Metastatic colorectal cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests.

Use of metastatic colorectal cancer nucleic acids

As described above, metastatic colorectal cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the metastatic colorectal cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The metastatic colorectal cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-26, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the metastatic colorectal cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al., supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/unigene/>).

Once the metastatic colorectal cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire metastatic colorectal cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant metastatic colorectal cancer nucleic acid can be further-used as a probe to identify and isolate other metastatic colorectal cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant metastatic colorectal cancer nucleic acids and proteins.

The metastatic colorectal cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the metastatic colorectal

cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the metastatic colorectal cancer nucleic acids that include coding regions of metastatic colorectal cancer proteins can be put into expression vectors for the expression of metastatic colorectal cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to metastatic colorectal cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the metastatic colorectal cancer nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical

equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize

sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo- or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of metastatic colorectal cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a metastatic colorectal cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of metastatic colorectal

cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication (Guatelli *et al.*, *Proc. Natl. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

Expression of metastatic colorectal cancer proteins from nucleic acids

In a preferred embodiment, metastatic colorectal cancer nucleic acids, e.g., encoding metastatic colorectal cancer proteins, are used to make a variety of expression vectors to express metastatic colorectal cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the metastatic colorectal cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the metastatic colorectal cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The metastatic colorectal cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a metastatic colorectal cancer protein, under the appropriate conditions to induce or cause expression of the metastatic colorectal cancer protein. Conditions appropriate for metastatic colorectal cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeabacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, SF9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the metastatic colorectal cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g., Fernandez & Hoeffler, supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation,

polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, metastatic colorectal cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the metastatic colorectal cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, metastatic colorectal cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, metastatic colorectal cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The metastatic colorectal cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies,

if the desired epitope is small, the metastatic colorectal cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the metastatic colorectal cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the metastatic colorectal cancer protein is a metastatic colorectal cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the metastatic colorectal cancer protein is purified or isolated after expression. Metastatic colorectal cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the metastatic colorectal cancer protein may be purified using a standard anti-metastatic colorectal cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the metastatic colorectal cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the metastatic colorectal cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of metastatic colorectal cancer proteins

In one embodiment, the metastatic colorectal cancer proteins are derivative or variant metastatic colorectal cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative metastatic colorectal cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the metastatic colorectal cancer peptide.

Also included within one embodiment of metastatic colorectal cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the metastatic colorectal cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell

culture as outlined above. However, variant metastatic colorectal cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the metastatic colorectal cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed metastatic colorectal cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of metastatic colorectal cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a metastatic colorectal cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the metastatic colorectal cancer proteins as needed. Alternatively, the variant may be designed or reorganized such that the biological activity of the metastatic colorectal cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of metastatic colorectal cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a metastatic colorectal cancer polypeptide with an

organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a metastatic colorectal cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking metastatic colorectal cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-metastatic colorectal cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the metastatic colorectal cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence metastatic colorectal cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express metastatic colorectal cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to metastatic colorectal cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence metastatic colorectal cancer polypeptide (for O-linked glycosylation sites). The metastatic colorectal cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the metastatic colorectal cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the metastatic colorectal cancer polypeptide is by chemical or enzymatic coupling of glycosides

to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the metastatic colorectal cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of metastatic colorectal cancer comprises linking the metastatic colorectal cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxoalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Metastatic colorectal cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a metastatic colorectal cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a metastatic colorectal cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the metastatic colorectal cancer polypeptide. The presence of such epitope-tagged forms of a metastatic colorectal cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the metastatic colorectal cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a metastatic colorectal cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al.*, *Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan *et al.*, *Molecular and Cellular Biology* 5:3610-3616 (1985));

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (*Paborsky et al.*, *Protein Engineering* 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (*Hopp et al.*, *BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (*Martin et al.*, *Science* 255:192-194 (1992)); tubulin epitope peptide (*Skinner et al.*, *J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (*Lutz-Freyermuth et al.*, *Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

Also included are other metastatic colorectal cancer proteins of the metastatic colorectal cancer family, and metastatic colorectal cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related metastatic colorectal cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the metastatic colorectal cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, *PCR Protocols, supra*).

Antibodies to metastatic colorectal cancer proteins

In a preferred embodiment, when a metastatic colorectal cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the metastatic colorectal cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller metastatic colorectal cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-26 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler & Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of Tables 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to metastatic colorectal cancer protein are capable of reducing or eliminating a biological function of a metastatic colorectal cancer protein, as is described below. That is, the addition of anti-metastatic colorectal cancer protein antibodies (either polyclonal or preferably monoclonal) to metastatic colorectal cancer tissue (or cells containing metastatic colorectal cancer) may reduce or eliminate the metastatic colorectal cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the metastatic colorectal cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact

human variable domain has been substituted by the corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in virtually all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of metastatic colorectal cancer with an antibody raised against a metastatic colorectal cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the metastatic colorectal cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted metastatic colorectal cancer protein.

In another preferred embodiment, the metastatic colorectal cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory,

antibodies used for this treatment typically bind the extracellular domain of the metastatic colorectal cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane metastatic colorectal cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the metastatic colorectal cancer protein. The antibody may be an antagonist of the metastatic colorectal cancer protein or may prevent activation of the transmembrane metastatic colorectal cancer protein. In some embodiments, when the antibody prevents the binding of other molecules to the metastatic colorectal cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, metastatic colorectal cancer is treated by administering to a patient antibodies directed against the transmembrane metastatic colorectal cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the metastatic colorectal cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the metastatic colorectal cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with metastatic colorectal cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to metastatic colorectal cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with metastatic colorectal cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like.

Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against metastatic colorectal cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane metastatic colorectal cancer proteins not only serves to increase the local concentration of therapeutic moiety in the metastatic colorectal cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the metastatic colorectal cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the metastatic colorectal cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The metastatic colorectal cancer antibodies of the invention specifically bind to metastatic colorectal cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of metastatic colorectal cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the metastatic colorectal cancer phenotype. Expression levels of genes in normal tissue (i.e., not undergoing metastatic colorectal cancer) and in metastatic colorectal cancer tissue (and in some cases, for varying severities of metastatic colorectal cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may

be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus metastatic colorectal cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the metastatic colorectal cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to metastatic colorectal cancer genes, i.e., those identified as being important in a metastatic colorectal cancer phenotype, can be evaluated in a metastatic colorectal cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The metastatic colorectal cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of metastatic colorectal cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the metastatic colorectal cancer protein are detected. Although DNA or RNA encoding the metastatic colorectal cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a metastatic colorectal cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a metastatic colorectal cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, metastatic colorectal cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of metastatic colorectal cancer. Detection of these proteins in putative metastatic colorectal cancer tissue

allows for detection or diagnosis of metastatic colorectal cancer. In one embodiment, antibodies are used to detect metastatic colorectal cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the metastatic colorectal cancer protein is detected, e.g., by immunoblotting with antibodies raised against the metastatic colorectal cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the metastatic colorectal cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the metastatic colorectal cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the metastatic colorectal cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of metastatic colorectal cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing metastatic colorectal cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of metastatic colorectal cancer proteins. Antibodies can be used to detect a metastatic colorectal cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous metastatic colorectal cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled metastatic colorectal cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue

samples, including metastatic colorectal cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g.*, Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to metastatic colorectal cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, metastatic colorectal cancer probes may be attached to biochips for the detection and quantification of metastatic colorectal cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the three classes of proteins as described herein are used in drug screening assays. The metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (*e.g.*, Zlokarnik, *et al.*, *Science* 279:84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified metastatic colorectal cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the metastatic colorectal cancer phenotype or an identified physiological function of a metastatic colorectal cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput

screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be applied. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in metastatic colorectal cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the metastatic colorectal cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing metastatic colorectal cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in metastatic colorectal cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in metastatic colorectal cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the metastatic colorectal cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the metastatic colorectal cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of metastatic colorectal cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more metastatic colorectal cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-26. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate metastatic colorectal cancer, modulate metastatic colorectal

cancer proteins, bind to a metastatic colorectal cancer protein, or interfere with the binding of a metastatic colorectal cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the metastatic colorectal cancer phenotype or the expression of a metastatic colorectal cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a metastatic colorectal cancer phenotype, e.g., to a normal tissue fingerprint. In another embodiment, a modulator induces a metastatic colorectal cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a metastatic colorectal cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a metastatic colorectal cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of

chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al.*, *J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton *et al.*, *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagiwara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho, *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)). *See, generally,* Gordon *et al.*, *J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al.*, *Nature Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual

synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of metastatic colorectal cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, *e.g.*, U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (*i.e.*, in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (*see, e.g.*, Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, *e.g.*, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, *e.g.*, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, *e.g.*, substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased"-random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of metastatic colorectal cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the

assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the metastatic colorectal cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a metastatic colorectal cancer expression pattern leading to a normal expression pattern, or to modulate a single metastatic colorectal cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated metastatic colorectal cancer tissue reveals genes that are not expressed in normal tissue or metastatic colorectal cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for metastatic colorectal cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated metastatic colorectal cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of metastatic colorectal cancer cells, that have an associated metastatic colorectal cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral

construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., metastatic colorectal cancer tissue may be screened for agents that modulate, e.g., induce or suppress the metastatic colorectal cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on metastatic colorectal cancer activity. By defining such a signature for the metastatic colorectal cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of metastatic colorectal cancer polypeptide activity, or of metastatic colorectal cancer or the metastatic colorectal cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of metastatic colorectal cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian metastatic colorectal cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a colorectal cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the metastatic colorectal cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively

binds to the metastatic colorectal cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the metastatic colorectal cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "metastatic colorectal cancer proteins." The metastatic colorectal cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the metastatic colorectal cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a metastatic colorectal cancer protein and a candidate compound, and determining the binding of the compound to the metastatic colorectal cancer protein. Preferred embodiments utilize

the human metastatic colorectal cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative metastatic colorectal cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the metastatic colorectal cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc.. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the metastatic colorectal cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the metastatic colorectal cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the metastatic colorectal cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all

or a portion of the metastatic colorectal cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a metastatic colorectal cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the metastatic colorectal cancer protein and thus is capable of binding to, and potentially modulating, the activity of the metastatic colorectal cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the metastatic colorectal cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the metastatic colorectal cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the metastatic colorectal cancer proteins. In this embodiment, the methods comprise combining a metastatic colorectal cancer protein and a competitor in a first sample. A second sample comprises a test compound, a metastatic colorectal cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the metastatic colorectal cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the metastatic colorectal cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native metastatic colorectal cancer protein, but cannot bind to modified metastatic colorectal cancer proteins. The structure of the metastatic colorectal cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a metastatic colorectal cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a metastatic colorectal cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising metastatic colorectal cancer proteins. Preferred cell types include almost any cell. The cells contain a

recombinant nucleic acid that encodes a metastatic colorectal cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate metastatic colorectal cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the metastatic colorectal cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting metastatic colorectal cancer cell division is provided. The method comprises administration of a metastatic colorectal cancer inhibitor. In another embodiment, a method of inhibiting metastatic colorectal cancer is provided. The method comprises administration of a metastatic colorectal cancer inhibitor. In a further embodiment, methods of treating cells or individuals with metastatic colorectal cancer are provided. The method comprises administration of a metastatic colorectal cancer inhibitor.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of metastatic colorectal cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed., 1994),

herein incorporated by reference. *See also*, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. *See* Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a metastatic colorectal cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. *See*, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (*see, e.g.*, Temin, *J. Natl. Cancer Insti.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.*, Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth*, in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor

angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman, *Angiogenesis and Cancer, Sem Cancer Biol.* (1992)).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkless *et al.*, *J. Biol. Chem.* 249:4295-4305 (1974); Strickland & Beers, *J. Biol. Chem.* 251:5694-5702 (1976); Whur *et al.*, *Br. J. Cancer* 42:305-312 (1980); Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.* in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985); Freshney *Anticancer Res.* 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate metastatic colorectal cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of metastatic colorectal cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the metastatic colorectal cancer gene is disrupted or in which a metastatic colorectal cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous metastatic colorectal cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous metastatic colorectal cancer gene with a mutated version of the metastatic colorectal cancer gene, or by mutating the endogenous metastatic colorectal cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi *et al.*, *Science* 244:1288 (1989)). Chimeric targeted mice can be derived according to Hogan *et al.*, *Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella *et al.*, *J. Natl. Cancer Inst.* 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley *et al.*, *Br. J. Cancer* 38:263 (1978); Selby *et al.*, *Br. J. Cancer* 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportion of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a metastatic colorectal cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth. Additionally, human tumor cells expressing the genes of the invention may be injected into immune compromised animals. Growth of these tumors, or xenografts, is compared to growth of similar human tumor cell that do not express the genes of the invention. These animals may also be used to binding assays and efficacy studies for therapeutic compounds that modulate metastatic colorectal cancer, such as antibodies or small molecules.

Polynucleotide modulators of metastatic colorectal cancer

Antisense Polynucleotides

In certain embodiments, the activity of a metastatic colorectal cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a metastatic colorectal cancer

protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the metastatic colorectal cancer protein mRNA. *See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.*

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for metastatic colorectal cancer molecules. A preferred antisense molecule is for a metastatic colorectal cancer sequence in Tables 1-26, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein & Cohen (*Cancer Res.* 48:2659 (1988) and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of metastatic colorectal cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g., Castanotto et al.*,

Adv. in Pharmacology 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al.*, *Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang *et al.*, *Proc. Natl. Acad. Sci. USA* 90:6340-6344 (1993); Yamada *et al.*, *Human Gene Therapy* 1:39-45 (1994); Leavitt *et al.*, *Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al.*, *Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al.*, *Virology* 205: 121-126 (1994)).

Polynucleotide modulators of metastatic colorectal cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of metastatic colorectal cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating metastatic colorectal cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-metastatic colorectal cancer antibody that reduces or eliminates the biological activity of an endogenous metastatic colorectal cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a metastatic colorectal cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the metastatic colorectal cancer sequence is down-regulated in metastatic colorectal cancer, such state may be reversed by increasing the amount of metastatic colorectal cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous metastatic colorectal cancer gene or administering a gene encoding the metastatic colorectal cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the

incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety.

Alternatively, e.g., when the metastatic colorectal cancer sequence is up-regulated in metastatic colorectal cancer, the activity of the endogenous metastatic colorectal cancer gene is decreased, e.g., by the administration of a metastatic colorectal cancer antisense nucleic acid.

In one embodiment, the metastatic colorectal cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to metastatic colorectal cancer proteins. Similarly, the metastatic colorectal cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify metastatic colorectal cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a metastatic colorectal cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The metastatic colorectal cancer antibodies may be coupled to standard affinity chromatography columns and used to purify metastatic colorectal cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the metastatic colorectal cancer protein.

Methods of identifying variant metastatic colorectal cancer-associated sequences

Without being bound by theory, expression of various metastatic colorectal cancer sequences is correlated with metastatic colorectal cancer. Accordingly, disorders based on mutant or variant metastatic colorectal cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant metastatic colorectal cancer genes, e.g., determining all or part of the sequence of at least one endogenous metastatic colorectal cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the metastatic colorectal cancer genotype of an individual, e.g., determining all or part of the sequence of at least one metastatic colorectal cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced metastatic colorectal cancer gene to a known metastatic colorectal cancer gene, i.e., a wild-type gene.

The sequence of all or part of the metastatic colorectal cancer gene can then be compared to the sequence of a known metastatic colorectal cancer gene to determine if any

differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the metastatic colorectal cancer gene of the patient and the known metastatic colorectal cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the metastatic colorectal cancer genes are used as probes to determine the number of copies of the metastatic colorectal cancer gene in the genome.

In another preferred embodiment, the metastatic colorectal cancer genes are used as probes to determine the chromosomal localization of the metastatic colorectal cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the metastatic colorectal cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a metastatic colorectal cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations* (1999)). As is known in the art, adjustments for metastatic colorectal cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the metastatic colorectal cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above,

including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the metastatic colorectal cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a metastatic colorectal cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that metastatic colorectal cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. It is also recognized that, after delivery to other

sites in the body (e.g., circulatory system, lymphatic system, or the tumor site) the metastatic colorectal cancer modulators of the invention may need to be protected from excretion, hydrolysis, proteolytic digestion or modification, or detoxification by the liver. In all these cases, protection is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier or by modifying the molecular size, weight, and/or charge of the modulator. Means of protecting agents from digestion degradation, and excretion are well known in the art.

The compositions for administration will commonly comprise a metastatic colorectal cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and *Goodman & Gillman, The Pharmacological Basis of Therapeutics* (Hardman *et al.*, eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., *Remington's Pharmaceutical Science* and *Goodman and Gillman, The Pharmacological Basis of Therapeutics, supra*.

The compositions containing modulators of metastatic colorectal cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its

complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present metastatic colorectal cancer protein-modulating compounds can be administered alone or in combination with additional metastatic colorectal cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of metastatic colorectal cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g., Berger & Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel et al., eds., Current Protocols* (supplemented through 1999), and Sambrook et al., *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989).

In a preferred embodiment, metastatic colorectal cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above.

Similarly, metastatic colorectal cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the metastatic colorectal cancer coding regions) can be administered in a gene therapy application. These metastatic colorectal cancer genes can include antisense applications, either as gene therapy (i.e., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Metastatic colorectal cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al., *J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al., *Molec. Immunol.* 28:287-294, (1991); Alonso et al., *Vaccine* 12:299-306 (1994); Jones et al., *Vaccine* 13:675-681 (1995)), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi et al., *Nature* 344:873-875 (1990); Hu et al., *Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (see, e.g., Tam, *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., In: *Concepts in vaccine development* (Kaufmann, ed., p. 379, 1996); Chakrabarti, et al., *Nature* 320:535 (1986); Hu et al., *Nature* 320:537 (1986); Kieny, et al., *AIDS Bio/Technology* 4:790 (1986); Top et al., *J. Infect. Dis.* 124:148 (1971); Chanda et al., *Virology* 175:535 (1990)), particles of viral or synthetic origin (see, e.g., Kofler et al., *J. Immunol. Methods*. 192:25 (1996); Eldridge et al., *Sem. Hematol.* 30:16 (1993); Falo et al., *Nature Med.* 7:649 (1995)), adjuvants (Warren et al., *Annu. Rev. Immunol.* 4:369 (1986); Gupta et al., *Vaccine* 11:293 (1993)), liposomes (Reddy et al., *J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, et al., *Science* 259:1745 (1993); Robinson et al., *Vaccine* 11:957 (1993); Shiver et al., In: *Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev. Immunol.* 12:923 (1994) and Eldridge et al., *Sem. Hematol.* 30:16 (1993)). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit,

MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quill A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode metastatic colorectal cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).

Methods for the use of genes as DNA vaccines are well known, and include placing a metastatic colorectal cancer gene or portion of a metastatic colorectal cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a metastatic colorectal cancer patient. The metastatic colorectal cancer gene used for DNA vaccines can encode full-length metastatic colorectal cancer proteins, but more preferably

encodes portions of the metastatic colorectal cancer proteins including peptides derived from the metastatic colorectal cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a metastatic colorectal cancer gene. For example, metastatic colorectal cancer-associated genes or sequence encoding subfragments of a metastatic colorectal cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the metastatic colorectal cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment metastatic colorectal cancer genes find use in generating animal models of metastatic colorectal cancer. When the metastatic colorectal cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense RNA directed to the metastatic colorectal cancer gene will also diminish or repress expression of the gene. Animal models of metastatic colorectal cancer find use in screening for modulators of a metastatic colorectal cancer-associated sequence or modulators of metastatic colorectal cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the metastatic colorectal cancer protein. When desired, tissue-specific expression or knockout of the metastatic colorectal cancer protein may be necessary.

It is also possible that the metastatic colorectal cancer protein is overexpressed in metastatic colorectal cancer. As such, transgenic animals can be generated that overexpress the metastatic colorectal cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of metastatic colorectal cancer and are additionally useful in screening for modulators to treat metastatic colorectal cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, metastatic colorectal cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative metastatic colorectal cancer polypeptides or polynucleotides, small molecules inhibitors of metastatic colorectal cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of metastatic colorectal cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a metastatic colorectal cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing metastatic colorectal cancer-associated activity. Optionally, the kit contains biologically active metastatic colorectal cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

Table 1

| Pkey | ExAccn | UnigeneID | Unigene Title | Ratio BS_Mats | Top 3 expressing cell lines |
|--------|----------|---|--|---------------|--|
| 103989 | AA314779 | Hs.105484 | ESTs; Weakly similar to LITHOSTATHINE 1 | 15.77 | EB_cells, HT29_cells, HMEC |
| 101169 | L15533 | Hs.423 | pancreatitis-associated protein | 11.98 | HMEC (total RNA), Fibroblasts 2, Fibroblasts 2 |
| 101880 | M97925 | Hs.72887 | defensin, alpha 5; Paneth cell-specific | 9.24 | Fibroblasts 2, MB231_cells, MB-MDA-453 |
| 129462 | D84239 | Hs.111732 | IgG Fc binding protein | 8.57 | EB_cells, OVCAR_cells, HS578T_cells |
| 131676 | C20785 | Hs.30514 | ESTs | 7.43 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 131861 | D11925 | Hs.184245 | KIAA0929 protein Msx2 interacting nuclea | 7.15 | HMEC, HMEC (total RNA), Fibroblasts 2 |
| 118823 | N79237 | Hs.50813 | ESTs; Weakly similar to long chain fatty | 6.72 | HMEC, HMEC (total RNA), Lu_AD_H23 |
| 101107 | L08010 | Hs.4158 | regenerating islet-derived 1 beta (pancr | 6.33 | BT474_cells, Fibroblasts 2, MB231_cells |
| 103466 | Y00339 | Hs.155097 | carbonic anhydrase II | 6.18 | OVCAR_cells, MCF7, 293T_cells |
| 102306 | U33317 | Hs.711 | defensin, alpha 6; Paneth cell-specific | 5.67 | Fibroblasts 2, HMEC, HT29_cells |
| 126419 | AA451775 | Hs.129064 | H sapiens chromosome 19; cosmid F22162 | 5.14 | HS578T_cells, HMEC (total RNA), HMEC |
| 101198 | L21988 | Hs.315 | mucin 2; intestinal/tracheal | 5.1 | EB_cells, HT29_cells, MB231_cells |
| 107652 | AA010195 | Hs.52642 | ESTs; Weakly similar to !!! ALU CLASS F | 4.94 | HMEC (total RNA), HMEC, EB_cells |
| 128145 | AI498467 | Hs.166669 | ESTs; Weakly similar to sodium bicarbona | 4.77 | HS578T_cells, HMEC, Lu_SQ_H520 |
| 110660 | H82117 | Hs.28043 | ESTs | 4.54 | HMEC, HS578T_cells, BT474_cells |
| 111669 | R19305 | Hs.110347 | H sapiens mRNA for alpha integrin bindin | 4.52 | HMEC, HS578T_cells, Caco2 |
| 124867 | R68971 | Hs.168500 | ESTs | 4.5 | HMEC, HMEC (total RNA), HS578T_cells |
| 127352 | AA416577 | Hs.189105 | ESTs | 4.41 | HMEC, HMEC (total RNA), MB-MDA-435s |
| 130736 | T99385 | Hs.18648 | EST | 4.29 | HMEC, EB_cells, HMEC (total RNA) |
| 128592 | AA470056 | Hs.113994 | ESTs; Weakly similar to alternatively sp | 4.18 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 108092 | AA045951 | Hs.169355 | ESTs; Weakly similar to TRANSCRIPTION RE | 4.04 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 133373 | S72487 | Hs.73946 | endothelial cell growth factor 1 (platelet | 4.03 | EB_cells, HMEC, HMEC (total RNA) |
| 100572 | HG2271 | Hs.46527 | Profilaggrin | 4.03 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 115775 | AA424030 | Hs.52788 | ESTs | 4.02 | HMEC, HMEC (total RNA), EB_cells |
| 120811 | AA346854 | Hs.52788 | fragile X mental retardation; autosomal | 4.01 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 111919 | R39926 | Hs.21031 | ESTs | 3.98 | EB_cells, HMEC (total RNA), HMEC |
| 117009 | H85422 | Hs.108556 | ESTs | 3.97 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 101124 | L10343 | Hs.112341 | protease inhibitor 3; skin-derived (SKAL | 3.89 | PC3_cells, RPWE_2, Caco2 |
| 106151 | AA424958 | Hs.33735 | ESTs | 3.88 | EB_cells, HMEC, HMEC (total RNA) |
| 134733 | U03644 | Hs.89421 | CBF1 interacting corepressor | 3.88 | EB_cells, HMEC, HMEC (total RNA) |
| 131739 | AA449749 | Hs.31386 | ESTs; Highly similar to secreted apoptos | 3.87 | HS578T_cells, MB-MDA-435s, HT29_cells |
| 116311 | AA490469 | Hs.48752 | ESTs | 3.84 | HS578T_cells, HMEC, LNCaP_cells |
| 134174 | U05259 | Hs.79630 | CD79A antigen (immunoglobulin-associated | 3.83 | DU145_cells, Lu_AD_H23, MB231_cells |
| 106753 | AA476944 | Hs.7331 | ESTs | 3.82 | LNCaP_cells, Lu_SC_H345, DU145_cells |
| 104842 | AA039854 | Hs.8065 | H sapiens mRNA full length insert cDNA c | 3.78 | HS578T_cells, A549_cells, CALU6_cells |
| 129161 | N27334 | Hs.181780 | ESTs | 3.75 | HMEC (total RNA), HMEC, BT474_cells |
| 105675 | AA284767 | Hs.252808 | ESTs; Highly similar to pulmonary surfac | 3.75 | 293T_cells, PRSC_con, HT29_cells |
| 100547 | HG2149 | Hs.57417 | Mucin (Gb)M57417) | 3.75 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 116857 | H65841 | Hs.186550 | ESTs | 3.73 | HS578T_cells, 293T_cells, HMEC |
| 113222 | T59570 | Hs.10515 | ESTs | 3.7 | HMEC, HS578T_cells, Caco2 |
| 118768 | N74467 | Hs.94304 | EST | 3.68 | HMEC, HS578T_cells, OVCAR_cells |
| 114542 | AA055768 | Hs.122576 | ESTs | 3.66 | EB_cells, MCF7, LNCaP_cells |
| 101640 | M50459 | Hs.180911 | ribosomal protein S4; Y-linked | 3.62 | DU145_cells, RPWE_2, A549_cells |
| 107754 | AA017462 | Hs.187571 | ESTs | 3.6 | HMEC (total RNA), Fibroblasts 2, Fibroblasts 2 |
| 104668 | AA007312 | Hs.183852 | ESTs; Weakly similar to polymerase [H]sa | 3.58 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 135377 | C21382 | Hs.99766 | H sapiens mRNA; cDNA DKFZp564J0323 (from | 3.58 | 3.56 HMEC, HMEC (total RNA), EB_cells |
| 127083 | Z44079 | Hs.91608 | otoferlin | 3.53 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 102329 | U35407 | Hs.158084 | peroxisome receptor 1 | 3.51 | HMEC, HMEC (total RNA), EB_cells |
| 117882 | N50101 | Hs.124724 | ESTs; Weakly similar to coded for by C. | 3.47 | HMEC (total RNA), HMEC, EB_cells |
| 126405 | U46278 | Hs.122489 | ESTs | 3.46 | LNCaP_cells, MCF7, DU145_cells |
| 131378 | AA463886 | Hs.203910 | small glutamine-rich tetrapeptide r | 3.45 | EB_cells, HMEC, HMEC (total RNA) |
| 111418 | R01084 | Hs.19081 | ESTs | 3.43 | HS578T_cells, EB_cells, Lu_AD_H23 |
| 135398 | AA194075 | Hs.99908 | nuclear receptor coactivator 4 | 3.4 | HS578T_cells, EB_cells, HMEC |
| 108710 | AA121960 | zm24g9.s1 Stratagene pancreas (#93728) H mRNA seq | | | EB_cells, HMEC, HMEC (total RNA) |
| 105437 | AA252191 | Hs.25199 | ESTs; Highly similar to match to ESTs AA | 3.38 | EB_cells, LNCaP_cells, RPWE_2 |
| 103448 | X99133 | Hs.204238 | lipocalin 2 (oncogene 24p3) | 3.38 | PC3_cells, EB_cells, HT29_cells |
| 130436 | M84526 | Hs.155597 | D component of complement (adipsin) | 3.37 | PRSC_con, EB_cells, Lu_AD_H23 |
| 112309 | R55021 | yJ76d5.s1 Soares breast 2NbHBst H sapien | | | EB_cells, HMEC, HMEC (total RNA) |
| 103211 | X73079 | Hs.205126 | polymeric immunoglobulin receptor | 3.35 | MB231_cells, HT29_cells, Lu_SC_H69 |
| 109012 | AA156576 | Hs.191466 | ESTs | 3.21 | EB_cells, HMEC, HMEC (total RNA) |
| 129989 | AF005887 | Hs.247433 | activating transcription factor 6 | 3.19 | HMEC (total RNA), HMEC, Lu_AD_H23 |
| 113466 | T86945 | Hs.16304 | ESTs | 3.18 | HMEC, MB231_cells, Caco2 |
| 103029 | X54489 | Hs.789 | GRO1 oncogene (melanoma growth stimulat | 3.16 | Lu_LC_H460, PC3_cells, Fibroblasts 2 |

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|--------|----------|-----------|--|------|--|
| 109374 | AA218727 | Hs.210785 | ESTs; Highly similar to lbd1 [H.sapiens] | 3.13 | Caco2, A549_cells, MB231_cells |
| 131403 | R55750 | Hs.26455 | ESTs | 3.13 | HS578T_cells, HMEC, MB231_cells |
| 113420 | T83964 | Hs.15400 | ESTs | 3.11 | HMEC (total RNA), HMEC, EB_cells |
| 112532 | R69824 | Hs.28313 | ESTs | 3.11 | HMEC, HMEC (total RNA), EB_cells |
| 117905 | N50782 | Hs.231713 | EST | 3.11 | HMEC, HS578T_cells, Caco2 |
| 125349 | T87826 | Hs.164480 | ESTs | 3.1 | HS578T_cells, EB_cells, MB-MDA-435s |
| 107072 | AA609113 | Hs.177533 | H.sapiens mRNA; cDNA DKFZp586N0318 (from N64583) | 3.05 | 3.1 Lu_SC_H69, MB-MDA-453, MB231_cells |
| 118389 | N64583 | Hs.182385 | ESTs | 3.04 | HMEC, HMEC, LNCaP_cells |
| 117653 | N38970 | Hs.194214 | ESTs | 3.04 | HMEC, HMEC (total RNA), Fibroblasts 2 |
| 101082 | L05072 | Hs.80645 | Interferon regulatory factor 1 | 3.04 | EB_cells, PRSC_con, DU145_cells |
| 126105 | H75323 | Hs.167614 | ESTs | 3.03 | HS578T_cells, HMEC (total RNA), HMEC |
| 120006 | W90108 | Hs.10848 | KIAA0187 gene product | 3.03 | HMEC, HMEC (total RNA), EB_cells |
| 127191 | AA297581 | | EST113160 Gall bladder ! H.sapiens cDNA | 3.02 | HMEC, Lu_AD_H23, Lu_SQ_H520 |
| 106899 | AA490107 | Hs.21753 | JM5 protein | 3.02 | EB_cells, HMEC (total RNA), HMEC |
| 112784 | R86306 | Hs.191290 | ESTs | 3.02 | EB_cells, HMEC, Lu_AD_358 |
| 113613 | T93337 | Hs.17167 | ESTs; Highly similar to LRR FLI4 Interactor | 3.02 | HMEC (total RNA), EB_cells, HMEC |
| 107631 | AA007230 | Hs.95026 | ESTs | 3.02 | Lu_SC_H345, HS578T_cells, Lu_LC_H460 |
| 101923 | S75256 | | HNL=neutrophil lipocalin [human, ovarian | 3.01 | PC3_cells, EB_cells, HT29_cells |
| 100695 | HG315T | | Beta-1-Glycoprotein 11, Pregnancy-Specific | 3.01 | Fibroblasts 2, Lu_AD_H23, MB-MDA-435s |
| 102523 | U53445 | Hs.15432 | downregulated in ovarian cancer 1 | 2.98 | PRSC_con, Fibroblasts 2, HMEC |
| 121588 | AA416615 | Hs.98242 | ESTs | 2.94 | HMEC, HS578T_cells, BT474_cells |
| 103714 | AA047055 | Hs.192943 | ESTs | 2.94 | HS578T_cells, EB_cells, HMEC |
| 104916 | AA056588 | Hs.16542 | ESTs | 2.93 | HMEC (total RNA), Fibroblasts 2, HMEC |
| 109298 | H05961 | Hs.26331 | ESTs | 2.92 | HMEC, MB231_cells, HS578T_cells |
| 104586 | R78309 | Hs.20787 | ESTs | 2.92 | PRSC_con, Fibroblasts 2, HMEC |
| 101236 | L29433 | Hs.47913 | coagulation factor X | 2.91 | EB_cells, MB-MDA-435s, BT474_cells |
| 134749 | L10955 | Hs.89485 | carbonic anhydrase IV | 2.9 | HS578T_cells, MCF7, HMEC (total RNA) |
| 124703 | R07294 | Hs.109108 | solute carrier family 22 (organic cation | 2.9 | HMEC, HMEC (total RNA), MB-MDA-435s |
| 114108 | Z38431 | Hs.27038 | ESTs; Moderately similar to X-linked ret | 2.89 | HMEC, HMEC (total RNA), EB_cells |
| 107857 | AA024687 | Hs.61208 | ESTs | 2.88 | HS578T_cells, MB231_cells, HMEC |
| 111586 | R10759 | Hs.15177 | ESTs | 2.88 | HS578T_cells, Lu_LC_H460, PRSC_con |
| 127553 | AA282433 | | H.sapiens p60 katanin mRNA; complete cds | 2.87 | EB_cells, MB-MDA-435s, RPWE_2 |
| 129881 | AA458952 | Hs.197728 | ESTs; Weakly similar to ZINC FINGER PROT | 2.86 | EB_cells, PC3_cells, HMEC |
| 116852 | H65459 | Hs.38323 | ESTs | 2.85 | HMEC, Caco2, HS578T_cells |
| 133468 | X03068 | Hs.73931 | major histocompatibility complex; class | 2.82 | MB-MDA-435s, BT474_cells, HT29_cells |
| 130998 | C00810 | Hs.21970 | guanine nucleotide binding protein (G pr | 2.82 | LNCAp_cells, Lu_SC_H345, EB_cells |
| 124075 | H05741 | Hs.101643 | ESTs | 2.82 | HMEC, HS578T_cells, HT29_cells |
| 128108 | A1247422 | Hs.129966 | ESTs | 2.82 | HS578T_cells, Lu_LC_H460, Lu_SC_H69 |
| 128096 | R15413 | Hs.164919 | ESTs; Highly similar to PROTEIN KINASE C | 2.8 | MB231_cells, Lu_AD_H23, RPWE_2 |
| 126619 | Z28861 | | HS8A7E032 STRATAGENE Human skeletal muscle cDNA clone A7E03, mRNA seq. | 2.77 | HMEC, Lu_AD_H23, HMEC (total RNA) |
| 114418 | AA011383 | Hs.177313 | ESTs | 2.77 | HS578T_cells, EB_cells, MCF7 |
| 120383 | AA228030 | Hs.120234 | ESTs | 2.77 | EB_cells, Fibroblasts 2, HMEC (total RNA) |
| 126535 | H73017 | Hs.250723 | ESTs; Weakly similar to atrophin-1 relat | 2.76 | Fibroblasts 2, PRSC_con, DU145_cells |
| 119347 | T64349 | | yc10408.s1 Stratagene lung (#937210) H.s | 2.76 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 126219 | N36358 | Hs.141438 | ESTs; Moderately similar to similar to C | 2.76 | Lu_AD_H23, HMEC (total RNA), MB-MDA-435s |
| 125426 | R43963 | Hs.169355 | ESTs; Weakly similar to TRANSCRIPTION RE | 2.75 | 2.75 HMEC, HMEC (total RNA), Lu_SC_H69 |
| 103005 | X52008 | Hs.2700 | glycine receptor, alpha 2 | 2.74 | HS578T_cells, HMEC, MB-MDA-435s |
| 109170 | AA180352 | Hs.191472 | ESTs | 2.74 | Fibroblasts 2, HMEC (total RNA), MB-MDA-435s |
| 101125 | L10373 | Hs.82749 | transmembrane 4 superfamily member 2 | 2.73 | Lu_LC_H460, 293T_cells, EB_cells |
| 130656 | Z20481 | Hs.174111 | KIAA0699 protein | 2.73 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 122933 | AA476728 | Hs.107537 | ESTs | 2.72 | HMEC, EB_cells, HMEC (total RNA) |
| 126033 | AA055978 | Hs.3807 | ESTs; Weakly similar to PHOSPHOLEMMAN PR | 2.71 | 2.71 Lu_SC_H345, Lu_SC_H69, 293T_cells |
| 111644 | R16539 | Hs.223649 | EST; Moderately similar to Cd-7 Metallo | 2.71 | EB_cells, HMEC, HMEC (total RNA) |
| 133719 | AA033790 | Hs.75736 | apolipoprotein D | 2.71 | Caco2, Fibroblasts 2, MB-MDA-435s |
| 127555 | AA582324 | Hs.192857 | ESTs | 2.7 | HMEC, HS578T_cells, HMEC (total RNA) |
| 113321 | T70580 | Hs.13759 | ESTs | 2.69 | HMEC (total RNA), Fibroblasts 2, PRSC_con |
| 109326 | AA210719 | Hs.86414 | ESTs | 2.68 | MB-MDA-435s, HS578T_cells, Lu_SC_H69 |
| 135003 | H42527 | Hs.92832 | ESTs | 2.68 | HS578T_cells, EB_cells, PRSC_con |
| 103650 | Z70220 | | H.sapiens mRNA for 5'UTR for unknown pro | 2.68 | HMEC, HS578T_cells, PRSC_con |
| 111507 | R07728 | Hs.191218 | ESTs | 2.67 | HMEC (total RNA), HMEC, EB_cells |
| 117084 | H93081 | Hs.41829 | ESTs | 2.67 | HS578T_cells, HMEC, MB231_cells |
| 103975 | AA306264 | Hs.176403 | ESTs; Moderately similar to !!! ALU SUB | 2.67 | DU145_cells, HS578T_cells, MB-MDA-435s |
| 132850 | R89741 | Hs.58215 | ESTs; Moderately similar to rholetin [M. | 2.66 | HS578T_cells, EB_cells, 293T_cells |
| 121599 | AA416770 | Hs.98255 | EST | 2.61 | HMEC (total RNA), HMEC, EB_cells |
| 124230 | H63111 | Hs.6655 | ESTs | 2.6 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 114174 | Z39055 | Hs.27264 | ESTs; Moderately similar to !!! ALU SUB | 2.58 | Caco2, MB-MDA-453, A549_cells |
| 128469 | T23724 | Hs.258677 | EST | 2.57 | Lu_LC_H460, Lu_SC_H69, MB-MDA-435s |
| 117399 | N26480 | Hs.43805 | lipoma HMGIC fusion partner-like 3 | 2.57 | HMEC, HMEC (total RNA), EB_cells |
| 129279 | AA460551 | Hs.184860 | ESTs; Weakly similar to EG-87B1.6 [D.mel | 2.57 | HS578T_cells, EB_cells, HT29_cells |
| 119817 | W74257 | Hs.159690 | ESTs | 2.57 | HMEC, HMEC (total RNA), Lu_SC_H69 |
| 114445 | AA019594 | Hs.250493 | ESTs; Weakly similar to KIAA0390 [H.sapi | 2.56 | HMEC, HT29_cells, Lu_LC_H460 |
| 120651 | AA287286 | Hs.98657 | ESTs | 2.55 | HMEC, HMEC (total RNA), Fibroblasts 2 |
| 105707 | AA291012 | Hs.37617 | ESTs; Weakly similar to KIAA0727 protein | 2.55 | HMEC (total RNA), EB_cells, BT474_cells |
| 128483 | T58588 | Hs.5148 | FLN29 gene product | 2.54 | HMEC, HS578T_cells, MB231_cells |
| 125890 | AA448739 | Hs.116708 | ESTs; Weakly similar to HYPOTHETICAL PRO | 2.54 | 2.54 HMEC (total RNA), HMEC, OVCAR_cells |

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| 134764 | M74715 | Hs.89560 | Iduronidase; alpha-L- | 2.54 | |
| 113404 | T82323 | Hs.70337 | immunoglobulin superfamily; member 4 | 2.54 | Caco2, HS578T_cells, HMEC |
| 129128 | AA423854 | Hs.108812 | ESTs | 2.54 | BT474_cells, MB-MDA-435s, HMEC |
| 101428 | M19584 | Hs.184929 | protease inhibitor 1 (alpha-1-antitrypsin) | 2.54 | HMEC, HT29_cells, HMEC (total RNA) |
| 103206 | X72755 | Hs.77367 | monokine induced by gamma Interferon | 2.53 | Fibroblasts 2, MB231_cells, HMEC (total RNA) |
| 132273 | AA489716 | Hs.43658 | DKFZP386L151 protein | 2.53 | EB_cells, HMEC, HMEC (total RNA) |
| 108392 | AA075124 | zm86a1.s1 | Stratagene ovarian cancer (#93 IMAGE:544776 3', mRNA seq | 2.52 | |
| 119508 | W37895 | Hs.45519 | ESTs | 2.52 | HMEC (total RNA), HMEC, HS578T_cells |
| 109828 | F13763 | Hs.19827 | ESTs | 2.52 | Lu_SC_H69, CALU6_cells, 293T_cells |
| 135096 | N89775 | Hs.132390 | zinc finger protein 36 (KOX 18) | 2.51 | PRSC_log, PRSC_con, HS578T_cells |
| 130860 | U66051 | Hs.241395 | protease; serine; 1 (trypsin 1) | 2.51 | HMEC, HS578T_cells, HT29_cells |
| 105725 | AA292228 | Hs.199791 | STAT Induced STAT Inhibitor 3 | 2.51 | OVCAR_cells, MB231_cells, PC3_cells |
| 110427 | H48579 | Hs.36275 | EST | 2.51 | HS578T_cells, HT29_cells, HMEC |
| 123762 | AA610013 | Hs.244553 | EST | 2.51 | HS578T_cells, Caco2, Lu_LC_H460 |
| 126406 | AA034096 | z106f05.r1 | Soares_fetal_liver_spleen_1NF IMAGE:430017 5', mRNA seq. | 2.5 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 129751 | AA346065 | Hs.111286 | KIAA0714 protein | 2.5 | Lu_AD_H23, HS578T_cells, Lu_AD_358 |
| 121704 | AA418743 | Hs.98306 | ESTs | 2.5 | HMEC, HS578T_cells, Fibroblasts 2 |
| 112595 | R77783 | Hs.22404 | protease; serine; 12 (neurotrypsin; moto | 2.5 | EB_cells, HMEC (total RNA), HMEC |
| 108499 | AA083103 | zn1b12.s1 | Stratagene hNT neuron (#937233 IMAGE:5477 3', mRNA seq | 2.5 | Fibroblasts 2, EB_cells, PRSC_con |
| 131968 | AA151333 | Hs.36029 | ESTs; Highly similar to basic helix-loop | 2.5 | LNCaP_cells, MB-MDA-453, HMEC |
| 112665 | R85661 | Hs.221447 | ESTs | 2.48 | Fibroblasts 2, A549_cells, 293T_cells |
| 115764 | AA421562 | Hs.91011 | anterior gradient 2 (<i>Xenopus laevis</i>) hom | 2.48 | Lu_AD_H23, HMEC, Lu_LC_H460 |
| 105959 | AA405540 | Hs.7001 | ESTs | 2.48 | EB_cells, Caco2, MCF7 |
| 125804 | R79519 | Hs.16899 | ESTs | 2.48 | OVCAR_cells, BT474_cells, Caco2 |
| 110102 | H16681 | Hs.180950 | guanine nucleotide binding protein (G pr | 2.46 | HMEC (total RNA), EB_cells, HMEC |
| 104680 | AA009809 | Hs.37599 | ESTs | 2.46 | HS578T_cells, HMEC, OVCAR_cells |
| 132339 | D80030 | Hs.45127 | chondroitin sulfate proteoglycan 5 (neur | 2.45 | HMEC, HS578T_cells, Caco2 |
| 121712 | AA419116 | Hs.193663 | ESTs; Weakly similar to III ALU SUBFAMI | 2.45 | OVCAR_cells, 293T_cells, HMEC (total RNA) |
| 129226 | M96843 | Hs.180919 | Inhibitor of DNA binding 2; dominant neg | 2.44 | Lu_SQLH520, Lu_AD_H23, Lu_SC_H69 |
| 128731 | AF005271 | Hs.104555 | neuropeptide FF-amide peptide precursor | 2.43 | MB-MDA-453, 293T_cells, Caco2 |
| 106670 | AA461174 | Hs.5943 | ESTs | 2.43 | HMEC, HMEC (total RNA), EB_cells |
| 119306 | T26914 | Hs.132785 | EAP30 subunit of ELL complex | 2.43 | EB_cells, HS578T_cells, Lu_SC_H69 |
| 133507 | X74295 | Hs.74369 | integrin; alpha 7 | 2.42 | EB_cells, HMEC (total RNA), HMEC |
| 125713 | AA367905 | Hs.77356 | transferrin receptor (p90; CD71) | 2.41 | Fibroblasts 2, Fibroblasts 2, Lu_AD_H23 |
| 107438 | W27841 | Hs.17118 | ESTs; Weakly similar to B0025.2 [C.elega | 2.41 | HMEC, HS578T_cells, MB231_cells |
| 101784 | M83186 | Hs.114346 | cytochrome c oxidase subunit VIIa polype | 2.41 | Fibroblasts 2, PRSC_con, PRSC_log |
| 134578 | AA194724 | Hs.182418 | endonuclease G | 2.4 | EB_cells, HMEC, Lu_AD_H23 |
| 125105 | T95642 | Hs.189759 | ESTs | 2.4 | EB_cells, A549_cells, HS578T_cells |
| 127087 | AA380418 | Hs.88012 | SHP2 interacting transmembrane adaptor | 2.4 | HMEC, HMEC (total RNA), EB_cells |
| 113118 | T47906 | Hs.220512 | ESTs | 2.39 | MB-MDA-435s, HS578T_cells, HMEC |
| 104791 | AA029046 | Hs.30377 | ESTs; Moderately similar to cAMP Inducib | 2.39 | LNCaP_cells, OVCAR_cells, PC3_cells |
| 115833 | AA428269 | Hs.125035 | ESTs | 2.38 | Caco2, LNCaP_cells, CALU6_cells |
| 132223 | R77451 | Hs.4245 | ESTs; Weakly similar to similar to S. ce | 2.38 | HMEC, HMEC (total RNA), EB_cells |
| 115836 | AA428863 | Hs.89388 | ESTs | 2.38 | HS578T_cells, HMEC, PRSC_con |
| 101891 | S45630 | Hs.1940 | crystallin; alpha B | 2.38 | HS578T_cells, OVCAR_cells, Lu_LC_H460 |
| 132894 | D82422 | Hs.5944 | ESTs | 2.37 | Caco2, MB-MDA-453, HT29_cells |
| 106939 | AA496048 | Hs.26570 | ESTs | 2.35 | LNCaP_cells, 293T_cells, EB_cells |
| 131104 | W27770 | Hs.258721 | ESTs | 2.35 | HMEC (total RNA), HMEC, HT29_cells |
| 122355 | AA443789 | Hs.189324 | ESTs | 2.34 | HMEC (total RNA), HMEC, EB_cells |
| 119343 | T26873 | yc3d2.s1 | Stratagene lung (#93721) H sapi | | |
| | | | to contains Altu repetitive element; mR | 2.34 | HS578T_cells, Lu_SC_H69, HT29_cells |
| | | | H sapiens mRNA; chromosome 1 specific tr | 2.33 | Lu_AD_H23, HMEC (total RNA), BT474_cells |
| | | | period (<i>Drosophila</i>) homolog 1 | 2.33 | HMEC, HMEC (total RNA), MB231_cells |
| | | | ESTs | 2.33 | HMEC (total RNA), EB_cells, HMEC |
| | | | ribophorin II | 2.33 | Lu_AD_H23, HMEC (total RNA), HMEC |
| | | | ESTs | 2.33 | HS578T_cells, HMEC, Lu_LC_H460 |
| | | | hypocretin (orexin) receptor 2 | 2.32 | HMEC, HMEC (total RNA), EB_cells |
| | | | H sapiens clone 23570 mRNA seq | 2.32 | MB231_cells, HMEC (total RNA), HMEC |
| | | | ESTs; Weakly similar to 15-HYDROXYPROSTA | 2.32 | 2.32 HMEC, HS578T_cells, MB231_cells |
| | | | H sapiens DNA seq from cosmid ICK0721Qo | | |
| | | | L12 LIKE protein ln an intron of the HS | 2.32 | |
| | | | ESTs | 2.32 | Caco2, PRSC_con, LNCaP_cells |
| | | | ESTs | 2.32 | HMEC (total RNA), HS578T_cells, HMEC |
| | | | ESTs | 2.32 | HMEC (total RNA), HMEC, MB-MDA-435s |
| | | | ESTs | 2.32 | Fibroblasts 2, HS578T_cells, MB-MDA-435s |
| | | | ESTs | 2.32 | PRSC_con, EB_cells, Lu_AD_358 |
| | | | ESTs | 2.31 | 293T_cells, LNCaP_cells, RPWE_2 |
| | | | ESTs; Weakly similar to GAGE-7 [H.sapien· | 2.31 | Caco2, HS578T_cells, HMEC |
| | | | ESTs | 2.31 | HMEC, Fibroblasts 2, HMEC (total RNA) |
| | | | ESTs | 2.31 | PC3_cells, HS578T_cells, HMEC |
| | | | ESTs | 2.3 | HMEC (total RNA), HMEC, OVCAR_cells |
| | | | ESTs | 2.3 | PRSC_log, PRSC_con, HS578T_cells |
| | | | ESTs | 2.3 | HMEC, HMEC (total RNA), EB_cells |
| | | | ESTs; Weakly similar to Gag polyprotein | 2.29 | EB_cells, Fibroblasts 2, HS578T_cells |

| | | | | | |
|--------|----------|-----------|---|------|--|
| 115540 | AA349954 | Hs.56281 | ESTs; Weakly similar to ASB-1 protein [H | 2.29 | Fibroblasts 2, BT474_cells, MB231_cells |
| 101622 | MS5621 | Hs.151513 | mannosyl (alpha-1,3)-glycoprotein beta- | 2.29 | PRSC_con, RPWE_2, PRSC_log |
| 103535 | Y13620 | Hs.122607 | B-cell CLL/lymphoma 9 | 2.28 | Lu_SC_H69, Lu_AD_358, Lu_AD_H23 |
| 127482 | AI337294 | Hs.155014 | ESTs | 2.28 | HS578T_cells, 293T_cells, CALU6_cells |
| 104297 | D31111 | Hs.106005 | ESTs; Highly similar to NY-REN-50 antigen | 2.27 | EB_cells, DU145_cells, HT29_cells |
| 112318 | R55470 | Hs.11067 | ESTs | 2.27 | MB-MDA-453, LNCAp_cells, OVCAR_cells |
| 101877 | M97496 | Hs.778 | guanylate cyclase activator 1B (retina) | 2.27 | HT29_cells, BT474_cells, Caco2 |
| 100760 | HG3576 | | Major Histocompatibility Complex, Class | 2.26 | MB-MDA-435s, MB231_cells, BT474_cells |
| 102362 | U39412 | Hs.75932 | N-ethylmaleimide-sensitive factor attach | 2.26 | LNCAp_cells, MB-MDA-453, Caco2 |
| 108142 | AA424590 | Hs.239531 | Golgi transport complex protein (90 kDa) | 2.26 | HMEC, HS578T_cells, Caco2 |
| 101461 | M22430 | Hs.76422 | phospholipase A2; group IIA (platelets; | 2.26 | LNCAp_cells, BT474_cells, Caco2 |
| 119336 | T55340 | Hs.208238 | ESTs | 2.26 | HS578T_cells, EB_cells, HMEC |
| 127619 | AA627122 | Hs.163787 | ESTs | 2.25 | Lu_SQ_H520, Lu_LC_H460, Lu_SC_H69 |
| 104113 | AA427510 | Hs.181202 | ESTs; Weakly similar to Wiscott-Aldrich | 2.25 | MB-MDA-435s, Fibroblasts 2, HMEC (total RNA) |
| 131219 | C00476 | Hs.24395 | small inducible cytokine subfamily B (Cy | 2.25 | Lu_SQ_H520, BT474_cells, Fibroblasts 2 |
| 118915 | N91481 | Hs.54713 | ESTs | 2.25 | HMEC (total RNA), HMEC, MCF7 |
| 127556 | AA679831 | Hs.180228 | ESTs | 2.24 | HS578T_cells, EB_cells, HMEC |
| 128700 | U59288 | Hs.103982 | small inducible cytokine subfamily B (Cy | 2.24 | HMEC, HS578T_cells, Fibroblasts 2 |
| 113674 | T96374 | Hs.5753 | inositol(myo)-1-(or 4)-monophosphatase 2 | 2.24 | A549_cells, DU145_cells, Lu_AD_358 |
| 133085 | M73720 | Hs.646 | carboxypeptidase A3 (mast cell) | 2.24 | HS578T_cells, Fibroblasts 2, HT29_cells |
| 106017 | AA411882 | Hs.26268 | ESTs | 2.24 | MB-MDA-453, OVCAR_cells, 293T_cells |
| 100582 | HG2348 | | Peptide Yy | 2.24 | HMEC, HS578T_cells, HMEC (total RNA) |
| 134811 | N66357 | Hs.89761 | ATP synthase; H+ transporting; mitochond | 2.23 | Lu_SQ_H520, LNCAp_cells, Lu_AD_H23 |
| 102543 | U57627 | Hs.234776 | oculocerebrorenal syndrome of Lowe | 2.23 | 293T_cells, EB_cells, LNCAp_cells |
| 127357 | AA452788 | | zx39g11.r1 Soares_total_fetus_Nb2HF8_9w IMAGE:788900 5; mRNA seq. | 2.23 | HS578T_cells, RPWE_2, HMEC (total RNA) |
| 135288 | AA402930 | Hs.97876 | ESTs | 2.23 | HS578T_cells, 293T_cells, OVCAR_cells |
| 105581 | AA278850 | Hs.28891 | ESTs; Weakly similar to !!! ALU SUBFAM1 | 2.23 | BT474_cells, BT474_cells, MB231_cells |
| 103812 | AA131707 | Hs.124094 | ESTs; Weakly similar to NFAT1-A [M.muscu | 2.23 | Lu_SC_H345, Lu_AD_H23, PRSC_con |
| 117016 | H87171 | Hs.52170 | ESTs | 2.22 | Fibroblasts 2, Lu_LC_H460, HMEC (total RNA) |
| 114607 | AA079342 | Hs.129057 | breast carcinoma amplified seq 1 | 2.22 | BT474_cells, HT29_cells, HT29_cells |
| 134000 | U29091 | Hs.7833 | selenin binding protein 1 | 2.22 | LNCAp_cells, MB-MDA-453, BT474_cells |
| 111069 | N58461 | Hs.22036 | ESTs | 2.22 | HMEC, Lu_SC_H345, HS578T_cells |
| 129048 | L27670 | Hs.108287 | intercellular adhesion molecule 4; Lands | 2.21 | Lu_AD_H23, HS578T_cells, Lu_SQ_H520 |
| 124995 | T52700 | Hs.110044 | ESTs | 2.2 | Caco2, MB-MDA-453, HT29_cells |
| 116678 | F05063 | Hs.251736 | ESTs | 2.2 | HS578T_cells, BT474_cells, 293T_cells |
| 118222 | N62263 | Hs.48501 | EST | 2.2 | HS578T_cells, BT474_cells, MB231_cells |
| 127888 | AI149662 | Hs.143590 | ESTs | 2.19 | BT474_cells, CALU6_cells, MB231_cells |
| 113790 | W33178 | Hs.26912 | ESTs | 2.19 | HMEC, HMEC (total RNA), Fibroblasts 2 |
| 100097 | AF002224 | | H.sapiens Angelman Syndrome Gene, E6-AP from promoter P1, 5'UTR | 2.19 | HS578T_cells, CALU6_cells, 293T_cells |
| 109151 | AA176800 | Hs.73452 | ESTs | 2.19 | CALU6_cells, Lu_AD_H23, Lu_SC_H69 |
| 135368 | AA086057 | Hs.9964 | ribosomal protein; mitochondrial; S12 | 2.19 | OVCAR_cells, A549_cells, Lu_AD_H23 |
| 109016 | AA156936 | Hs.58069 | ESTs; Highly similar to type II cAMP-dep | 2.19 | HS578T_cells, BT474_cells, A549_cells |
| 124300 | H92575 | Hs.105859 | ESTs; Weakly similar to !!! ALU SUBFAM1 | 2.18 | Lu_AD_358, Lu_SC_H69, Lu_SC_H345 |
| 123450 | AA598913 | Hs.111207 | ESTs | 2.18 | HMEC (total RNA), HMEC, MB-MDA-435s |
| 117435 | N27628 | | yw50b08.s1 Weizmann Olfactory Epithelium | 2.18 | LNCAp_cells, DU145_cells, Lu_SQ_H520 |
| 119860 | W80709 | Hs.58485 | ESTs | 2.18 | HS578T_cells, MB231_cells, Caco2 |
| 123833 | AA620717 | Hs.112889 | ESTs | 2.18 | Lu_AD_H23, Lu_SQ_H520, Lu_AD_358 |
| 107938 | AA029446 | Hs.53115 | ESTs | 2.17 | Caco2, 293T_cells, 293T_cells |
| 119380 | T83659 | Hs.184407 | ESTs | 2.16 | Lu_AD_H23, Lu_AD_358, PRSC_con |
| 114066 | Z38152 | Hs.26920 | ESTs | 2.15 | HMEC (total RNA), HMEC, EB_cells |
| 128748 | T59001 | Hs.10475 | ESTs | 2.15 | HMEC, HT29_cells, MB231_cells |
| 130414 | M21121 | Hs.241392 | small inducible cytokine A5 (RANTES) | 2.15 | HS578T_cells, PC3_cells, A549_cells |
| 123490 | AA599723 | | TAP binding protein (tapasin) | 2.15 | HS578T_cells, EB_cells, Lu_SC_H69 |
| 112588 | R77302 | Hs.20226 | ESTs | 2.14 | HMEC (total RNA), HMEC, Fibroblasts 2 |
| 110548 | H58715 | Hs.14706 | ESTs | 2.14 | HMEC, HMEC (total RNA), HT29_cells |
| 101581 | M34996 | Hs.198253 | major histocompatibility complex; class | 2.14 | MB-MDA-435s, HMEC, HMEC |
| 115248 | AA278887 | Hs.194530 | ESTs; Weakly similar to unknown [H.sapi | 2.14 | HT29_cells, BT474_cells, CALU6_cells |
| 105619 | AA280810 | Hs.24003 | ESTs; Moderately similar to LEYDIG CELL | 2.14 | Lu_SQ_H520, MB-MDA-435s, LNCAp_cells |
| 128058 | AI126617 | Hs.132449 | ESTs | 2.14 | HS578T_cells, EB_cells, HMEC (total RNA) |
| 134573 | AA442125 | Hs.171873 | ESTs; Weakly similar to PUTATIVE STEROID | 2.14 | EB_cells, MB231_cells, Caco2 |
| 134863 | AA353903 | Hs.183373 | ATX1 (antioxidant protein 1; yeast) homo | 2.14 | Lu_SC_H345, HT29_cells, BT474_cells |
| 128811 | H17317 | Hs.169100 | ESTs; Weakly similar to HPBRI-7 protein | 2.13 | Caco2, Lu_SC_H345, EB_cells |
| 112368 | R59371 | Hs.26653 | EST | 2.13 | HMEC, HMEC (total RNA), Lu_SQ_H520 |
| 108395 | AA075144 | | zmb86f.s1 Stratagene ovarian cancer (#93 gbX1664 TRANSLATIONALLY CONTROLLED TUM | 2.13 | HMEC (total RNA), HMEC, OVCAR_cells |
| 129611 | D45680 | Hs.11614 | ESTs | 2.13 | HMEC, HS578T_cells, Caco2 |
| 101253 | L34355 | Hs.9931 | sarcoglycan; alpha (50kD dystrophin-ass | 2.12 | HS578T_cells, OVCAR_cells, CALU6_cells |
| 126701 | AA515212 | Hs.202590 | ESTs; Weakly similar to mucin glycoprote | 2.12 | EB_cells, Lu_AD_H23, Lu_AD_H23 |
| 111628 | R15825 | Hs.4014 | KIAA0946 protein; Huntingtin interacting | 2.12 | A549_cells, BT474_cells, MB-MDA-435s |
| 108675 | AA115240 | Hs.61816 | ESTs | 2.12 | Lu_AD_H23, MB-MDA-453, PRSC_con |
| 127131 | Z44658 | Hs.105460 | DKFZP564O0823 protein | 2.12 | EB_cells, Lu_SC_H69, Lu_SC_H69 |
| 109590 | F02465 | Hs.27281 | ESTs | 2.12 | HMEC, HS578T_cells, HMEC (total RNA) |
| 116539 | D12124 | Hs.242890 | EST | 2.12 | Lu_AD_H23, Caco2, BT474_cells |
| 112117 | R45402 | Hs.23789 | ESTs | 2.12 | EB_cells, Lu_AD_H23, Lu_SQ_H520 |

| | | | | | |
|--------|----------|-----------|--|------|--|
| 126367 | AA477929 | Hs.25584 | ESTs | 2.12 | |
| 135252 | U62966 | Hs.97207 | solute carrier family 28 (sodium-coupled | 2.11 | Lu_SC_H69, Lu_AD_H23, Lu_AD_358 |
| 117565 | N34301 | Hs.248426 | EST | 2.11 | MB-MDA-435s, 293T_cells, CALU6_cells |
| 129430 | AA258842 | Hs.197877 | H sapiens clone 23777 putative transmemb | 2.11 | HMEC, HS578T_cells, MB231_cells |
| 120256 | AA169801 | | sema domain; Immunoglobulin domain (Ig); | 2.11 | HS578T_cells, Lu_AD_358, MB-MDA-435s |
| 134169 | D20342 | Hs.178137 | transducer of ERBB2; 1 (TOB1) | 2.11 | HMEC, HMEC (total RNA), EB_cells |
| 130397 | AA487452 | Hs.155344 | DNA fragmentation factor, 45 kD; alpha s | 2.11 | HMEC (total RNA), 293T_cells, OVCAR_cells |
| 132859 | D20925 | Hs.5842 | ESTs | 2.11 | 293T_cells, Caco2, Lu_AD_H23 |
| 117633 | N36404 | Hs.44807 | ESTs | 2.11 | HMEC (total RNA), Fibroblasts 2, HMEC |
| 125003 | T59442 | Hs.100445 | ESTs | 2.11 | HMEC, Caco2, HS578T_cells |
| 125239 | AA825437 | Hs.58875 | ESTs | 2.11 | MB-MDA-435s, HMEC (total RNA), HT29_cells |
| 114055 | Z38149 | Hs.134015 | uronid 2-sulfotransferase | 2.11 | HS578T_cells, PRSC_con, PRSC_log |
| 120718 | AA292747 | Hs.97286 | ESTs | 2.11 | MB-MDA-435s, 293T_cells, PRSC_con |
| 133869 | T49444 | Hs.77031 | Sp2 transcription factor | 2.1 | HT29_cells, Lu_AD_H23, Lu_SC_H69 |
| 135351 | AA430179 | Hs.9933 | putative Ac-like transposon | 2.1 | Lu_LC_H460, Lu_AD_358, RPWE_2 |
| 110973 | N51529 | Hs.118047 | ESTs | 2.09 | HS578T_cells, EB_cells, HMEC |
| 131879 | AA017161 | Hs.33792 | ESTs | 2.09 | EB_cells, HS578T_cells, MCF7 |
| 116656 | F03935 | Hs.241640 | EST | 2.09 | HMEC (total RNA), MB231_cells, BT474_cells |
| 120311 | AA194074 | Hs.193401 | ESTs | 2.09 | HS578T_cells, Lu_SC_H69 |
| 108024 | AA040433 | Hs.61688 | DKFZP586N2124 protein | 2.09 | OVCAR_cells, HMEC (total RNA), HMEC |
| 105871 | AA399633 | Hs.24872 | ESTs | 2.09 | HMEC (total RNA), BT474_cells, HT29_cells |
| 120206 | Z40805 | Hs.91668 | ESTs | 2.09 | Fibroblasts 2, A549_cells, HS578T_cells |
| 112333 | R56222 | Hs.26514 | ESTs | 2.09 | BT474_cells, MB-MDA-453, EB_cells |
| 116746 | H04811 | Hs.79027 | ESTs | 2.08 | Lu_AD_H23, Fibroblasts 2, Lu_LC_H460 |
| 121529 | AA412257 | Hs.98121 | ESTs | 2.08 | MB-MDA-435s, HMEC (total RNA), Lu_SC_H345 |
| 105592 | AA279337 | Hs.180549 | ESTs; Highly similar to R26660_1; parfia | 2.08 | HMEC, HMEC (total RNA), HS578T_cells |
| 108582 | AA088231 | Hs.91732 | ESTs | 2.08 | LNCaP_cells, PRSC_log, PRSC_log |
| 123197 | AA489250 | Hs.59403 | serine palmitoyltransferase; subunit II | 2.08 | HS578T_cells, Lu_SC_H345, Lu_SC_H69 |
| 134965 | J05480 | Hs.92 | protein phosphatase 3 (formerly 2B); cat | 2.08 | EB_cells, Lu_SC_H69, Lu_SC_H345 |
| 123856 | AA620814 | Hs.144959 | ESTs | 2.08 | LNCaP_cells, MB-MDA-435s, HMEC |
| 132058 | AA251737 | Hs.172818 | Apg12 (autophagy 12; S. cerevisiae)-like | 2.07 | HS578T_cells, BT474_cells, BT474_cells |
| 126476 | R94666 | Hs.195155 | ESTs; Weakly similar to transporter prot | 2.07 | HS578T_cells, MCF7, HMEC |
| 106087 | AA418740 | Hs.21111 | ESTs | 2.07 | PRSC_log, Lu_LC_H460, RPWE_2 |
| 103802 | AA122003 | Hs.62954 | ferritin; heavy polypeptide 1 | 2.07 | OVCAR_cells, A549_cells, Lu_AD_H23 |
| 125633 | AA908225 | Hs.126841 | ESTs | 2.07 | HMEC, HMEC (total RNA), HS578T_cells |
| 112817 | R98491 | Hs.14584 | ESTs | 2.07 | EB_cells, Fibroblasts 2, Lu_SC_H69 |
| 111050 | N56984 | Hs.74335 | heat shock 90kD protein 1; beta | 2.07 | HMEC, HMEC (total RNA), Fibroblasts 2 |
| 133072 | AA425294 | Hs.64322 | ESTs; Weakly similar to Closely related | 2.07 | LNCaP_cells, DU145_cells, 293T_cells |
| 118270 | N62868 | Hs.48653 | ESTs | 2.07 | LNCaP_cells, MB-MDA-453, Caco2 |
| 105035 | AA128486 | Hs.8859 | ESTs | 2.07 | HMEC (total RNA), HMEC, EB_cells |
| 102337 | U36922 | | Human fork head domain protein (FKHR) mRNA | 2.07 | LNCaP_cells, PC3_cells, EB_cells |
| 109687 | F09380 | Hs.182859 | lifeguard | 2.06 | 293T_cells, HMEC, HT29_cells |
| 109802 | F10789 | Hs.12439 | ESTs | 2.06 | BT474_cells, BT474_cells, Lu_AD_H23 |
| 128103 | AA905960 | Hs.48516 | ESTs | 2.06 | EB_cells, EB_cells, Caco2 |
| 128278 | A1018343 | Hs.131275 | ESTs | 2.06 | HT29_cells, HMEC (total RNA), HMEC |
| 131873 | H39997 | Hs.33716 | ESTs | 2.06 | PRSC_con, Lu_SC_H345, HS578T_cells |
| 122683 | AA455528 | Hs.96772 | ESTs | 2.05 | HMEC (total RNA), HMEC, EB_cells |
| 128066 | AA884838 | Hs.189171 | ESTs | 2.05 | LNCaP_cells, Lu_AD_H23, HS578T_cells |
| 131451 | N28028 | Hs.26968 | H sapiens mRNA from chromosome 5q21-22; | 2.05 | HMEC, HMEC (total RNA), Fibroblasts 2 |
| 120887 | AA365644 | Hs.97043 | ESTs | 2.05 | MB-MDA-435s, Lu_LC_H460, Lu_SQ_H520 |
| 103966 | AA303166 | Hs.127270 | ESTs | 2.05 | HS578T_cells, PRSC_con, HMEC |
| 105861 | AA399260 | Hs.28454 | ESTs | 2.05 | HMEC (total RNA), LNCaP_cells, PC3_cells |
| 104627 | AA001976 | Hs.19603 | ESTs | 2.05 | Fibroblasts 2, HMEC (total RNA), EB_cells |
| 108794 | AA128468 | Hs.203392 | ESTs | 2.04 | HS578T_cells, HMEC, BT474_cells |
| 111896 | R38936 | Hs.24894 | H sapiens clone 25248 mRNA seq | 2.04 | HS578T_cells, HMEC, A549_cells |
| 101849 | M94167 | Hs.172816 | neuregulin 1 | 2.04 | HS578T_cells, PC3_cells, 293T_cells |
| 119913 | W85931 | Hs.58785 | ESTs | 2.04 | HMEC, HS578T_cells, HMEC (total RNA) |
| 130785 | A242828 | Hs.19405 | caspase recruitment domain 4 | 2.04 | HMEC, BT474_cells, MB231_cells |
| 124702 | R06984 | Hs.7745 | ESTs; Weakly similar to TESTIS-SPECIFIC | 2.03 | HMEC, HS578T_cells, BT474_cells |
| 106769 | AA478001 | Hs.225935 | dacylglycerol O-acyltransferase (mouse) | 2.03 | Fibroblasts 2, PRSC_con, HMEC |
| 132219 | N46862 | Hs.172971 | ESTs | 2.03 | PC3_cells, EB_cells, HS578T_cells |
| 122033 | AA431334 | Hs.109297 | ESTs | 2.03 | HT29_cells, PC3_cells, A549_cells |
| 120461 | AA251301 | | zs10b02.s1 NCI(CGAP_GCB1 H sapiens cDNA | 2.03 | OVCAR_cells, A549_cells, Caco2 |
| 134959 | U90550 | Hs.91813 | contains Alu repetitive element; mRNA | 2.03 | HS578T_cells, EB_cells, EB_cells |
| 104909 | AA055892 | Hs.14543 | butyrophillin; subfamily 2 member A2 | 2.03 | HMEC, Fibroblasts 2, EB_cells |
| 101950 | S79219 | Hs.80741 | ESTs | 2.03 | Lu_SC_H345, PC3_cells, DU145_cells |
| 133878 | D78947 | Hs.7718 | propionyl Coenzyme A carboxylase; alpha | 2.03 | Lu_SC_H69, EB_cells, CALU6_cells |
| 103459 | X99894 | Hs.32938 | ESTs; Weakly similar to weak similarity | 2.02 | EB_cells, MCF7, MB231_cells |
| 125507 | A1436377 | Hs.258590 | insulin promoter factor 1; homeodomain t | 2.02 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 116657 | F04014 | Hs.65996 | tetraspanin TM4-B | 2.02 | A549_cells, Lu_SQ_H520, Lu_AD_H23 |
| 112920 | T10234 | Hs.4275 | ESTs | 2.01 | HS578T_cells, HMEC, MB231_cells |
| 105533 | AA258572 | Hs.6418 | ESTs; Moderately similar to seven transm | 2.01 | HS578T_cells, EB_cells, PRSC_con |
| 126762 | AA064671 | | zm13b04.r1 Stratagene pancreas (#937208) | 2.01 | HS578T_cells, EB_cells |
| 128999 | R37808 | Hs.107765 | similar to TR:G413842 G413842 NONCLASSI | 2.01 | RPWE_2, Lu_AD_H23, Lu_AD_358 |
| | | | | | HS578T_cells, OVCAR_cells, EB_cells |

WO 02/068677

PCT/US02/06001

133902 AA114858 Hs.7745 ESTs; Weakly similar to TESTIS-SPECIFIC 2

Fibroblasts 2, PRSC_conn, DU145_cells

Table 2

| Pkey | Ex Accn | UniG_ID | Complete_Title | Ratio Meta/BS | Top 3 expressing cell lines |
|--------|----------|--|---|---------------|--|
| 101447 | M21305 | Hs.247946 | Human alpha satellite and satellite 3 ju | 110.98 | EB_cells, Fibroblasts 2, A549_cells |
| 105039 | AA130349 | Hs.36475 | ESTs | 9.13 | EB_cells, OVCAR_cells, Lu_SC_H345 |
| 106094 | AA419461 | Hs.18127 | ESTs | 8.51 | HT29_cells, MB-MDA-453, HS578T_cells |
| 105777 | AA348412 | Hs.23096 | ESTs | 8.4 | 293T_cells, OVCAR_cells, EB_cells |
| 129818 | N54841 | Hs.172572 | ESTs | 7.2 | Lu_SC_H69, EB_cells, Lu_SC_H345 |
| 118475 | N66845 | Hs.165411 | ESTs; Weakly similar to !!!! ALU CLASS B | 7 | DU145_cells, EB_cells, Caco2 |
| 112170 | R48744 | Hs.192878 | ESTs | 6.91 | 293T_cells, DU145_cells, HT29_cells |
| 114918 | AA236813 | Hs.72324 | ESTs; Highly similar to unknown [H.sapien] | 6.6 | EB_cells, 293T_cells, DU145_cells |
| 104590 | R79750 | Hs.83623 | nuclear receptor subfamily 1; group I; m | 6.58 | 293T_cells, OVCAR_cells, HMEC |
| 120825 | AA285053 | Hs.107168 | ESTs | 6.55 | CALU6_cells, OVCAR_cells, EB_cells |
| 115650 | AA404564 | Hs.47094 | ESTs | 6.43 | EB_cells, LNCaP_cells, Lu_SC_H345 |
| 124568 | N67086 | Hs.102000 | ESTs | 6.35 | PC3_cells, A549_cells, DU145_cells |
| 134238 | R81509 | Hs.184571 | splicing factor; arginine/serine-rich 11 | 6.32 | 293T_cells, Lu_SC_H345, HMEC |
| 114721 | AA131450 | Hs.103822 | ESTs | 6.13 | Caco2, MB-MDA-435s, PRSC_low |
| 106145 | AA424791 | Hs.5734 | KIAA0679 protein | 6 | OVCAR_cells, EB_cells, 293T_cells |
| 114610 | AA081079 | zn32h9.s1 Stralagene endothelial cell 93 IMAGE:549183 3', mRNA seq | | 5.97 | |
| 130281 | R12777 | Hs.15395 | ESTs; Weakly similar to ARGINYL-TRNA SYN | 5.94 | PRSC_low, DU145_cells, HS578T_cells |
| 124690 | R05818 | Hs.173830 | ESTs | 5.92 | |
| 113490 | T88700 | Hs.173374 | ESTs | 5.81 | LNCaP_cells, EB_cells, OVCAR_cells |
| 104425 | H88496 | Hs.40583 | ESTs | 5.77 | DU145_cells, PC3_cells, HMEC (total RNA) |
| 118828 | N79496 | Hs.50824 | EST | 5.45 | OVCAR_cells, HS578T_cells, A549_cells |
| 129076 | AA262179 | Hs.169343 | ESTs | 5.35 | LNCaP_cells, OVCAR_cells, DU145_cells |
| 109684 | F09317 | Hs.140885 | ESTs; Weakly similar to LINE-1 REVERSE T | 5.34 | 293T_cells, BT474_cells, MCF7 |
| 104558 | R56578 | Hs.88959 | Human DNA seq from clone 967N21 on chr 2 part of KIAA0172; the gene for a novel | 5.32 | Fibroblasts 2, Lu_SC_H69, DU145_cells |
| 109032 | AA158234 | Hs.72222 | ESTs | 5.23 | EB_cells, PC3_cells, Lu_SC_H345 |
| 129350 | U50535 | Hs.110630 | Human BRCA2 region; mRNA seq CG006 | 5.2 | HT29_cells, PC3_cells, Lu_AD_358 |
| 112662 | R85436 | Hs.193150 | ESTs | 5.2 | 293T_cells, EB_cells, DU145_cells |
| 132902 | AA490969 | Hs.168147 | ESTs | 5.18 | MB-MDA-435s, PRSC_low, MB-MDA-435s |
| 126872 | AA136653 | ESTs | | 5.04 | PC3_cells, LNCaP_cells, CALU6_cells |
| 122528 | AA449804 | Hs.250992 | EST | 5.04 | EB_cells, Fibroblasts 2, A549_cells |
| 102193 | U20758 | Hs.313 | secreted phosphoprotein 1 (osteopontin; | 5.02 | Lu_SC_H345, PRSC_low, LNCaP_cells |
| 121332 | AA404384 | Hs.97921 | ESTs | 5.01 | Lu_LC_H460, A549_cells, MB-MDA-435s |
| 135357 | AA235803 | Hs.79572 | cathepsin D (lysosomal aspartyl protease | 4.96 | EB_cells, MCF7, DU145_cells |
| 109141 | AA176428 | Hs.193380 | ESTs | 4.86 | DU145_cells, PC3_cells, PRSC_low |
| 135324 | AA082041 | Hs.9873 | ESTs | 4.83 | EB_cells, Lu_SC_H345, HS578T_cells |
| 124875 | R70506 | Hs.207693 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 4.75 | DU145_cells, OVCAR_cells, LNCaP_cells |
| 102380 | U40434 | Hs.155981 | mesothelin | 4.71 | OVCAR_cells, Lu_AD_H23, RPWE_2 |
| 127956 | AA826117 | Hs.194013 | ESTs | 4.69 | EB_cells, HS578T_cells, DU145_cells |
| 125038 | T78089 | Hs.168887 | ESTs | 4.58 | OVCAR_cells, 293T_cells, DU145_cells |
| 102515 | U52636 | Human adrenal Creb-rp hmg (Creb-rp), com | | 4.57 | Lu_SC_H345, Lu_SC_H69, HT29_cells |
| 109027 | AA157818 | Hs.238380 | Human endogenous retroviral protease mRN | 4.57 | PC3_cells, EB_cells, Lu_SC_H345 |
| 115096 | AA255991 | Hs.175319 | ESTs | 4.57 | OVCAR_cells, 293T_cells, PC3_cells |
| 123470 | AA599106 | Hs.194208 | ESTs | 4.55 | LNCaP_cells, Lu_SC_H69, 293T_cells |
| 113219 | T59257 | Hs.194407 | ESTs | 4.55 | A549_cells, 293T_cells, 293T_cells |
| 123433 | AA598661 | Hs.112478 | ESTs | 4.55 | EB_cells, OVCAR_cells, HT29_cells |
| 135182 | M28170 | Hs.96023 | CD19 antigen | 4.53 | OVCAR_cells, DU145_cells, EB_cells |
| 121721 | AA419470 | Hs.199961 | ESTs | 4.51 | DU145_cells, LNCaP_cells, EB_cells |
| 129126 | H88486 | Hs.108806 | ESTs | 4.45 | LNCaP_cells, Caco2, EB_cells |
| 135232 | AA342457 | Hs.96800 | ESTs; Moderately similar to !!!! ALU SUB | 4.43 | LNCaP_cells, DU145_cells, OVCAR_cells |
| 124847 | R60044 | Hs.105706 | ESTs; Highly similar to BETA-CATENIN [H. | 4.42 | OVCAR_cells, CALU6_cells, CALU6_cells |
| 110349 | H40988 | ESTs; Weakly similar to !!!! ALU SUBFAMI | | 4.39 | DU145_cells, OVCAR_cells, LNCaP_cells |
| 134402 | U25165 | Hs.82712 | fragile X mental retardation; autosomal | 4.38 | HS578T_cells, OVCAR_cells, DU145_cells |
| 115494 | AA290603 | Hs.255617 | ESTs | 4.36 | Lu_SC_H345, OVCAR_cells, PC3_cells |
| 119174 | R71234 | y54c08.s1 Soares placenta Nb2HP H saple transcript, (rRNA); gb:S41458 ROD CGMP-BETA-SUBUNIT (HUMAN); contain | | 4.33 | DU145_cells, OVCAR_cells, LNCaP_cells |
| 121943 | AA429265 | Hs.126759 | ESTs | 4.3 | EB_cells, HT29_cells, Lu_SC_H69 |
| 110856 | N33063 | Hs.23291 | ESTs; Weakly similar to S164 [H.sapiens] | 4.28 | OVCAR_cells, EB_cells, Lu_SC_H69 |
| 102474 | U49973 | Human Tigger1 transposable element, comp | | 4.28 | DU145_cells, LNCaP_cells, OVCAR_cells |
| 123458 | AA598963 | Hs.112499 | KIAA0612 protein | 4.27 | A549_cells, A549_cells, BT474_cells |
| 116459 | AA621399 | Hs.64193 | ESTs | 4.22 | Caco2, HS578T_cells, MB-MDA-435s |
| 126301 | N62371 | Hs.100043 | ESTs; Weakly similar to Similar to cutic | 4.22 | PC3_cells, DU145_cells, Lu_SC_H345 |
| 123461 | AA598990 | Hs.251119 | EST | 4.22 | Lu_SC_H345, Lu_SC_H69, OVCAR_cells |

| | | | | | |
|--------|----------|--|--|------|--|
| 130588 | AA287735 | Hs.16411 | Human DNA seq from clone 1189B24 on chro MLRQ subunit (EC 1.6.5.3; EC 1.6.99.3; Tyrosine-protein Kinase FER (EC 2.7.1.1 | 4.2 | |
| 125756 | W25498 | Hs.81634 | ATP synthase; H+ transporting; mitochondrion ESTs | 4.19 | EB_cells, LNCaP_cells, MCF7 HMEC, EB_cells, DU145_cells |
| 135009 | AA040507 | Hs.251865 | | 4.18 | 293T_cells, EB_cells, DU145_cells |
| 107001 | AA598589 | Hs.24492 | ESTs | 4.18 | 293T_cells, DU145_cells, EB_cells |
| 124896 | R82063 | Hs.101594 | EST | 4.16 | OVCAR_cells, Lu_SC_H345, HMEC (total RNA) |
| 119404 | T92950 | | ye27c10.s1 Stratagene lung (#937210) H s ye20f05.s1 Stratagene lung (#937210) H s contains Atu repetitive element; contain | 4.15 | DU145_cells, PC3_cells, Fibroblasts 2 |
| 125090 | T91518 | | | 4.14 | LNCaP_cells, DU145_cells, OVCAR_cells |
| 117348 | N24157 | Hs.139615 | ESTs | 4.1 | Lu_SC_H345, Lu_SC_H69, PRSC_log |
| 111389 | N95837 | Hs.169111 | ESTs; Weakly similar to L82A [D.melanogaster] | 4.1 | DU145_cells, MCF7, LNCaP_cells |
| 134977 | AA464698 | Hs.19390 | ESTs; Weakly similar to bullous pemphigo | 4.09 | OVCAR_cells, Fibroblasts 2, Lu_SC_H69 |
| 124696 | R06273 | Hs.186467 | ESTs; Moderately similar to IIII ALU SUB | 4.09 | OVCAR_cells, Lu_SC_H345, PRSC_con |
| 124090 | H09570 | Hs.143032 | ESTs; Weakly similar to neuronal thread | 3.98 | DU145_cells, OVCAR_cells, Lu_SC_H345 |
| 133992 | R46354 | Hs.169832 | zinc finger protein 42 (myeloid-specific) | 3.98 | HT29_cells, MB231_cells, BT474_cells |
| 126009 | H51652 | Hs.242985 | hemoglobin; gamma G | 3.96 | Lu_SC_H69, OVCAR_cells, EB_cells |
| 114161 | Z38904 | Hs.22385 | ESTs; Weakly similar to KIAA0970 protein | 3.94 | HS578T_cells, EB_cells, PRSC_con |
| 109171 | AA180356 | Hs.73700 | EST | 3.94 | 293T_cells, MB-MDA-435s, A549_cells |
| 122007 | AA430529 | Hs.98564 | ESTs | 3.93 | PC3_cells, A549_cells, OVCAR_cells |
| 131936 | AA094855 | Hs.179972 | interferon; alpha-inducible protein (clotting) | 3.9 | CALU6_cells, EB_cells, Lu_SC_H69 |
| 128668 | AA194849 | Hs.103422 | ESTs | 3.9 | Lu_AD_H23, EB_cells, Lu_SC_H69 |
| 124977 | T33859 | Hs.190452 | KIAA0365 gene product | 3.89 | 293T_cells, DU145_cells, EB_cells |
| 107048 | AA600012 | Hs.10669 | ESTs; Moderately similar to KIAA0400 [H. r.] | 3.89 | PC3_cells, HS578T_cells, DU145_cells |
| 105358 | AA236034 | Hs.25362 | ESTs | 3.89 | Caco2, EB_cells, CALU6_cells |
| 135106 | AA599037 | Hs.9456 | SWI/SNF related; matrix associat; actin de | 3.86 | EB_cells, LNCaP_cells, Caco2 |
| 106688 | AA463215 | Hs.29896 | ESTs; Weakly similar to proline-rich pro | 3.85 | OVCAR_cells, DU145_cells, EB_cells |
| 132093 | AA400091 | Hs.39421 | ESTs | 3.85 | OVCAR_cells, OVCAR_cells, LNCaP_cells |
| 128651 | AA446990 | Hs.103135 | ESTs | 3.84 | EB_cells, LNCaP_cells, OVCAR_cells |
| 102459 | Y48836 | | Human amiloride-sensitive epithelial sod | 3.84 | HT29_cells, BT474_cells, Lu_SC_H69 |
| 113732 | T98288 | Hs.193295 | ESTs; Weakly similar to IIII ALU SUBFAMI | 3.82 | DU145_cells, OVCAR_cells, LNCaP_cells |
| 116000 | AA448710 | Hs.41327 | ESTs | 3.82 | DU145_cells, MB-MDA-453, Lu_SC_H69 |
| 120748 | AA303153 | Hs.237994 | EST; Weakly similar to IIII ALU SUBFAMIL | 3.82 | DU145_cells, DU145_cells, Lu_SC_H345 |
| 116318 | AA490830 | Hs.58570 | delted in cancer 1; RNA helicase HDB/DI | 3.79 | MB-MDA-453, CALU6_cells, EB_cells |
| 114366 | Z41747 | Hs.469 | succinate dehydrogenase complex; subunit | 3.78 | DU145_cells, Fibroblasts 2, Caco2 |
| 107248 | D59894 | Hs.34782 | ESTs | 3.75 | LNCaP_cells, DU145_cells, EB_cells |
| 132713 | AA286906 | Hs.55335 | ESTs | 3.75 | OVCAR_cells, EB_cells, Lu_SC_H345 |
| 102222 | U24683 | Hs.159386 | Immunoglobulin heavy variable 4-4 | 3.73 | EB_cells, OVCAR_cells, 293T_cells |
| 108201 | AA057518 | Hs.633394 | ESTs | 3.72 | 293T_cells, DU145_cells, EB_cells |
| 119940 | W86779 | Hs.171807 | DKFZP586B0319 protein | 3.71 | EB_cells, Caco2, DU145_cells |
| 106508 | AA452590 | Hs.30348 | ESTs | 3.67 | EB_cells, LNCaP_cells, 293T_cells |
| 114360 | Z41592 | Hs.22129 | hypothetical protein | 3.67 | HT29_cells, Lu_SQ_H520, Lu_SQ_H520 |
| 100991 | J03764 | Hs.82085 | plasmogen activator inhibitor; type I | 3.67 | Fibroblasts 2, HS578T_cells, MB231_cells |
| 107580 | AA002091 | Hs.175476 | ESTs; Weakly similar to IIII ALU SUBFAMI | 3.67 | OVCAR_cells, LNCaP_cells, Lu_SC_H345 |
| 111685 | R21408 | Hs.106095 | ESTs | 3.66 | OVCAR_cells, A549_cells, 293T_cells |
| 128336 | AZ42720 | Hs.146043 | ESTs; Weakly similar to alternatively sp | 3.66 | Lu_SC_H345, Caco2, OVCAR_cells |
| 130868 | AA004900 | Hs.171917 | ESTs; Weakly smir to smir to glycerophos | 3.61 | EB_cells, HS578T_cells, LNCaP_cells |
| 116802 | H44061 | Hs.194026 | ESTs | 3.6 | Lu_SC_H345, OVCAR_cells, DU145_cells |
| 130753 | Z46632 | Hs.189 | phosphodiesterase 4C; cAMP-specific (dun | 3.6 | Lu_SC_H69, Lu_AD_H23, Lu_SC_H345 |
| 123074 | AA485117 | Hs.105653 | ESTs | 3.6 | 293T_cells, MB231_cells, Fibroblasts 2 |
| 114317 | Z41038 | Hs.469 | succinate dehydrogenase complex; subunit | 3.6 | DU145_cells, HS578T_cells, CALU6_cells |
| 134194 | AA233231 | Hs.78828 | ESTs | 3.59 | BT474_cells, MB231_cells, HT29_cells |
| 127752 | AA808388 | Hs.211167 | ESTs | 3.59 | Lu_SQ_H520, MB-MDA-453, DU145_cells |
| 123526 | AA608657 | | ESTs; Moderately similar to IIII ALU SUB | 3.59 | DU145_cells, OVCAR_cells, LNCaP_cells |
| 127917 | AA211895 | Hs.118831 | EST; Highly similar to dJ1163J1.2.1 [H.s. s. | 3.58 | Lu_SC_H345, OVCAR_cells, PRSC_con |
| 105941 | AA404427 | Hs.10669 | ESTs; Moderately similar to KIAA0400 [H. | 3.58 | PC3_cells, DU145_cells, HS578T_cells |
| 124694 | R08108 | Hs.135258 | ESTs | 3.56 | Lu_AD_H23, Lu_SQ_H520, Lu_AD_358 |
| 105658 | AA282571 | Hs.203772 | FSHD region gene 1 | 3.56 | DU145_cells, EB_cells, A549_cells |
| 111168 | N66951 | Hs.238380 | Human endogenous retroviral protease mRNA | 3.55 | PC3_cells, EB_cells, MB231_cells |
| 133254 | AA156670 | Hs.180780 | H sapiens agrin precursor mRNA; partial | 3.54 | OVCAR_cells, DU145_cells, PC3_cells |
| 132640 | U33821 | | Tax1 (human T-cell leukemia virus type I) | 3.53 | MB231_cells, CALU6_cells, BT474_cells |
| 116562 | D25807 | Hs.90145 | ESTs | 3.52 | MB231_cells, BT474_cells, Lu_SC_H345 |
| 126045 | N80361 | Hs.14248 | ESTs | 3.51 | DU145_cells, Lu_SC_H345, OVCAR_cells |
| 122878 | AA465341 | Hs.99640 | ESTs | 3.47 | HT29_cells, OVCAR_cells, HMEC |
| 105220 | AA210695 | Hs.17212 | ESTs | 3.47 | MB-MDA-453s, HT29_cells, HT29_cells |
| 127001 | AA731636 | Hs.59319 | ESTs; Weakly similar to IIII ALU SUBFAMI | 3.45 | LNCAp_cells, DU145_cells, Lu_SC_H345 |
| 112693 | R88741 | Hs.91065 | ESTs; Moderately similar to proliferatio | 3.44 | EB_cells, LNCAp_cells, DU145_cells |
| 104935 | AA063280 | Hs.35552 | ESTs | 3.43 | LNCAp_cells, CALU6_cells, 293T_cells |
| 128710 | J04813 | Hs.104117 | cytochrome P450; subfamily IIIA (nphedi | 3.41 | HT29_cells, A549_cells, Fibroblasts 2 |
| 131996 | D86956 | Hs.36927 | heat shock 105kD | 3.4 | EB_cells, PC3_cells, Lu_SC_H345 |
| 119229 | T03229 | H sapiens (clone 104) retinoblastoma 1 g | | 3.4 | DU145_cells, Lu_SC_H345, EB_cells |
| 128046 | AA873285 | Hs.137947 | ESTs | 3.39 | EB_cells, LNCAp_cells, DU145_cells |
| 105175 | AA166804 | Hs.25740 | ESTs; Weakly similar to ubiquitous TPR m | 3.39 | PC3_cells, MCF7, DU145_cells |
| 132349 | Y00705 | Hs.181286 | serine protease inhibitor; Kazal type 1 | 3.38 | Caco2, EB_cells, Lu_SC_H69 |
| 101559 | M32053 | | Human H19 RNA gene, complete cds | 3.37 | Lu_SC_H69, MCF7, OVCAR_cells |
| 116389 | AA599011 | | troponin T1; skeletal; slow | 3.36 | DU145_cells, LNCAp_cells, OVCAR_cells |

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|--------|----------|-----------|---|------|--|
| 130641 | AA182001 | Hs.17155 | ESTs | 3.36 | DU145_cells, MB-MDA-435s, HS578T_cells |
| 109362 | AA214615 | Hs.194348 | ESTs | 3.33 | HT29_cells, Fibroblasts 2, BT474_cells |
| 106278 | AA432292 | Hs.23388 | ESTs; Moderately similar to !!! ALU SUB | 3.33 | EB_cells, Fibroblasts 2, BT474_cells |
| 127241 | AA321849 | Hs.248340 | H sapiens mRNA; cDNA DKFZp564J2116 (from | 3.32 | LNCaP_cells, DU145_cells, EB_cells |
| 133339 | N64588 | Hs.71252 | ESTs | 3.32 | DU145_cells, EB_cells, Caco2 |
| 113260 | T64896 | Hs.237992 | ESTs | 3.32 | Lu_SC_H345, LNCaP_cells, Lu_SC_H69 |
| 133349 | N75791 | Hs.7153 | L-3-hydroxyacyl-Coenzyme A dehydrogenase | 3.31 | Caco2, EB_cells, OVCAR_cells |
| 107149 | AA621159 | Hs.23284 | ESTs | 3.29 | HS578T_cells, DU145_cells, PRSC_con |
| 133195 | AA350744 | Hs.181409 | KIAA1007 protein | 3.29 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 111302 | N73838 | Hs.15049 | ESTs | 3.29 | DU145_cells, EB_cells, HS578T_cells |
| 106414 | AA447971 | Hs.28827 | ESTs | 3.28 | A549_cells, OVCAR_cells, PC3_cells |
| 121768 | AA421561 | Hs.251664 | insulin-like growth factor 2 (somatomedi | 3.28 | Caco2, PRSC_con, PRSC_log |
| 117176 | H98670 | Hs.49753 | ESTs; Weakly similar to hypothetical pro | 3.28 | PRSC_log, CALU6_cells, OVCAR_cells |
| 131320 | AA171948 | Hs.145696 | splicing factor (CC1.3) | 3.28 | EB_cells, LNCaP_cells, DU145_cells |
| 100700 | HG3227-H | | Guanine Nucleotide-Binding Protein Hsr1 | 3.27 | EB_cells, RPWE_2, Lu_AD_H23 |
| 134275 | AA132328 | Hs.3688 | acid-inducible phosphoprotein | 3.26 | EB_cells, DU145_cells, LNCaP_cells |
| 117667 | N39214 | Hs.44708 | Ser-Thr protein kinase related to the my | 3.26 | LNCaP_cells, DU145_cells, MB-MDA-453 |
| 124889 | R78604 | Hs.101570 | ESTs | 3.25 | Lu_AD_H23, Lu_SC_H69, Lu_SC_H345 |
| 126631 | W95117 | Hs.193337 | ESTs | 3.25 | Lu_SC_H345, OVCAR_cells, Lu_SC_H69 |
| 105643 | AA282069 | Hs.173802 | KIAA0603 gene product | 3.24 | Caco2, EB_cells, 293T_cells |
| 132718 | AA056731 | Hs.554 | Sjogren syndrome antigen A2 (60kD; ribon | 3.24 | CALU6_cells, OVCAR_cells, A549_cells |
| 116417 | AA609309 | Hs.239302 | ESTs; Weakly similar to !!! ALU SUBFAM1 | 3.24 | A549_cells, CALU6_cells, 293T_cells |
| 108039 | AA041341 | Hs.46670 | ESTs | 3.24 | 293T_cells, EB_cells, Caco2 |
| 114116 | Z38496 | Hs.103283 | KIAA0594 protein | 3.23 | DU145_cells, OVCAR_cells, EB_cells |
| 124514 | N58045 | Hs.142737 | ESTs | 3.22 | EB_cells, Caco2, Lu_SC_H520 |
| 110802 | N26651 | Hs.252748 | ESTs | 3.22 | LNCaP_cells, MB-MDA-435s, MB-MDA-453 |
| 106920 | AA490899 | Hs.24462 | ESTs | 3.22 | DU145_cells, EB_cells, OVCAR_cells |
| 123523 | AA608588 | Hs.193634 | ESTs | 3.21 | DU145_cells, LNCaP_cells, OVCAR_cells |
| 131564 | AA491465 | Hs.28792 | ESTs | 3.2 | HS578T_cells, HMEC (total RNA), HMEC |
| 119423 | T99544 | Hs.173734 | ESTs; Weakly similar to !!! ALU CLASS B | 3.2 | EB_cells, DU145_cells, Caco2 |
| 128736 | F03934 | Hs.104607 | ESTs | 3.19 | PC3_cells, Lu_SC_H520, Lu_SC_H69 |
| 101511 | M27826 | Hs.238380 | Human endogenous retroviral protease mRNA | 3.18 | PC3_cells, DU145_cells, Lu_SC_H520 |
| 114509 | AA043551 | Hs.95249 | ESTs | 3.18 | EB_cells, Lu_SC_H345, DU145_cells |
| 124196 | H52617 | Hs.144167 | ESTs | 3.17 | BT474_cells, MB231_cells, HMEC |
| 129095 | L12350 | Hs.108623 | thrombospondin 2 | 3.17 | Fibroblasts 2, PRSC_con, PRSC_log |
| 116457 | AA621367 | Hs.119683 | ESTs | 3.17 | 293T_cells, Lu_SC_H345, CALU6_cells |
| 117040 | H89112 | yw25e5.s1 | Morton Fetal Cochlea H sapiens | 3.16 | OVCAR_cells, 293T_cells, EB_cells |
| 129112 | N32521 | Hs.108738 | ESTs | 3.16 | EB_cells, Fibroblasts 2, MB231_cells |
| 130418 | J03242 | Hs.251664 | Insulin-like growth factor 2 (somatomedi | 3.16 | Caco2, PRSC_con, PRSC_log |
| 131199 | R80048 | Hs.234433 | ESTs; Weakly similar to transporter prot | 3.15 | PC3_cells, EB_cells, OVCAR_cells |
| 110357 | H41529 | Hs.33549 | ESTs; Highly similar to sulfonyleurea rec | 3.15 | Lu_SC_H345, PRSC_con, Lu_AD_H23 |
| 130068 | AA608903 | Hs.106220 | KIAA0336 gene product | 3.15 | OVCAR_cells, CALU6_cells, HS578T_cells |
| 127423 | T47546 | Hs.119252 | tumor protein; translationally-controld | 3.15 | EB_cells, PRSC_con, LNCaP_cells |
| 105028 | AA126719 | Hs.25282 | ESTs | 3.14 | LNCaP_cells, PC3_cells, EB_cells |
| 102349 | U37547 | Hs.75263 | apoptosis inhibitor 1 | 3.14 | DU145_cells, HS578T_cells, LNCaP_cells |
| 105126 | AA157814 | Hs.36288 | ESTs | 3.13 | EB_cells, HS578T_cells, LNCaP_cells |
| 115465 | AA286941 | Hs.43691 | ESTs | 3.12 | EB_cells, DU145_cells, 293T_cells |
| 133246 | AA086452 | Hs.58731 | tfardin | 3.12 | Lu_SC_H520, Lu_AD_H23, PRSC_log |
| 122698 | AA456112 | Hs.99410 | ESTs | 3.12 | DU145_cells, OVCAR_cells, A549_cells |
| 123553 | AA608841 | Hs.111977 | ESTs | 3.12 | EB_cells, Caco2, DU145_cells |
| 133437 | R57419 | Hs.7370 | ESTs | 3.11 | HS578T_cells, 293T_cells, Caco2 |
| 104956 | AA074880 | Hs.120975 | ESTs; Weakly similar to hypothetical pro | 3.11 | OVCAR_cells, Fibroblasts 2, Caco2 |
| 116314 | AA490588 | Hs.43118 | ESTs | 3.11 | EB_cells, MB-MDA-435s, HT29_cells |
| 120562 | AA280036 | Hs.173912 | eukaryotic translation initiation factor | 3.11 | LNCaP_cells, DU145_cells, EB_cells |
| 108770 | AA127845 | Hs.71027 | EST | 3.11 | Lu_IC_H460, Lu_SC_H345, Lu_AD_358 |
| 129791 | F02778 | Hs.173887 | KIAA0876 protein | 3.1 | Lu_SC_H345, Lu_SC_H69, PRSC_log |
| 115783 | AA244487 | Hs.72289 | ESTs; Weakly similar to LIV-1 protein [H | 3.09 | Lu_AD_358, EB_cells, PC3_cells |
| 107630 | AA007218 | Hs.60178 | ESTs | 3.07 | Lu_SC_H345, CALU6_cells, Lu_SC_H69 |
| 124339 | H99093 | Hs.6179 | H sapiens mRNA; cDNA DKFZp586K2322 (from | 3.07 | 3.07 293T_cells, MB-MDA-453, Caco2 |
| 122314 | AA442257 | Hs.192076 | ESTs | 3.07 | 293T_cells, LNCaP_cells, PC3_cells |
| 104589 | R79299 | Hs.241160 | ESTs; Moderately similar to !!! ALU SUB | 3.07 | 293T_cells, DU145_cells, EB_cells |
| 115687 | AA410508 | Hs.183765 | ESTs; Moderately smlr to ORF derived frm | 3.06 | Caco2, EB_cells, MB231_cells |
| 123796 | AA620390 | Hs.247444 | ESTs | 3.06 | Lu_SC_H345, LNCaP_cells, DU145_cells |
| 106483 | AA451676 | Hs.30299 | IGF-II mRNA-binding protein 2 | 3.06 | OVCAR_cells, HMEC (total RNA), HMEC |
| 133318 | AA256168 | Hs.70838 | ESTs | 3.05 | OVCAR_cells, LNCaP_cells, 293T_cells |
| 117244 | N20979 | Hs.1757 | L1 cell adhesion molecule (hydrocephalus | 3.05 | MB231_cells, MCF7, CALU6_cells |
| 130797 | AA430050 | Hs.180948 | thumbs) syndrome; spastic paraplegia 1) | 3.05 | EB_cells, DU145_cells, DU145_cells |
| 128959 | D79791 | Hs.107381 | KIAA0729 protein | 3.05 | LNCaP_cells, HS578T_cells, Lu_SC_H520 |
| 120481 | AA252703 | Hs.191754 | ESTs; Weakly similar to F38A5.1 [C.elega | 3.04 | EB_cells, Fibroblasts 2, PRSC_con |
| 126649 | AA856990 | Hs.125058 | ESTs | 3.03 | OVCAR_cells, LNCaP_cells, 293T_cells |
| 106970 | AA504835 | Hs.24252 | ESTs | 3.03 | EB_cells, OVCAR_cells, 293T_cells |
| 126488 | N34935 | Hs.25633 | ESTs; Highly similar to ARF GTPase-activ | 3.03 | Lu_AD_358, MCF7, MB231_cells |
| 119498 | W37226 | Hs.55573 | ESTs | 3.01 | 293T_cells, HS578T_cells, CALU6_cells |
| 129967 | H99653 | Hs.138618 | ESTs | 3.01 | Lu_SC_H345, Lu_SC_H69, PRSC_log |
| 130698 | AA037357 | Hs.188212 | ESTs | 3.01 | OVCAR_cells, LNCaP_cells, DU145_cells |

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|--------|----------|------------|---|------|---|
| 111018 | N54067 | Hs.3628 | mitogen-activated protein kinase kinase | 3.01 | PC3_cells, Caco2, Fibroblasts 2 |
| 123196 | AA489250 | Hs.59403 | serine palmitoyltransferase; subunit II | 3 | Lu_SC_H345, BT474_cells, Lu_SC_H69 |
| 133229 | AA203433 | Hs.6834 | KIAA1014 protein | 3 | OVCAR_cells, 293T_cells, EB_cells |
| 130405 | H88359 | Hs.155396 | nuclear factor (erythroid-derived 2)-like | 3 | PRSC_con, EB_cells, DU145_cells |
| 107881 | AA025567 | Hs.61273 | H_sapiens chromosome 19; cosmid R32611 | 3 | Lu_SQ_H520, MCF7, Lu_AD_358 |
| 116589 | D59570 | Hs.17132 | ESTs | 3 | EB_cells, A549_cells, HS578T_cells |
| 105479 | AA255546 | Hs.23467 | ESTs | 2.99 | Lu_SC_H345, PC3_cells, OVCAR_cells |
| 115560 | AA393812 | Hs.50575 | ESTs; Moderately similar to !!! ALU SUB | 2.99 | EB_cells, Lu_SC_H69, Fibroblasts 2 |
| 130166 | AA350690 | Hs.151411 | KIAA0916 protein | 2.98 | LNCaP_cells, EB_cells, 293T_cells |
| 123355 | AA504773 | Hs.160857 | ESTs | 2.98 | PRSC_con, PRSC_log, PRSC_log |
| 109546 | F01449 | Hs.26954 | ESTs | 2.97 | Lu_SC_H345, HT29_cells, BT474_cells |
| 129001 | AA448946 | Hs.107812 | ESTs; Weakly similar to proline-rich pro | 2.97 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 102259 | U28369 | Hs.82222 | sema domain; immunoglobulin domain (Ig); | 2.97 | EB_cells, MB231_cells, OVCAR_cells |
| 105583 | AA278907 | Hs.24549 | ESTs | 2.96 | EB_cells, DU145_cells, 293T_cells |
| 131859 | M90657 | Hs.3337 | transmembrane 4 superfamily member 1 | 2.96 | A549_cells, PC3_cells, DU145_cells |
| 114533 | AA053401 | Hs.177526 | ESTs | 2.96 | 293T_cells, Lu_LC_H460, PC3_cells |
| 110220 | H23543 | Hs.27090 | ESTs | 2.95 | PRSC_log, Lu_SC_H345, MB231_cells |
| 124917 | R91241 | Hs.75470 | hypothetical protein; expressed in osteo | 2.95 | Lu_SC_H345, Lu_SC_H69, PRSC_log |
| 127111 | AA805728 | Hs.220509 | ESTs | 2.94 | HS578T_cells, 293T_cells, 293T_cells |
| 134882 | NT3762 | Hs.30638 | ESTs | 2.94 | EB_cells, MB-MDA-435, Fibroblasts 2 |
| 121788 | AA423968 | Hs.178113 | ESTs; Moderately similar to kinesin like | 2.94 | HT29_cells, CALU6_cells, HMEC |
| 128530 | AA504343 | Hs.183475 | H_sapiens clone 25061 mRNA seq | 2.94 | DU145_cells, Lu_SC_H345, Caco2 |
| 128435 | A1301201 | Hs.147112 | ESTs | 2.93 | EB_cells, Lu_SQ_H520, PRSC_con |
| 113782 | W15580 | Hs.15342 | phosphate cytidylyltransferase 1; cholin | 2.93 | EB_cells, Lu_AD_H23, PRSC_log |
| 127569 | AA588536 | Hs.191783 | ESTs | 2.93 | EB_cells, HS578T_cells, Lu_AD_358 |
| 109642 | F04465 | Hs.22394 | ESTs; Weakly similar to weak similarity | | |
| | | | protein US1 [C.elegans] | 2.92 | PC3_cells, EB_cells, OVCAR_cells |
| 114615 | AA083812 | Hs.159456 | DKFZP566F123 protein | 2.92 | A549_cells, HS578T_cells, PRSC_con |
| 126808 | AA086320 | | zn52d12.s1 Stratagene muscle 937209 H sa | 2.92 | Lu_SC_H69, Lu_SC_H345, EB_cells |
| 113847 | W84768 | Hs.141742 | ESTs | 2.92 | DU145_cells, Fibroblasts 2, MCF7 |
| 129455 | W27301 | Hs.187991 | DKFZP564A122 protein | 2.91 | OVCAR_cells, DU145_cells, CALU6_cells |
| 107772 | AA018587 | Hs.40515 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.91 | OVCAR_cells, EB_cells, PC3_cells |
| 127159 | AA284097 | Hs.237955 | RAB7; member RAS oncogene family | 2.91 | 293T_cells, OVCAR_cells, PC3_cells |
| 124792 | R44357 | Hs.132784 | ESTs; Weakly similar to cDNA EST EMBL:T0 | 2.91 | DU145_cells, DU145_cells, CALU6_cells |
| 109751 | F10210 | Hs.6679 | H_sapiens mRNA; cDNA DKFZp586A0424 (from | | 2.91 EB_cells, Lu_SC_H69, 293T_cells |
| 128926 | AA481403 | Hs.107213 | ESTs; Highly similar to NY-REN-6 antigen | 2.9 | CALU6_cells, EB_cells, OVCAR_cells |
| 106637 | AA459951 | Hs.250824 | ESTs | 2.9 | EB_cells, Caco2, MB-MDA-435s |
| 132164 | U84573 | Hs.41270 | procollagen-lysine; 2-oxoglutarate 5-dio | 2.9 | DU145_cells, HS578T_cells, A549_cells |
| 128099 | AA905327 | | ESTs | 2.9 | MCF7, HMEC (total RNA), 293T_cells |
| 104818 | AA034947 | Hs.24831 | ESTs | 2.9 | EB_cells, Lu_LC_H460, 293T_cells |
| 126050 | H27287 | Hs.75860 | hydroxyacyl-Coenzyme A dehydrogenase/3-k | | |
| | | | -Coenzyme A hydratase (trifunctional pro | 2.89 | LNCaP_cells, DU145_cells, OVCAR_cells |
| 116696 | F09780 | Hs.66124 | EST | 2.89 | CALU6_cells, 293T_cells, 293T_cells |
| 135204 | AA421146 | Hs.183418 | cell division cycle 2-like 1 (PITSRE pr | 2.89 | PC3_cells, EB_cells, LNCaP_cells |
| 134946 | AA406534 | Hs.193053 | ESTs; Weakly similar to hwi [H.sapiens] | 2.88 | EB_cells, LNCaP_cells, Caco2 |
| 114975 | AA250850 | Hs.13944 | adrenergic; beta; receptor kinase 2 | 2.88 | EB_cells, EB_cells, EB_cells |
| 113792 | W35212 | Hs.17691 | ESTs; Weakly similar to env protein [H.s | 2.88 | MB-MDA-435s, Lu_SC_H69, CALU6_cells |
| 102322 | U34982 | Hs.54473 | cardiac-specific homeo box | 2.88 | 293T_cells, HT29_cells, Lu_AD_H23 |
| 125642 | A1096849 | Hs.25274 | ESTs; Moderately similar to putative sev | 2.88 | PC3_cells, CALU6_cells, 293T_cells |
| 100288 | D43951 | Hs.153834 | Human mRNA for KIAA0099 gene; complete | 2.88 | 293T_cells, LNCaP_cells, EB_cells |
| 105878 | AA400184 | Hs.24656 | cDNA DKFZp586A0424 (from | | OVCAR_cells, DU145_cells, 293T_cells |
| 125252 | W88755 | Hs.108514 | ESTs; Highly similar to Trbo [H.sapiens] | 2.88 | DU145_cells, HS578T_cells, MB231_cells |
| 114419 | AA011448 | Hs.106532 | ESTs; Weakly similar to transposon LRE2 | 2.88 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 130639 | D59711 | Hs.17132 | ESTs | 2.87 | EB_cells, A549_cells, OVCAR_cells |
| 130972 | AA370302 | Hs.21739 | H_sapiens mRNA; cDNA DKFZp586A1518 (from | | 2.87 293T_cells, A549_cells, Lu_LC_H460 |
| 126906 | H66949 | Hs.158069 | ESTs; Highly similar to CALCIUM-BINDING | 2.87 | Lu_SC_H345, Lu_SC_H69, LNCaP_cells |
| 121807 | AA424507 | Hs.247478 | H_sapiens Mut S homolog 5 gene; partial | | |
| | | | 1C7; LST-1; lymphotxin beta; tumor necr | 2.87 | Lu_SC_H69, HT29_cells, RPWE_2 |
| 105474 | AA255440 | Hs.219614 | F-box protein FBL11 | 2.87 | Lu_AD_H23, Caco2, EB_cells |
| 122348 | AA443695 | Hs.231476 | ESTs | 2.87 | HT29_cells, Lu_SC_H69, BT474_cells |
| 116368 | AA521186 | Hs.94217 | ESTs | 2.86 | MB-MDA-435, OVCAR_cells, Lu_SC_H69 |
| 135143 | AA102644 | Hs.69559 | KIAA1096 protein | 2.86 | PC3_cells, EB_cells, 293T_cells |
| 106711 | AA464741 | Hs.143187 | Human DNA from chromosome 19-specific co | 2.86 | EB_cells, Lu_AD_H23, Lu_LC_H460 |
| 128583 | L32832 | Hs.101842 | AT-blinding transcription factor 1 | 2.85 | LNCaP_cells, Caco2, EB_cells |
| 132139 | AA213410 | Hs.111554 | ADP-ribosylation factor-like 7 | 2.85 | A549_cells, HS578T_cells, Caco2 |
| 114484 | AA034378 | Hs.2522351 | HERV-H LTR-associating 2 | 2.85 | PC3_cells, Lu_SQ_H520, MB231_cells |
| 124620 | N74051 | Hs.194032 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.85 | Lu_SC_H345, MB231_cells, Fibroblasts 2 |
| 100403 | D85527 | Hs.142051 | H_sapiens mRNA for LIM domain, partial c | 2.84 | Lu_AD_358, Lu_AD_358, MB231_cells |
| 129795 | AA448627 | Hs.125163 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.84 | Lu_SC_H345, OVCAR_cells, PC3_cells |
| 128258 | T70214 | Hs.183548 | ESTs | 2.84 | DU145_cells, DU145_cells, OVCAR_cells |
| 102662 | U70321 | Hs.130227 | tumor necrosis factor receptor superfam | 2.84 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 132232 | AA252030 | Hs.42640 | ESTs | 2.84 | EB_cells, OVCAR_cells, Lu_SC_H345 |
| 106111 | AA421638 | Hs.6451 | ESTs | 2.83 | EB_cells, Lu_LC_H460, OVCAR_cells |
| 123963 | C13961 | Hs.210115 | EST | 2.83 | DU145_cells, LNCaP_cells, Lu_SC_H345 |
| 122783 | AA459895 | Hs.98988 | ESTs | 2.83 | EB_cells, MCF7, Lu_SC_H69 |
| 112788 | R96586 | Hs.163630 | ESTs | 2.82 | DU145_cells, Lu_SC_H345, EB_cells |

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|--------|----------|-----------|---|------|---|
| 120823 | AA347546 | Hs.185780 | ESTs | 2.82 | HT29_cells, HMEC (total RNA), BT474_cells |
| 100378 | D80009 | Hs.10848 | KIAA0187 gene product | 2.82 | Caco2, PC3_cells, OVCAR_cells |
| 114677 | AA114163 | Hs.188877 | ESTs | 2.81 | DU145_cells, MCF7, EB_cells |
| 108085 | AA045602 | Hs.62863 | ESTs; Moderately similar to serine/threonine kinase 1 | 2.81 | EB_cells, Lu_AD_H23, HT29_cells |
| 104938 | AA064627 | Hs.18341 | ESTs; Highly similar to CGI-72 protein [Homo sapiens] | 2.81 | PC3_cells, HS578T_cells, OVCAR_cells |
| 128743 | AA237013 | Hs.2730 | heterogeneous nuclear ribonucleoprotein | 2.8 | OVCAR_cells, LNCaP_cells, Caco2 |
| 124314 | H94877 | Hs.215766 | GTP-binding protein | 2.8 | LNCaP_cells, DU145_cells, Caco2 |
| 134227 | D79986 | Hs.80338 | KIAA0164 gene product | 2.8 | LNCaP_cells, A549_cells, EB_cells |
| 122922 | AA476268 | zw44h1.s1 | Soares_lata_fetus_Nb2HF8_9w H | 2.79 | |
| | | | contains Alu repetitive element; contains | 2.79 | |
| 126096 | H42968 | Hs.155606 | paired mesoderm homeo box 1 | 2.78 | Lu_SC_H345, OVCAR_cells, Lu_SC_H69 |
| 129295 | AA424782 | Hs.110121 | SEC7 homolog | 2.78 | Lu_AD_H23, Lu_SC_H69, Lu_LC_H460 |
| 116155 | AA460957 | Hs.76053 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide | 2.78 | Lu_AD_H23, EB_cells, Lu_SC_H345 |
| 105911 | AA041809 | Hs.189910 | ESTs | 2.77 | EB_cells, OVCAR_cells, 293T_cells |
| 119232 | T03475 | Hs.258624 | EST | 2.77 | 293T_cells, HS578T_cells, DU145_cells |
| 131168 | AA482007 | Hs.23788 | ESTs; Weakly similar to homology with Is | 2.77 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 106048 | AA416697 | Hs.15330 | ESTs | 2.76 | EB_cells, Lu_LC_H460, MCF7 |
| 124352 | N21626 | Hs.102406 | ESTs | 2.76 | OVCAR_cells, Lu_SC_H345, 293T_cells |
| 129349 | D86974 | Hs.110613 | KIAA0220 protein | 2.76 | MCF7, MB-MDA-453, CALU6_cells |
| 106120 | AA423808 | Hs.8765 | RNA helicase-related protein | 2.76 | DU145_cells, HT29_cells, Lu_SC_H69 |
| 100643 | HG2755-H | | T-Plastin | 2.75 | OVCAR_cells, EB_cells, 293T_cells |
| 128500 | U60521 | Hs.100641 | caspase 9; apoptosis-related cysteine pr | 2.75 | 293T_cells, PC3_cells, HS578T_cells |
| 126090 | R44789 | Hs.119486 | ESTs; Weakly similar to rostral cerebellum | 2.75 | Lu_AD_358, Lu_SC_H69, Lu_SC_H345 |
| 127064 | Z43709 | | HSC1JA091 normalized infant brain cDNA H | 2.75 | Lu_SC_H69, Lu_SC_H345, BT474_cells |
| 132989 | AA480074 | Hs.394 | adrenomedullin | 2.75 | Caco2, A549_cells, HT29_cells |
| 108888 | AA135606 | Hs.189384 | ESTs; Weakly similar to IIII ALU SUBFAMI | 2.75 | EB_cells, OVCAR_cells, DU145_cells |
| 119579 | W42429 | Hs.150507 | ESTs | 2.74 | OVCAR_cells, LNCaP_cells, DU145_cells |
| 100387 | D83777 | Hs.75137 | KIAA0193 gene product | 2.74 | 293T_cells, DU145_cells, PC3_cells |
| 114744 | AA135407 | Hs.252351 | HERV-H LTR-associating 2 | 2.74 | CALU6_cells, DU145_cells, Caco2 |
| 129092 | AA011243 | Hs.63525 | poly(rC)-binding protein 2 | 2.74 | PC3_cells, Lu_SQL520, RPWE_2 |
| 125360 | AA677978 | Hs.189741 | ESTs | 2.74 | EB_cells, MCF7, DU145_cells |
| 107874 | AA025305 | Hs.25218 | ESTs; Weakly similar to reverse transcriptase | 2.74 | Lu_AD_358, Lu_AD_358, PRSC_log |
| 114086 | Z38266 | Hs.12770 | H sapiens PAC clone DJ0777023 from 7p14 | 2.74 | Lu_SC_H345, Lu_LC_H460, HT29_cells |
| 116180 | AA463902 | Hs.94964 | ESTs | 2.73 | EB_cells, LNCaP_cells, BT474_cells |
| 126027 | M61982 | | ESTs | 2.73 | Lu_SC_H69, PRSC_con, Lu_AD_H23 |
| 116339 | AA496257 | Hs.72165 | ESTs; Weakly similar to R26984_1 [H.sapiens] | 2.73 | LNCaP_cells, DU145_cells, A549_cells |
| 105387 | AA236951 | Hs.108636 | chromosome 1 open reading frame 9 | 2.72 | EB_cells, DU145_cells, OVCAR_cells |
| 111359 | N91273 | Hs.27179 | ESTs | 2.72 | PC3_cells, EB_cells, Caco2 |
| 106680 | AA461458 | Hs.24789 | ESTs | 2.72 | EB_cells, LNCaP_cells, 293T_cells |
| 118598 | NG9136 | Hs.214343 | ESTs | 2.72 | PC3_cells, Lu_SC_H345, Caco2 |
| 107913 | AA027161 | Hs.59523 | ESTs; Highly similar to G1 TO S PHASE TR | 2.71 | MB-MDA-453, 293T_cells, BT474_cells |
| 134315 | AA136269 | Hs.81648 | ESTs; Weakly similar to S164 [H.sapiens] | 2.71 | EB_cells, MCF7, Lu_SC_H345 |
| 135233 | AA127463 | Hs.9683 | protein-kinase; interferon-inducible dou | 2.71 | EB_cells, DU145_cells, HMEC |
| 112932 | T15470 | Hs.189810 | ESTs | 2.7 | EB_cells, OVCAR_cells, Caco2 |
| 119053 | R11501 | | yf28f1.s1 Soares fetal liver spleen 1NFL | 2.7 | 293T_cells, Lu_AD_H23, PC3_cells |
| | | | contains Alu repetitive element; mRNA | 2.7 | |
| 131206 | AA044078 | Hs.24210 | ESTs | 2.7 | Lu_SC_H345, Lu_SC_H69, DU145_cells |
| 126759 | AA063642 | | ESTs; Highly similar to (define not available) | 2.7 | Caco2, Lu_SC_H345, HS578T_cells |
| 131060 | AA160890 | Hs.22564 | myosin VI | 2.7 | LNCaP_cells, Lu_SC_H345, Lu_SC_H69 |
| 132135 | N69101 | Hs.40730 | ESTs | 2.7 | LNCaP_cells, MCF7, HT29_cells |
| 120835 | AA348448 | Hs.56806 | ESTs | 2.7 | EB_cells, 293T_cells, OVCAR_cells |
| 113815 | W45311 | Hs.14756 | ESTs | 2.7 | Fibroblasts 2, CALU6_cells, RPWE_2 |
| 133234 | T80092 | Hs.6853 | ESTs; Weakly similar to IIII ALU SUBFAMI | 2.69 | EB_cells, PC3_cells, DU145_cells |
| 126819 | AA305536 | Hs.161489 | ESTs | 2.69 | Lu_SC_H345, OVCAR_cells, DU145_cells |
| 125198 | W69474 | Hs.225550 | ESTs | 2.69 | EB_cells, DU145_cells, Caco2 |
| 108394 | AA075144 | | zm8616.s1 Stratagene ovarian cancer (#93 | 2.69 | Lu_SC_H345, Lu_AD_H23, Lu_AD_H23 |
| | | | gb:X1664 TRANSLATIONALLY CONTROLLED TUM | 2.69 | HMEC, HMEC (total RNA), Fibroblasts 2 |
| 134456 | X59405 | Hs.83532 | membrane cofactor protein (CD46; trophoblast) | 2.69 | EB_cells, LNCaP_cells, DU145_cells |
| 111720 | R23739 | Hs.23585 | KIAA1078 protein | 2.68 | PC3_cells, HMEC (total RNA), OVCAR_cells |
| 114617 | AA084148 | Hs.110659 | ESTs | 2.68 | DU145_cells, LNCaP_cells, OVCAR_cells |
| 127787 | AA731764 | | ESTs; Weakly similar to IIII ALU CLASS C | 2.68 | HT29_cells, Lu_SC_H345, MB231_cells |
| 101437 | M20681 | Hs.7594 | solute carrier family 2 (facilitated glucose) | 2.68 | Caco2, Lu_LC_H460, Fibroblasts 2 |
| 133761 | AA477223 | Hs.75922 | brain protein I3 | 2.68 | EB_cells, Lu_AD_H23, Lu_SC_H345 |
| 105869 | AA399574 | Hs.19086 | ESTs | 2.68 | PC3_cells, MCF7, MB231_cells |
| 125191 | W67257 | Hs.138871 | ESTs; Weakly similar to IIII ALU CLASS B | 2.68 | OVCAR_cells, DU145_cells, LNCaP_cells |
| 116238 | AA479362 | Hs.47144 | DKFZP586N0819 protein | 2.67 | OVCAR_cells, DU145_cells, LNCaP_cells |
| 124770 | R40555 | Hs.120429 | ESTs | 2.67 | Lu_AD_H23, Lu_SC_H69, PRSC_con |
| 101764 | M80563 | Hs.81256 | S100 calcium-binding protein A4 (calcium binding protein) | 2.67 | A549_cells, MB231_cells, OVCAR_cells |
| 130897 | AA063428 | Hs.21022 | adaptor-related protein complex 3; beta | 2.67 | EB_cells, Lu_AD_H23, HMEC |
| 133303 | H61046 | Hs.237352 | EST | 2.66 | Lu_SC_H345, Lu_SC_H69, PRSC_con |
| 124724 | R12405 | Hs.112423 | H sapiens mRNA; cDNA DKFZp586I1420 (from | 2.66 | 2.66 Lu_SC_H345, BT474_cells, OVCAR_cells |
| 123697 | AA609601 | Hs.221224 | ESTs | 2.66 | OVCAR_cells, 293T_cells, Lu_SC_H69 |
| 111548 | R09170 | Hs.258707 | ESTs | 2.66 | 293T_cells, CALU6_cells, A549_cells |
| 107005 | AA598679 | Hs.194215 | ESTs | 2.66 | Lu_SC_H345, OVCAR_cells, Lu_AD_H23 |
| 105569 | AA278399 | Hs.20596 | ESTs | 2.65 | MCF7, HT29_cells, BT474_cells |

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|--------|----------|--|---|------|---|
| 132687 | AB002301 | Hs.54985 | KIAA0303 protein | 2.65 | HMEC (total RNA), HMEC, LNCaP_cells Lu_SC_H345, Lu_SC_H69, DU145_cells |
| 104105 | AA422123 | Hs.42457 | ESTs | 2.65 | EB_cells, Fibroblasts 2, DU145_cells |
| 121335 | AA404418 | Hs.144953 | ESTs | 2.65 | Lu_SC_H69, 293T_cells, EB_cells |
| 124853 | R61693 | Hs.172330 | ESTs; Weakly similar to Wiskott-Aldrich | 2.64 | DU145_cells, OVCAR_cells, Lu_SC_H345 |
| 124253 | H69742 | Hs.102201 | ESTs | 2.64 | EB_cells, Lu_SC_H69, Lu_SC_H345 |
| 123044 | AA481549 | Hs.165694 | ESTs | 2.64 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 129535 | AA608852 | Hs.112603 | EST | 2.64 | EB_cells, DU145_cells, Caco2 |
| 131397 | AB002336 | Hs.26395 | erythrocyte membrane protein band 4.1-II | 2.64 | Fibroblasts 2, PRSC_con, HS578T_cells |
| 130175 | X75593 | Hs.151536 | RAB13; member RAS oncogene family | 2.64 | EB_cells, Lu_AD_H23, Lu_SC_H460 |
| 127507 | A1188445 | Hs.152618 | ESTs | 2.63 | Caco2, EB_cells, CALU6_cells |
| 105377 | AA236702 | Hs.24371 | ESTs | 2.63 | EB_cells, DU145_cells, Caco2 |
| 114671 | AA112679 | Hs.252291 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 2.63 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 133726 | W19983 | Hs.75761 | SFRS protein kinase 1 | 2.63 | |
| 132380 | H68018 | yr76h05.r1 Soares fetal liver spleen 1NF IMAGE:211257 5', mRNA seq. | | 2.62 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 127986 | AI370418 | Hs.192050 | ESTs; Weakly similar to !!!! ALU CLASS A | 2.62 | DU145_cells, OVCAR_cells, LNCaP_cells |
| 116208 | AA476333 | Hs.42532 | ESTs | 2.61 | DU145_cells, PRSC_con, Fibroblasts 2 |
| 130946 | AA059456 | Hs.21490 | KIAA0438 gene product | 2.6 | LNCaP_cells, DU145_cells, HS578T_cells |
| 106687 | AA463234 | Hs.118387 | KIAA0792 gene product | 2.59 | EB_cells, MB-MDA-453, Caco2 |
| 101551 | M31606 | Hs.196177 | phosphorylase kinase; gamma 2 (testis) | 2.59 | LNCaP_cells, EB_cells, MB-MDA-453 |
| 114479 | AA032084 | Hs.124841 | ESTs; Moderately similar to transformati | 2.59 | DU145_cells, Caco2, OVCAR_cells |
| 111863 | R37495 | Hs.23578 | ESTs | 2.59 | HT29_cells, MB231_cells, Lu_SO_H520 |
| 128018 | AA029793 | Hs.107979 | small membrane protein 1 | 2.59 | A549_cells, EB_cells, HS578T_cells |
| 107058 | AA600357 | Hs.239489 | TIA1 cytotoxic granule-associated RNA-b1 | 2.58 | DU145_cells, Lu_SC_H345, EB_cells |
| 126175 | AA056181 | Hs.17311 | DKFZP434N161 protein | 2.58 | Lu_SC_H345, DU145_cells, LNCaP_cells |
| 131979 | D52154 | Hs.172458 | Iduronate 2-sulfatase (Hunter syndrome) | 2.58 | DU145_cells, PC3_cells, A549_cells |
| 126122 | H80181 | ESTs | | 2.58 | DU145_cells, OVCAR_cells, LNCaP_cells |
| 106961 | AA504110 | Hs.18063 | ESTs | 2.58 | HMEC, DU145_cells, DU145_cells |
| 114730 | AA133527 | Hs.126925 | ESTs; Weakly similar to The KIAA0138 gen | 2.58 | DU145_cells, LNCaP_cells, MCF7 |
| 117342 | N24020 | Hs.132913 | ESTs | 2.58 | HS578T_cells, DU145_cells, LNCaP_cells |
| 131622 | AA442483 | Hs.29592 | ESTs | 2.57 | PRSC_con, PRSC_log, HS578T_cells |
| 104904 | AA055560 | Hs.13179 | ESTs; Moderately similar to !!!! ALU SUB | 2.57 | Lu_SC_H345, Lu_SC_H69, BT474_cells |
| 117359 | N24848 | Hs.114062 | ESTs; Weakly similar to T15B7.2 [C.eleg | 2.57 | HS578T_cells, PRSC_con, EB_cells |
| 123331 | AA497013 | Hs.188740 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 2.57 | Lu_SC_H69, Caco2, PRSC_con |
| 125324 | R07785 | yf15c06.r1 Soares fetal liver spleen 1NF contains Alu repetitive element; contain | | 2.57 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 129813 | T33462 | Hs.12600 | ESTs | 2.57 | Lu_SC_H345, 293T_cells, Lu_SC_H69 |
| 100265 | D38521 | Hs.75935 | KIAA0077 protein | 2.57 | EB_cells, LNCaP_cells, PC3_cells |
| 134890 | T40902 | Hs.90786 | ATP-binding cassette; sub-family C (CFTR | 2.57 | A549_cells, DU145_cells, EB_cells |
| 133582 | AA421874 | Hs.75087 | Fas-activated serine/threonine kinase | 2.56 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 135011 | H73161 | Hs.92991 | ESTs; Weakly similar to C13F10.4 [C.eleg | 2.56 | EB_cells, LNCaP_cells, MB-MDA-453 |
| 107226 | D58185 | Hs.21945 | ESTs | 2.56 | Lu_SC_H345, Lu_SC_H69, HMEC (total RNA) |
| 126042 | H62441 | Hs.157082 | H sapiens PAC clone DJ0988G15 from 7q33- | 2.56 | HMEC (total RNA), HMEC, RPWE_2 |
| 114472 | AA028924 | Hs.177407 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.56 | Lu_SC_H345, Lu_SC_H69, DU145_cells |
| 126291 | N42090 | yy05b07.r1 Soares melanocytes 2NbHM H sap | | 2.56 | HMEC, HMEC (total RNA), PC3_cells |
| 113349 | T79021 | Hs.14438 | ESTs; Moderately similar to histamine N- | 2.56 | HT29_cells, PRSC_log, Lu_SC_H345 |
| 105769 | AA347485 | Hs.25477 | ESTs; Moderately similar to fgf-1 protel | 2.56 | Lu_AD_H23, RPWE_2, Lu_SO_H520 |
| 110918 | N46423 | Hs.24283 | ESTs | 2.56 | EB_cells, CALU6_cells, DU145_cells |
| 117170 | H98153 | Hs.42500 | ADP-ribosylation factor-like 5 | 2.56 | OVCAR_cells, EB_cells, LNCaP_cells |
| 105159 | AA173981 | Hs.30490 | CD2-associated protein | 2.55 | LNCaP_cells, EB_cells, DU145_cells |
| 105726 | AA292328 | Hs.9754 | activating transcription factor 5 | 2.55 | MCF7, EB_cells, MB-MDA-453 |
| 132079 | H67984 | Hs.38694 | ESTs | 2.55 | EB_cells, DU145_cells, HS578T_cells |
| 131813 | X51757 | Hs.3268 | heat shock 70kD protein 6 (HSP70B) | 2.55 | Lu_AD_H23, MB231_cells, Fibroblasts 2 |
| 133538 | L14837 | Hs.74614 | tight junction protein 1 (zona occcludens | 2.54 | DU145_cells, Caco2, A549_cells |
| 124981 | T40849 | Hs.114034 | maternal G10 transcript | 2.54 | EB_cells, Caco2, LNCaP_cells |
| 122028 | AA431306 | Hs.98722 | ESTs | 2.54 | Fibroblasts 2, BT474_cells, HMEC (total RNA) |
| 122487 | AA448332 | Rs.80598 | transcription elongation factor A (SII); | 2.54 | Lu_SC_H345, MCF7, MB-MDA-453 |
| 119315 | T41152 | Hs.90485 | ESTs | 2.54 | Lu_SC_H345, MB-MDA-435s, PRSC_con |
| 107957 | AA031948 | Hs.57548 | ESTs | 2.54 | A549_cells, RPWE_2, DU145_cells |
| 122457 | AA447780 | Hs.96418 | ESTs | 2.54 | DU145_cells, EB_cells, A549_cells |
| 103572 | Z25749 | Hs.75538 | ribosomal protein S7 | 2.54 | EB_cells, CALU6_cells, DU145_cells |
| 124395 | N29963 | Hs.193977 | ESTs | 2.54 | HMEC (total RNA), HMEC, RPWE_2 |
| 116024 | AA451748 | Hs.83883 | Human DNA seq from clone 718J7 on chromo | | |
| | | | phosphoenolpyruvate carboxykinase 1; ES | 2.53 | LNCaP_cells, RPWE_2, MB-MDA-453 |
| 134381 | D43682 | Hs.82208 | acyl-Coenzyme A dehydrogenase; very long | 2.53 | LNCaP_cells, CALU6_cells, DU145_cells |
| 130420 | U60975 | Human hybrid receptor gp25 precursor mRNA | | 2.53 | EB_cells, HMEC (total RNA), Caco2 |
| 100336 | D63478 | Hs.8127 | KIAA0144 gene product | 2.53 | BT474_cells, HT29_cells, Lu_AD_358 |
| 105519 | AA258063 | Hs.23438 | ESTs | 2.53 | EB_cells, Caco2, MB-MDA-435s |
| 124684 | R02401 | Hs.221078 | ESTs | 2.53 | Lu_SC_H345, OVCAR_cells, Lu_SC_H69 |
| 105852 | AA398933 | Hs.172613 | solute carrier family 12 (potassium/chlo | 2.52 | LNCaP_cells, DU145_cells; EB_cells |
| 105012 | AA116036 | Hs.9329 | chromosome 20 open reading frame 1 | 2.52 | CALU6_cells, Caco2, DU145_cells |
| 128534 | W39128 | Hs.247901 | Human DNA seq from clone 881 on chromo | | |
| | | | -CELL MEMBRANE GLYCOPROTEIN PC-1; the | | |
| 135334 | AA053134 | Hs.241558 | ariadne-2 (D. melanogaster) homolog (all | 2.52 | 2.52 BT474_cells, LNCaP_cells, Lu_AD_H23 |
| 128538 | R44214 | Hs.101189 | ESTs | 2.52 | 2.52 293T_cells, CALU6_cells, DU145_cells |
| 109865 | H02566 | Hs.191268 | H sapiens mRNA; cDNA DKFZp434N174 (from | | EB_cells, Lu_AD_H23, Lu_SC_H345 |
| | | | | 2.52 | DU145_cells, LNCaP_cells, OVCAR_cells |

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|--------|-----------|--|------|--|
| 118579 | N68905 | small inducible cytokine A5 (RANTES) | 2.51 | Lu_SC_H345, LNCaP_cells, Lu_SC_H69 |
| 117590 | N34904 | ESTs; Moderately similar to !!! ALU SUB | 2.51 | Lu_SC_H345, DU145_cells, Lu_SC_H69 |
| 104340 | F15201 | ESTs | 2.51 | Lu_SC_H345, PRSC_con, PRSC_log |
| 122455 | AA447744 | Hs.99141 EST | 2.51 | Caco2, Lu_SC_H69, 293T_cells |
| 109339 | AA211901 | Hs.86430 ESTs | 2.51 | EB_cells, DU145_cells, CALU6_cells |
| 123258 | AA490929 | Hs.105274 ESTs | 2.51 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 118467 | N66763 | Hs.43080 ESTs | 2.51 | CALU6_cells, HS578T_cells, OVCAR_cells |
| 106044 | AA416546 | Hs.149436 kinesin family member 5B | 2.51 | EB_cells, Caco2, DU145_cells |
| 107480 | W58057 | Hs.74304 periplakin | 2.5 | Caco2, OVCAR_cells, HMEC (total RNA) |
| 111760 | R26892 | Hs.221434 ESTs | 2.5 | Lu_AD_H23, EB_cells, Lu_AD_358 |
| 132474 | N68018 | Hs.180933 TBP-associated factor 172 | 2.5 | LNCaP_cells, EB_cells, DU145_cells |
| 103423 | X97249 | Hs.123122 FSH primary response (LRPR1; rat) homolog | 2.5 | HS578T_cells, Lu_SC_H345, PC3_cells |
| 123488 | AA599708 | Hs.187764 ESTs; Weakly similar to !!! ALU SUBFAMI | 2.49 | OVCAR_cells, Lu_SC_H345, DU145_cells |
| 100475 | D90276 | Hs.12 carcinoembryonic antigen-related cell ad | 2.49 | MB-MDA-453, 293T_cells, CALU6_cells |
| 112003 | R42547 | Hs.172551 ESTs | 2.49 | EB_cells, Lu_AD_H23, Lu_SC_H345 |
| 114315 | Z41027 | Hs.26297 ESTs | 2.49 | Lu_SC_H69, OVCAR_cells, Lu_AD_H23 |
| 105291 | AA233311 | Hs.28752 ESTs | 2.49 | EB_cells, CALU6_cells, DU145_cells |
| 135354 | AA188934 | Hs.99367 ESTs | 2.49 | MB-MDA-453, Lu_SC_H69, 293T_cells |
| 107521 | X78262 | H.spliens mRNA for TRE5 | 2.49 | Lu_SC_H345, Lu_SC_H69, PRSC_con |
| 108373 | AA074393 | Hs.61950 ESTs; Weakly similar to nuclear protein | 2.49 | MCF7, MB-MDA-453, Lu_SC_H345 |
| 108336 | AA132061 | Hs.222727 ESTs; Weakly similar to ubiquitous TPR m | 2.48 | DU145_cells, Lu_SC_H345, Lu_SC_H345 |
| 110386 | H45516 | Hs.33268 ESTs | 2.48 | PC3_cells, OVCAR_cells, Lu_SQL_H520 |
| 129658 | M22348 | Hs.131255 ubiquinol-cytochrome c reductase binding | 2.48 | LNCaP_cells, CALU6_cells, PC3_cells |
| 134283 | H12651 | Hs.8107 H.spliens mRNA; cDNA DKFZp586B0918 (from | 2.48 | 2.48 HMEC (total RNA), HS578T_cells, HMEC |
| 101844 | M93425 | Hs.62 protein tyrosine phosphatase; non-recept | 2.48 | DU145_cells, EB_cells, CALU6_cells |
| 133461 | M33318 | Hs.183584 cytochrome P450; subfamily IIa (phenobar | 2.48 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 103545 | Z14000 | Hs.35384 ring finger protein 1 | 2.47 | HT29_cells, Lu_SQL_H520, BT474_cells |
| 128440 | N76763 | ESTs | 2.47 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 134992 | H05625 | Hs.92414 ESTs | 2.47 | Lu_SC_H345, CALU6_cells, Lu_SC_H69 |
| 116295 | AA489016 | Hs.91216 ESTs; Highly similar to partial CDS; hum | 2.47 | MB-MDA-453, 293T_cells, MB-MDA-435s |
| 107004 | AA598675 | Hs.239475 ESTs | 2.47 | LNCaP_cells, Caco2, OVCAR_cells |
| 132137 | AA282312 | Hs.4076 CTD (carboxy-terminal domain; RNA polyme | 2.46 | Lu_SC_H69, HMEC, EB_cells |
| 126390 | W28286 | Hs.100090 tetraspan 3 | 2.46 | EB_cells, DU145_cells, LNCaP_cells |
| 113050 | T28366 | Hs.22711 EST; Weakly similar to 60S RIBOSOMAL PRO | 2.46 | 2.46 Lu_LC_H460, EB_cells, Lu_AD_358 |
| 101667 | M60858 | Hs.79110 nucleolin | 2.46 | PC3_cells, 293T_cells, A549_cells |
| 108569 | AA085398 | zn7e3.81 Stratagene hNT neuron (#937233) IMAGE:546748 3', mRNA seq | 2.45 | HT29_cells, BT474_cells, Lu_SQL_H520 |
| 117186 | H98988 | Hs.46212 ESTs | 2.45 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 129091 | AA044622 | Hs.183755 Human Chromosome 16 BAC clone CIT987SK-A | 2.45 | 2.45 EB_cells, Lu_AD_H23, Lu_AD_H23 |
| 128468 | T23625 | Hs.258674 EST | 2.45 | Lu_AD_H23, EB_cells, Lu_SC_H69 |
| 117498 | N31726 | Hs.44268 ESTs; Highly similar to myelin gene expr | 2.45 | Lu_SC_H69, DU145_cells, OVCAR_cells |
| 105407 | AA243478 | Hs.5208 ESTs | 2.45 | EB_cells, 293T_cells, PC3_cells |
| 128941 | R55763 | Hs.107287 ESTs | 2.44 | EB_cells, LNCaP_cells, A549_cells |
| 116486 | C14128 | Hs.251980 EST | 2.44 | MB-MDA-435s, HS578T_cells, 293T_cells |
| 134889 | T35288 | Hs.90421 ESTs; Moderately similar to !!! ALU SUB | 2.44 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 130564 | R03049 | Hs.17625 ESTs | 2.44 | PC3_cells, EB_cells, A549_cells |
| 107985 | AA035638 | Hs.71988 H.spliens mRNA; cDNA DKFZp564F053 (from | 2.44 | 2.44 PRSC_con, PRSC_log, Caco2 |
| 110300 | H37820 | Hs.124147 ESTs | 2.44 | MB-MDA-453, Caco2, OVCAR_cells |
| 113471 | T87174 | Hs.16341 ESTs; Moderately similar to !!! ALU SUB | 2.44 | Caco2, OVCAR_cells, LNCaP_cells |
| 131474 | U28749 | Hs.2726 high-mobility group (nonhistone chromoso | 2.44 | CALU6_cells, OVCAR_cells, 293T_cells |
| 120791 | AA342802 | Hs.194031 ESTs | 2.44 | Lu_AD_H23, Lu_SQL_H520, PRSC_con |
| 133733 | AA416973 | Hs.75798 Human DNA seq from clone 1183I21 on chro to predicted fly and worm proteins. Con | 2.43 | EB_cells, Caco2, DU145_cells |
| 119977 | W88579 | Hs.124744 ESTs | 2.43 | HT29_cells, HMEC (total RNA), HMEC |
| 134921 | W60186 | Kreisler (mouse) maf-related leucine zip | 2.43 | LNCaP_cells, HS578T_cells, MB-MDA-453 |
| 132295 | H66351 | Hs.181042 Dmx-like 1 | 2.43 | Lu_SC_H69, BT474_cells, Lu_SQL_H520 |
| 133395 | AA491296 | Hs.72805 ESTs | 2.43 | EB_cells, LNCaP_cells, OVCAR_cells |
| 106728 | AA463555 | Hs.153768 U3 snoRNP-associated 55-kDa protein | 2.43 | EB_cells, Lu_AD_H23, PC3_cells |
| 116370 | AA521256 | Hs.236204 ESTs; Moderately similar to NUCLEAR PORE 2.43 | 2.43 | EB_cells, A549_cells, 293T_cells |
| 113936 | W81552 | Hs.83623 nuclear receptor subfamily 1; group I; m | 2.43 | 293T_cells, OVCAR_cells, Fibroblasts 2 |
| 128862 | R61297 | Hs.106673 eukaryotic translation initiation factor | 2.43 | EB_cells, DU145_cells, DU145_cells |
| 111614 | R12581 | Hs.191146 ESTs | 2.43 | HMEC (total RNA), Fibroblasts 2, MB-MDA-435s |
| 111993 | R42241 | Hs.106359 ESTs | 2.43 | A549_cells, DU145_cells, CALU6_cells |
| 131554 | AA100026 | Hs.28669 ESTs; Weakly similar to PROTEIN-TYROSINE | 2.43 | 2.43 EB_cells, LNCaP_cells, Caco2 |
| 130983 | N71215 | Hs.21862 NCK-associated protein 1 | 2.42 | EB_cells, Caco2, A549_cells |
| 131654 | AA4497050 | Hs.30204 ESTs | 2.42 | MCF7, MB-MDA-435s, Lu_SC_H345 |
| 105014 | AA121123 | Hs.191374 ESTs | 2.42 | EB_cells, Lu_AD_H23, Lu_LC_H460 |
| 106300 | AA4435840 | Hs.19114 high-mobility group (nonhistone chromoso | 2.42 | EB_cells, Lu_SC_H345, A549_cells |
| 102386 | U40998 | Hs.81728 unc119 (C.elegans) homolog | 2.42 | OVCAR_cells, EB_cells, DU145_cells |
| 112517 | R68589 | Hs.23721 ESTs | 2.42 | Caco2, MCF7, DU145_cells |
| 125375 | H72971 | KIAA0277 gene product | 2.42 | Lu_SC_H345, OVCAR_cells, Lu_SC_H69 |
| 123808 | AA620552 | Hs.25682 ESTs; Weakly similar to PHOSPHATIDYLETHA | 2.42 | 2.42 EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 114950 | AA243503 | Hs.11801 adenosine A2b receptor pseudogene | 2.42 | MB-MDA-453, HT29_cells, Lu_LC_H460 |
| 129906 | H39216 | Hs.239970 ESTs; Weakly similar to ZNF91L [H.sapien | 2.41 | Lu_SC_H345, Fibroblasts 2, DU145_cells |
| 103408 | X95876 | Hs.198252 G protein-coupled receptor 9 | 2.41 | RPWE_2, PRSC_log, Lu_SC_H345 |
| 129703 | AA401348 | Hs.179999 ESTs | 2.41 | EB_cells, 293T_cells, DU145_cells |

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|--------|----------|------------------------|--|------|---|
| 105693 | AA287104 | Hs.181368 | U5 snRNP-specific protein (220 kD); orth | 2.41 | 293T_cells, CALU6_cells, A549_cells |
| 106532 | AA453628 | Hs.37443 | ESTs | 2.41 | EB_cells, OVCAR_cells, Caco2 |
| 132132 | AA010933 | Hs.4055 | core promoter element binding protein | 2.41 | HMEC, HMEC (total RNA), EB_cells |
| 111409 | R00311 | Hs.18798 | EST; Weakly similar to !!!! ALU SUBFAMIL | 2.41 | Lu_SC_H345, Lu_SC_H69, PRSC_con |
| 133813 | M26657 | Hs.250711 | dipeptidyl carboxypeptidase 1 (angiotens | 2.41 | HT29_cells, BT474_cells, MB231_cells |
| 127240 | AA888387 | Hs.243845 | ESTs; Moderately similar to !!!! ALU SUB | 2.41 | Lu_SC_H345, DU145_cells, LNCaP_cells |
| 104975 | AA086071 | Hs.50758 | chromosome-associated polypeptide C | 2.41 | OVCAR_cells, DU145_cells, PC3_cells |
| 118078 | N54321 | Hs.47790 | EST | 2.41 | EB_cells, Fibroblasts 2, HMEC (total RNA) |
| 115840 | AA429253 | Hs.58103 | A kinase (PRKA) anchor protein 9 | 2.41 | OVCAR_cells, EB_cells, PC3_cells |
| 101186 | L20298 | Hs.179881 ¹ | core-binding factor; beta subunit | 2.4 | EB_cells, DU145_cells, CALU6_cells |
| 113098 | T40936 | Hs.8349 | ESTs | 2.4 | Caco2, HT29_cells, EB_cells |
| 115185 | AA259140 | Hs.60238 | ESTs | 2.4 | Lu_SC_H69, EB_cells, Caco2 |
| 113778 | W15263 | Hs.5422 | ESTs | 2.4 | Caco2, MB-MDA-435s, LNCaP_cells |
| 128261 | A1061213 | Hs.13179 | ESTs; Moderately similar to !!!! ALU SUB | 2.4 | DU145_cells, LNCaP_cells, OVCAR_cells |
| 132210 | AA235013 | Hs.42322 | A kinase (PRKA) anchor protein 2 | 2.4 | Caco2, DU145_cells, PRSC_log |
| 112561 | R72427 | Hs.129873 | ESTs; Weakly similar to CYTOCHROME P450 | 2.4 | 2.4 Lu_SQ_H520, Lu_AD_H23, EB_cells |
| 127598 | AA610577 | Hs.168851 | ESTs | 2.4 | LNCaP_cells, DU145_cells, OVCAR_cells |
| 106684 | AA460969 | Hs.7510 | mitogen-activated protein kinase kinase | 2.4 | OVCAR_cells, 293T_cells, A549_cells |
| 131367 | AA456687 | Hs.26057 | ESTs | 2.4 | EB_cells, MB-MDA-453, 293T_cells |
| 103163 | X67683 | Hs.863 | H.sapiens mRNA for keratin 4 | 2.39 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 109639 | F04444 | Hs.6217 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 2.39 | EB_cells, Lu_SC_H345, Lu_SC_H69 |
| 112007 | R42671 | Hs.140853 | EST; Weakly similar to !!!! ALU SUBFAMIL | 2.39 | MB-MDA-435s, Lu_SC_H345, Lu_AD_H23 |
| 100023 | | | AFX3 control BioC-3 | 2.39 | Caco2, Lu_AD_358, LNCaP_cells |
| 119923 | W86214 | Hs.184642 | ESTs | 2.39 | EB_cells, HS578T_cells, DU145_cells |
| 127705 | AJ003307 | Hs.184642 | AJ003307 Selected chr 21 cDNA library H | 2.39 | Lu_AD_H23, Lu_SC_H345, Lu_LC_H460 |
| 130362 | AA182658 | Hs.179817 | DKFPZ586F0222 protein | 2.39 | EB_cells, DU145_cells, PC3_cells |
| 100168 | D14874 | Hs.394 | adrenomedullin | 2.39 | Fibroblasts 2, Caco2, HS578T_cells |
| 134261 | AA227678 | Hs.8084 | Human DNA seq from clone 465N24 on chr 1 | 1 | |
| | | | Contains two novel genes; ESTs; GSSs an | 2.39 | PRSC_con, MB-MDA-453, LNCaP_cells |
| | | | H.sapiens dbl/abp gene exon 1 & 2 | 2.38 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 129888 | U81001 | Hs.131891 | Human SNRPN mRNA; 3' UTR; partial seq | 2.38 | LNCaP_cells, Lu_SC_H69, Lu_LC_H460 |
| 130119 | T12649 | Hs.251653 | tubulin; beta; 2 | 2.38 | Lu_AD_H23, Lu_LC_H460, Lu_LC_H460 |
| 118136 | N57710 | Hs.233952 | proteasome (prosome; macropain) subunit; | 2.38 | 293T_cells, OVCAR_cells, HS578T_cells |
| 131163 | H80107 | Hs.23754 | ESTs | 2.38 | Lu_AD_H23, Lu_SC_H69, Lu_SC_H345 |
| 115964 | AA446622 | Hs.74313 | ESTs | 2.38 | EB_cells, LNCaP_cells, DU145_cells |
| 135026 | H59730 | Hs.93231 | ESTs | 2.37 | EB_cells, 293T_cells, Lu_SC_H69 |
| 133300 | D51401 | Hs.70333 | ESTs | 2.37 | OVCAR_cells, Caco2, CALU6_cells |
| 129948 | H69281 | Hs.13643 | ESTs | 2.37 | EB_cells, Lu_AD_H23, Lu_SC_H345 |
| 112505 | R57923 | Hs.23368 | ESTs | 2.37 | DU145_cells, OVCAR_cells, 293T_cells |
| 130715 | T98227 | Hs.171952 | occludin | 2.37 | Caco2, LNCaP_cells, DU145_cells |
| 120301 | AA192163 | Hs.104085 | EST | 2.37 | Lu_AD_H23, EB_cells, PRSC_con |
| 128062 | AA379500 | Hs.193155 | ESTs | 2.37 | EB_cells, LNCaP_cells, DU145_cells |
| 127154 | AA789101 | Hs.198860 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 2.37 | HS578T_cells, MCF7, Lu_SC_H69 |
| 102814 | U90716 | Hs.79187 | coxsackie virus and adenovirus receptor | 2.37 | OVCAR_cells, DU145_cells, Lu_SC_H345 |
| 120239 | Z41691 | Hs.65919 | ESTs | 2.37 | EB_cells, DU145_cells, LNCaP_cells |
| 106829 | AA481883 | Hs.31236 | ESTs; Weakly similar to Unknown [H.sapi | 2.37 | EB_cells, DU145_cells, OVCAR_cells |
| 132681 | AA435762 | Hs.54894 | ESTs; Highly similar to unknown [H.sapi | 2.37 | EB_cells, LNCaP_cells, PRSC_con |
| 108845 | AA132946 | Hs.68864 | ESTs | 2.36 | Lu_AD_H23, Lu_AD_358, Lu_SQ_H520 |
| 133226 | T85327 | Hs.169552 | ESTs | 2.36 | Caco2, MB-MDA-453, MCF7 |
| 105789 | AA478726 | Hs.26373 | ESTs; Moderately similar to !!!! ALU SUB | 2.36 | MB-MDA-453, Caco2, OVCAR_cells |
| 119236 | T10166 | Hs.237297 | ESTs | 2.36 | EB_cells, 293T_cells, LNCaP_cells |
| 106619 | AA459255 | Hs.23956 | ESTs | 2.36 | LNCaP_cells, A549_cells, Caco2 |
| 109178 | AA181600 | Hs.62741 | ESTs | 2.36 | Lu_SC_H345, LNCaP_cells, EB_cells |
| 112724 | R91753 | Hs.17757 | ESTs | 2.36 | Caco2, EB_cells, DU145_cells |
| 112655 | R85069 | Hs.141139 | ESTs | 2.36 | Fibroblasts 2, Lu_AD_H23, Lu_LC_H460 |
| 132820 | AA454988 | Hs.57621 | ESTs | 2.36 | EB_cells, OVCAR_cells, HS578T_cells |
| 106155 | AA425309 | Hs.33287 | nuclear factor I/B | 2.36 | OVCAR_cells, Lu_SC_H345, MB-MDA-453 |
| 114632 | AA084742 | Hs.194380 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 2.35 | Lu_SC_H345, Lu_LC_H460, Lu_AD_H23 |
| 134776 | J05582 | Hs.89603 | much 1; transmembrane | 2.35 | DU145_cells, Lu_AD_H23, Lu_AD_358 |
| 101192 | L20859 | Hs.78452 | solute carrier family 20 (phosphate tran | 2.35 | PC3_cells, CALU6_cells, MB-MDA-435s |
| 130349 | W16686 | Hs.171825 | basic helix-loop-helix domain containing | 2.35 | A549_cells, DU145_cells, HT29_cells |
| 106389 | AA446949 | Hs.6236 | ESTs | 2.35 | LNCaP_cells, PC3_cells, DU145_cells |
| 109637 | F04426 | Hs.23131 | kinesin family member C3 | 2.35 | MB-MDA-435s, A549_cells, Lu_LC_H460 |
| 101483 | M24486 | Hs.76768 | procollagen-proline; 2-oxoglutarate 4-di | 2.35 | PC3_cells, HS578T_cells, EB_cells |
| 131751 | H18335 | Hs.31562 | ESTs | 2.35 | DU145_cells, MB231_cells, HMEC |
| 131050 | X13987 | Hs.2250 | leukemia Inhibitory factor (cholinergic | 2.35 | Lu_AD_H23, PC3_cells, PRSC_log |
| 130097 | N21159 | Hs.14845 | forkhead box O3A | 2.34 | EB_cells, LNCaP_cells, LNCaP_cells |
| 134533 | AA013468 | Hs.241493 | natural killer-tumor recognition seq | 2.34 | EB_cells, HT29_cells, HMEC |
| 134839 | D63479 | Hs.115907 | diacylglycerol kinase; delta (130kD) | 2.34 | Lu_LC_H460, Caco2, DU145_cells |
| 115690 | AA410894 | Hs.44159 | ESTs | 2.34 | PC3_cells, EB_cells, OVCAR_cells |
| 129079 | N91011 | Hs.108502 | ESTs | 2.34 | Lu_AD_H23, Lu_SC_H69, Lu_AD_358 |
| 123517 | AA608525 | Hs.243059 | EST | 2.34 | Lu_SC_H345, PC3_cells, MB-MDA-435s |
| 126239 | AA527215 | Hs.75879 | ribosomal protein L19 | 2.34 | BT474_cells, Lu_LC_H460, Lu_AD_H23 |
| 124440 | N46435 | Hs. | ESTs | 2.34 | Lu_SC_H69, HT29_cells, MB-MDA-435s |
| 111468 | R05809 | Hs.205481 | ESTs | 2.34 | Lu_AD_H23, PRSC_log, Lu_SQ_H520 |
| 129560 | H18428 | Hs.113613 | ESTs; Moderately similar to !!!! ALU SUB | 2.34 | Lu_SC_H69, Lu_SC_H345, LNCaP_cells |

| | | | | | |
|--------|----------|-----------|---|------|---|
| 104857 | AA043219 | Hs.19058 | ESTs | 2.34 | Lu_AD_H23, Lu_SC_H345, Lu_SC_H345 |
| 109847 | F04587 | Hs.28241 | ESTs | 2.34 | HS578T_cells, A549_cells, CALU6_cells |
| 117160 | H97817 | Hs.183302 | ESTs | 2.34 | EB_cells, Fibroblasts 2, Lu_SC_H69 |
| 112352 | R58974 | Hs.167343 | ESTs | 2.34 | EB_cells, Lu_SC_H345, HT29_cells |
| 113553 | T95745 | Hs.187433 | ESTs | 2.34 | MB-MDA-435s, MB-MDA-453, Lu_SC_H345 |
| 131606 | W56804 | Hs.29385 | AFG3 (ATPase family gene 3; yeast)-like | 2.34 | OVCAR_cells, Fibroblasts 2, MB-MDA-435s |
| 101525 | M29536 | Hs.12163 | eukaryotic translation initiation factor | 2.34 | EB_cells, Caco2, DU145_cells |
| 125921 | AA775029 | Hs.122591 | ESTs | 2.33 | 293T_cells, PRSC_log, Lu_SC_H345 |
| 125775 | AA213555 | Hs.29205 | alpha integrin binding protein 63 | 2.33 | EB_cells, DU145_cells, LNCaP_cells |
| 108743 | AA126917 | Hs.71074 | ESTs | 2.33 | Lu_AD_H23, Lu_AD_358, Lu_LC_H460 |
| 133735 | AC002045 | Hs.251928 | nuclear pore complex interacting protein | 2.33 | LNCaP_cells, Lu_SC_H69, DU145_cells |
| 120403 | AA234916 | Hs.243851 | ESTs | 2.33 | MB231_cells, Lu_SC_H345, Lu_SC_H69 |
| 134998 | R02207 | Hs.92679 | ESTs; Weakly similar to microtubule-base | 2.33 | LNCaP_cells, BT474_cells, MCF7 |
| 108456 | AA079326 | Hs.143654 | ESTs | 2.33 | HT29_cells, Lu_AD_H23, RPWE_2 |
| 130552 | M86667 | Hs.179662 | nucleosome assembly protein 1-like 1 | 2.33 | EB_cells, A549_cells, DU145_cells |
| 111114 | N63391 | Hs.9238 | ESTs | 2.33 | Caco2, EB_cells, MB-MDA-453 |
| 127767 | A1269498 | Hs.125543 | ESTs; Moderately similar to TADA1 protein | 2.33 | CALU6_cells, 293T_cells, PC3_cells |
| 106546 | AA454725 | Hs.21056 | H sapiens mRNA from chromosome 5q21-22; | 2.33 | OVCAR_cells, Caco2, LNCaP_cells |
| 122379 | AA446110 | Hs.250998 | EST | 2.33 | BT474_cells, Fibroblasts 2, MB-MDA-435s |
| 133650 | D84294 | Hs.118174 | tetratricopeptide repeat domain 3 | 2.33 | Lu_SC_H345, EB_cells, EB_cells |
| 106434 | AA449099 | Hs.8151 | ESTs; Weakly similar to atopy related au | 2.33 | EB_cells, LNCaP_cells, Caco2 |
| 105297 | AA233451 | Hs.183858 | transcriptional intermediary factor 1 | 2.33 | EB_cells, LNCaP_cells, Caco2 |
| 115976 | AA447442 | Hs.86327 | ESTs | 2.33 | EB_cells, 293T_cells, Lu_SC_H69 |
| 105788 | AA351031 | Hs.23965 | solute carrier family 22 (organic anion | 2.33 | EB_cells, Lu_AD_H23, Lu_SC_H345 |
| 113774 | W04550 | Hs.9927 | H sapiens mRNA; cDNA DKFZp664D156 (from | 2.32 | 2.32 OVCAR_cells, EB_cells, Lu_SC_H69 |
| 110617 | H68772 | Hs.35820 | ESTs; Weakly similar to b3418.1 [H.sapi | 2.32 | Lu_SC_H345, Lu_AD_H23, PRSC_con |
| 102234 | U26312 | Hs.8123 | chromobox homolog 3 (Drosophila HP1 gamm | 2.32 | CALU6_cells, LNCaP_cells, A549_cells |
| 114777 | AA151699 | Hs.184519 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.32 | HT29_cells, Fibroblasts 2, Lu_SC_H345 |
| 125518 | R20148 | Hs.193851 | ESTs | 2.32 | HT29_cells, HMEC (total RNA), MB231_cells |
| 130814 | AA256695 | Hs.19813 | ESTs | 2.32 | MB-MDA-435s, Lu_SC_H69, PRSC_log |
| 123473 | AA599143 | | ESTs; Moderately similar to !!! ALU SUB | 2.32 | LNCaP_cells, DU145_cells, Lu_SC_H345 |
| 134310 | AA313444 | Hs.8148 | H sapiens clone 24856 mRNA seq; complete | 2.32 | PC3_cells, LNCaP_cells, OVCAR_cells |
| 119192 | R85375 | Hs.237262 | EST | 2.32 | Lu_SC_H69, PRSC_log, PRSC_con |
| 114391 | AA004876 | Hs.133100 | ESTs | 2.32 | PC3_cells, 293T_cells, 293T_cells |
| 119133 | R49144 | Hs.119756 | ESTs | 2.32 | PRSC_log, 293T_cells, 293T_cells |
| 109710 | F09792 | Hs.12929 | ESTs | 2.32 | Lu_AD_H23, Lu_SC_H69, Lu_SC_H345 |
| 116726 | F13681 | Hs.42309 | ESTs | 2.32 | MCF7, BT474_cells, MB-MDA-453 |
| 133206 | R32993 | Hs.6762 | ESTs; Weakly similar to similar to leucy | 2.31 | DU145_cells, 293T_cells, EB_cells |
| 135163 | AA125988 | Hs.199955 | ESTs | 2.31 | Lu_SC_H345, LNCaP_cells, DU145_cells |
| 111219 | N68836 | Hs.19247 | ESTs | 2.31 | OVCAR_cells, LNCaP_cells, 293T_cells |
| 110283 | H29565 | Hs.12271 | ESTs | 2.31 | BT474_cells, MB231_cells, MB-MDA-453 |
| 103772 | AA092473 | Hs.8123 | chromobox homolog 3 (Drosophila HP1 gamm | 2.31 | CALU6_cells, MCF7, DU145_cells |
| 122766 | AA459386 | Hs.194058 | ESTs; Weakly similar to atypical PKC spe | 2.31 | HT29_cells, BT474_cells, HMEC |
| 120886 | AA365566 | Hs.132736 | ESTs; Weakly similar to allograft inflam | 2.31 | DU145_cells, A549_cells, Lu_LC_H460 |
| 123512 | AA600248 | Hs.142245 | HERV-H LTR-associating 3 | 2.31 | PC3_cells, 293T_cells, DU145_cells |
| 106644 | AA460239 | Hs.12680 | ESTs | 2.31 | HS578T_cells, MB231_cells, Lu_SQ_H520 |
| 127359 | H72971 | | KIAA0277 gene product | 2.31 | Lu_SC_H345, DU145_cells, OVCAR_cells |
| 105919 | AA402494 | Hs.3990 | ESTs | 2.31 | HS578T_cells, DU145_cells, LNCaP_cells |
| 125241 | W86291 | Hs.121593 | ESTs | 2.3 | HMEC, HMEC (total RNA), EB_cells |
| 104624 | AA001936 | Hs.184721 | ESTs | 2.3 | DU145_cells, PC3_cells, PRSC_log |
| 128765 | AA101767 | Hs.10494 | ESTs | 2.3 | EB_cells, HMEC (total RNA), Lu_LC_H460 |
| 108360 | AA071539 | | zm74b6.s1 Stratagene neuroepithelium (#9 | | |
| | | | HYDROXYSTEROID DEHYDROGENASE/DELTA-5-DEL | | |
| 115682 | AA410300 | Hs.44618 | ESTs | 2.3 | 2.3 HT29_cells, RPWE_2, Lu_AD_H23 |
| 134528 | M23161 | Hs.84775 | Human transposon-like element mRNA | 2.3 | HT29_cells, Lu_SQ_H520, Lu_AD_H23 |
| 111091 | N59858 | Hs.33032 | H sapiens mRNA; cDNA DKFZp434N185 (from | | EB_cells, CALU6_cells, A549_cells |
| 134044 | AA262475 | Hs.78746 | phosphodiesterase 8A | 2.29 | 2.3 LNCaP_cells, DU145_cells, PRSC_log |
| 118229 | N62339 | Hs.180532 | heat shock 90kD protein 1; alpha | 2.29 | DU145_cells, A549_cells, MCF7 |
| 110188 | H20522 | Hs.20969 | ESTs | 2.29 | MCF7, DU145_cells, EB_cells |
| 125073 | T87185 | Hs.193638 | ESTs; Weakly similar to !!! ALU CLASS C | 2.29 | Fibroblasts 2, MB-MDA-435s, Lu_LC_H460 |
| 111495 | R07210 | Hs.19913 | ESTs | 2.29 | EB_cells, Lu_SC_H345, Lu_SC_H69 |
| 124024 | F03077 | Hs.10672 | ESTs | 2.29 | CALU6_cells, EB_cells, MCF7 |
| 126230 | AA984074 | Hs.176757 | ESTs | 2.29 | HS578T_cells, RPWE_2, LuAD_358 |
| 125471 | AA477571 | Hs.152601 | UDP-glucose ceramide glucosyltransferase | 2.29 | LNCaP_cells, DU145_cells, OVCAR_cells |
| 120734 | AA299949 | | EST12545 Uterus tumor I H sapiens cDNA 3 | 2.28 | DU145_cells, PRSC_con, PRSC_log |
| 134349 | AA405373 | Hs.8208 | ESTs | 2.28 | Lu_AD_H23, Lu_SC_H345, Lu_SC_H69 |
| 123412 | AA521443 | Hs.187763 | ESTs | 2.28 | DU145_cells, PC3_cells, LNCaP_cells |
| 116297 | AA469042 | Hs.59498 | ESTs | 2.28 | BT474_cells, BT474_cells, Lu_SC_H69 |
| 104476 | N33807 | Hs.223014 | protease; serine; 15 | 2.28 | EB_cells, 293T_cells, MB-MDA-453 |
| 101004 | J04101 | Hs.248109 | v-ets avian erythroblastosis virus E26 o | 2.28 | LNCaP_cells, MCF7, PC3_cells |
| 109991 | H09813 | Hs.12898 | KIAA1034 protein | 2.28 | HT29_cells, MB-MDA-435s, HMEC (total RNA) |
| 118934 | N32571 | Hs.54808 | ESTs | 2.28 | EB_cells, CALU6_cells, 293T_cells |
| 125096 | T94328 | Hs.194533 | ESTs | 2.28 | HS578T_cells, 293T_cells, A549_cells |
| 117514 | N32226 | Hs.124058 | ESTs | 2.28 | Lu_SC_H345, Lu_SC_H69, 293T_cells |
| 132792 | AA401903 | Hs.242985 | hemoglobin; gamma G | 2.28 | CALU6_cells, HMEC, Lu_AD_H23 |
| 129009 | AA131421 | Hs.107884 | ESTs | 2.28 | OVCAR_cells, Lu_SC_H69, MCF7 |
| | | | | | HS578T_cells, CALU6_cells, Caco2 |

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|--------|----------|-----------|--|------|--|
| 111658 | R16981 | Hs.15276 | ESTs | 2.28 | MB-MDA-435s, 293T_cells, A549_cells |
| 112322 | R55757 | Hs.26457 | EST | 2.28 | Lu_SC_H345, Lu_SC_H69, Lu_AD_358 |
| 133477 | W69310 | Hs.740 | PTK2 protein tyrosine kinase 2 | 2.28 | EB_cells, PC3_cells, DU145_cells |
| 132149 | T10822 | Hs.4095 | ESTs | 2.28 | LNCaP_cells, EB_cells, PC3_cells |
| 115119 | AA256524 | Hs.46847 | Human DNA seq from clone 30M3 on chromos yeast and archaea bacterial genes; and small nuclear ribonucleoprotein D3 polyp | 2.27 | A549_cells, EB_cells, LNCaP_cells |
| 102130 | U15009 | Hs.1575 | ESTs | 2.27 | LNCaP_cells, Caco2, EB_cells |
| 114343 | Z41424 | Hs.21259 | ESTs | 2.27 | HT29_cells, OVCAR_cells, Fibroblasts 2 |
| 105746 | AA476436 | Hs.7991 | ESTs | 2.27 | Lu_AD_358, RPWE_2, Lu_AD_H23 |
| 119359 | T71021 | Hs.93334 | ESTs; Highly similar to WS basic-helix-1 | 2.27 | Lu_SC_H69, 293T_cells, DU145_cells |
| 105301 | AA435867 | Hs.168212 | kinase family member 3B | 2.27 | OVCAR_cells, LNCaP_cells, EB_cells |
| 130280 | L13738 | Hs.153937 | activated p21cd42Hs kinase | 2.27 | MB-MDA-453, DU145_cells, DU145_cells |
| 119724 | W69468 | Hs.47622 | ESTs | 2.27 | PC3_cells, HT29_cells, A549_cells |
| 108960 | AA150199 | Hs.49378 | DKFZP586D0919 protein | 2.27 | EB_cells, HS578T_cells, Lu_AD_358 |
| 103489 | Y08614 | Hs.79090 | exportin 1 (CRM1; yeast; homolog) | 2.26 | EB_cells, CALU6_cells, DU145_cells |
| 107711 | AA015736 | Hs.220687 | ESTs | 2.26 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 131950 | WB4704 | Hs.35380 | ESTs | 2.26 | HS578T_cells, OVCAR_cells, MB-MDA-435s |
| 107093 | AA609800 | Hs.10018 | ESTs | 2.26 | LNCaP_cells, OVCAR_cells, DU145_cells |
| 113649 | T95641 | Hs.16400 | ESTs; Weakly similar to Hrs [H.sapiens] | 2.26 | Lu_AD_H23, Lu_SC_H69, PRSC_log |
| 105255 | AA227498 | Hs.3623 | ESTs | 2.26 | HS578T_cells, 293T_cells, Lu_SC_H345 |
| 130094 | H43286 | Hs.167017 | gamma-aminobutyric acid (GABA) B recepto | 2.26 | Fibroblasts 2, MB231_cells, 293T_cells |
| 111874 | R37959 | Hs.13358 | ESTs | 2.26 | CALU6_cells, Lu_SQ_H520, 293T_cells |
| 107890 | AA026030 | Hs.61311 | ESTs; Weakly similar to CALPAIN 2; LARGE | 2.26 | HT29_cells, MB-MDA-453, PC3_cells |
| 124628 | N74702 | Hs.102834 | ESTs | 2.26 | 293T_cells, CALU6_cells, CALU6_cells |
| 119707 | W67569 | Hs.44143 | ESTs; Weakly similar to SNF2alpha protein | 2.26 | 293T_cells, OVCAR_cells, Lu_SC_H345 |
| 106737 | AA470080 | Hs.36237 | ESTs; Moderately similar to CGI-34 prote | 2.26 | LNCaP_cells, DU145_cells, MB-MDA-435s |
| 117305 | N22798 | Hs.43248 | EST | 2.26 | HT29_cells, BT474_cells, Fibroblasts 2 |
| 134470 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 2.26 | DU145_cells, CALU6_cells, LNCaP_cells |
| 130734 | T99337 | Hs.18624 | KIAA1052 protein | 2.26 | Lu_AD_H23, Lu_SC_H345, Lu_SC_H69 |
| 128551 | R69227 | Hs.101489 | ESTs | 2.26 | Lu_SC_H345, DU145_cells, OVCAR_cells |
| 100670 | HG2992-H | | Beta-Hexosaminidase, Alpha Polypeptide, | 2.26 | HT29_cells, BT474_cells, Lu_SC_H345 |
| 115953 | AA443958 | Hs.90960 | ESTs | 2.26 | Caco2, 293T_cells, DU145_cells |
| 129612 | H17476 | Hs.11615 | ESTs; Highly similar to map kinase phosph | 2.25 | CALU6_cells, LNCaP_cells, PC3_cells |
| 111362 | N91973 | Hs.23595 | deoxyribonuclease III; dnaQ/mutD (E. col | 2.25 | Lu_SQ_H520, Lu_AD_H23, RPWE_2 |
| 116275 | AA485453 | Hs.250911 | interleukin 13 receptor; alpha 1 | 2.25 | OVCAR_cells, 293T_cells, DU145_cells |
| 114461 | AA024848 | Hs.125705 | ESTs | 2.25 | EB_cells, Lu_AD_H23, Lu_AD_H23 |
| 134083 | AA278393 | Hs.79013 | ESTs | 2.25 | 293T_cells, EB_cells, OVCAR_cells |
| 132470 | Z24724 | Hs.4934 | H.sapiens polyA site DNA | 2.25 | EB_cells, HS578T_cells, Caco2 |
| 114718 | AA131328 | | z08d1.s1 Stratagene neuroepithelium NT2R SW:COX2_MOUSE P45 CYTOCHROME C OXIDASE P | 2.25 | 2.25 MB-MDA-435s, HT29_cells, Lu_SC_H69 |
| 129499 | R40395 | Hs.242808 | lecithin-cholesterol acyltransferase | 2.25 | HMEC (total RNA), Fibroblasts 2, HMEC |
| 124758 | R38422 | Hs.169168 | ESTs | 2.25 | 293T_cells, RPWE_2, Lu_LC_H460 |
| 130301 | X83127 | Hs.172471 | potassium voltage-gated channel; shaker- | 2.25 | EB_cells, OVCAR_cells, A549_cells |
| 131263 | R38334 | Hs.24950 | regulator of G-protein signalling 5 | 2.25 | Lu_AD_H23, EB_cells, Lu_SC_H69 |
| 107159 | AA521340 | Hs.10600 | ESTs; Weakly similar to ORF YKR081c [S.c | 2.25 | LNCaP_cells, HMEC, EB_cells |
| 133262 | N72009 | Hs.205710 | ESTs | 2.24 | Lu_SC_H345, DU145_cells, LNCaP_cells |
| 132985 | AA093619 | Hs.62113 | KIAA0717 protein | 2.24 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 114172 | Z39043 | Hs.21421 | ESTs; Weakly similar to cysteine desulfu | 2.24 | 293T_cells, CALU6_cells, Lu_SQ_H520 |
| 127847 | AA913387 | Hs.126717 | ESTs | 2.24 | LNCaP_cells, DU145_cells, Lu_SC_H69 |
| 106499 | AA452244 | Hs.16727 | ESTs | 2.24 | Lu_SC_H345, MB-MDA-453, Lu_SC_H69 |
| 105095 | AA150098 | Hs.27023 | KIAA0917 protein | 2.24 | DU145_cells, LNCaP_cells, CALU6_cells |
| 108876 | AA134361 | Hs.191453 | ESTs | 2.24 | EB_cells, Lu_SC_H345, Lu_AD_H23 |
| 121971 | AA429667 | Hs.120405 | ESTs | 2.24 | Lu_AD_H23, 293T_cells, CALU6_cells |
| 114334 | Z41342 | Hs.22941 | ESTs | 2.24 | DU145_cells, PC3_cells, EB_cells |
| 114565 | AA063001 | Hs.103527 | SH2 domain protein 2A | 2.24 | Lu_LC_H460, MCF7, HMEC (total RNA) |
| 115766 | AA421761 | Hs.77603 | ESTs | 2.24 | Fibroblasts 2, MB-MDA-435s, MB231_cells |
| 130989 | AA608546 | Hs.21906 | ESTs | 2.24 | PC3_cells, LNCaP_cells, DU145_cells |
| 116304 | AA489461 | Hs.64742 | H.sapiens mRNA for KIAA0540 protein; par | 2.24 | BT474_cells, EB_cells, LNCaP_cells |
| 111154 | N66545 | Hs.29169 | ESTs | 2.24 | OVCAR_cells, MB-MDA-435s, HMEC |
| 105561 | AA262881 | Hs.16029 | ESTs; Weakly similar to alternatively sp | 2.23 | HS578T_cells, A549_cells, HMEC |
| 105939 | AA404421 | Hs.12258 | ESTs | 2.23 | EB_cells, LNCaP_cells, DU145_cells |
| 126379 | AI085342 | Hs.166146 | Homer; neuronal immediate early gene; 3 | 2.23 | HS578T_cells, PC3_cells, RPWE_2 |
| 106510 | AA458882 | Hs.4832 | ESTs; Moderately similar to Lasp-1 prote | 2.23 | DU145_cells, MCF7, Lu_SC_H345 |
| 132786 | AA424545 | Hs.56851 | H.sapiens mRNA expressed in placenta | 2.23 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 107206 | D20728 | Hs.30767 | ESTs | 2.23 | BT474_cells, Fibroblasts 2, MB-MDA-435s |
| 133708 | R42172 | Hs.75667 | synaptophysin | 2.23 | Lu_SC_H345, CALU6_cells, Lu_SC_H69 |
| 135123 | AA227557 | Hs.9482 | target of myo1 (chicken) homolog | 2.23 | BT474_cells, MB231_cells, EB_cells |
| 132156 | AA157401 | Hs.4113 | S-adenosylhomocysteine hydrolase-like 1 | 2.23 | DU145_cells, 293T_cells, LNCaP_cells |
| 116934 | H75624 | Hs.39662 | ESTs | 2.23 | CALU6_cells, Lu_SC_H345, Lu_LC_H460 |
| 133660 | R87373 | | ym88e05.r1 Soares adult brain N2b4HB55Y IMAGE:166016 5', mRNA seq. | 2.23 | DU145_cells, A549_cells, PC3_cells |
| 119468 | W23633 | Hs.125043 | ESTs | 2.23 | 293T_cells, MB-MDA-453, OVCAR_cells |
| 101247 | L33801 | Hs.78802 | glycogen synthase kinase 3 beta | 2.23 | LNCaP_cells, EB_cells, MB-MDA-435s |
| 126008 | AA253460 | | zs06f04.s1 NCI(CGAP_GCB1 H saptens cDNA | 2.23 | 2.23 HT29_cells, PRSC_log, Fibroblasts 2 |
| 122938 | AA477119 | | zu3767.s1 Soares ovary tumor NbHOT H sap TR:G288289 G288289 MITOCHONDRIAL D-LOOP | 2.23 | PC3_cells, MCF7, MB-MDA-435s |

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|-----------------|--|---|------|--|
| 114148 Z38804 | Hs.184777 | ESTs; Moderately similar to OP/OID BINDI MOLECULE PRECURSOR [H.sapiens] | 2.23 | HS578T_cells, Fibroblasts 2, Lu_SC_H345 |
| 103433 X98001 | Hs.78948 | Rab geranylgeranyltransferase; beta subu | 2.22 | LNCaP_cells, EB_cells, 293T_cells |
| 132954 AA027112 | Hs.216194 | ESTs | 2.22 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 133228 N90029 | Hs.6831 | H.sapiens clone 1400 unknown protein mRN | 2.22 | 293T_cells, PC3_cells, DU145_cells |
| 103891 AA242887 | Hs.124186 | ring finger protein 2 | 2.22 | EB_cells, Lu_SC_H69, Lu_SC_H345 |
| 124883 R75630 | Hs.177242 | ESTs | 2.22 | EB_cells, Lu_AD_H23, Lu_SC_H345 |
| 105921 H05734 | Hs.30559 | ESTs | 2.22 | Lu_SQL_H520, 293T_cells, RPWE_2 |
| 127306 AI305162 | Hs.193687 | ESTs | 2.22 | MCF7, HT29_cells, MB-MDA-453 |
| 102707 U77456 | Hs.78103 | nucleosome assembly protein 1-like 4 | 2.22 | Caco2, EB_cells, CALU6_cells |
| 106193 AA427625 | Hs.23272 | ESTs | 2.22 | 293T_cells, EB_cells, A549_cells |
| 118819 N79045 | Hs.50800 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 2.22 | Lu_SC_H345, Lu_SC_H69, DU145_cells |
| 134326 U16306 | Hs.81800 | chondroitin sulfate proteoglycan 2 (vers | 2.22 | HS578T_cells, PRSC_log, CALU6_cells |
| 112241 R51248 | Hs.16027 | ESTs | 2.22 | 293T_cells, HMEC (total RNA), HMEC (total RNA) |
| 123593 AA609591 | Hs.112728 | ESTs | 2.22 | HT29_cells, HMEC (total RNA), BT474_cells |
| 129052 AA496297 | Hs.182740 | ribosomal protein S11 | 2.22 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 122481 AA448271 | Hs.99126 | ESTs | 2.21 | Lu_AD_H23, HT29_cells, Lu_AD_358 |
| 128895 R37753 | Hs.106985 | ESTs | 2.21 | EB_cells, Lu_AD_H23, Lu_SC_H345 |
| 124691 R05835 | Hs.110153 | ESTs; Weakly similar to B-CELL GROWTH FA | 2.21 | 2.21 EB_cells, Lu_AD_H23, Lu_AD_358 |
| 131556 AA442853 | Hs.2869 | cyclin-dependent kinase 5; regulatory su | 2.21 | HT29_cells, Lu_LC_H460, Lu_SC_H69 |
| 128869 AA424570 | Hs.105736 | ESTs | 2.21 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 107114 AA610089 | Hs.11776 | U4/U6-associated RNA splicing factor | 2.21 | MCF7, Lu_SC_H345, DU145_cells |
| 106255 AA431191 | Hs.161489 | ESTs | 2.21 | EB_cells, Caco2, DU145_cells |
| 130724 AA370091 | Hs.179680 | ESTs | 2.2 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 105483 AA255874 | Hs.23458 | ESTs | 2.2 | LNCaP_cells, DU145_cells, PC3_cells |
| 118970 N93503 | Hs.54961 | stoned B/TFIIB-alpha/beta-like factor | 2.2 | 293T_cells, HS578T_cells, OVCAR_cells |
| 120805 AA346041 | Hs.96844 | ESTs | 2.2 | HT29_cells, HS578T_cells, 293T_cells |
| 106158 AA425382 | Hs.6553 | ESTs | 2.2 | CALU6_cells, PC3_cells, EB_cells |
| 102121 U14391 | Hs.82251 | myostatin | 2.2 | A549_cells, EB_cells, Caco2 |
| 109446 AA223215 | Hs.87062 | ESTs | 2.2 | HT29_cells, Lu_LC_H460, CALU6_cells |
| 129515 AA490882 | Hs.112227 | ESTs | 2.2 | Lu_SC_H345, BT474_cells, Caco2 |
| 113128 T49325 | Hs.8977 | ESTs | 2.2 | Lu_SQL_H520, Lu_AD_H23, Lu_AD_358 |
| 127289 AI041014 | Hs.220752 | ESTs | 2.2 | EB_cells, Lu_AD_H23, Lu_AD_H23 |
| 129912 AA047344 | Hs.107213 | ESTs; Highly similar to NY-REN-6 antigen | 2.2 | CALU6_cells, A549_cells, EB_cells |
| 115700 AA411685 | Hs.67709 | ESTs | 2.2 | OVCAR_cells, EB_cells, Caco2 |
| 105287 AA431873 | Hs.4988 | H.sapiens clone 24711 mRNA seq | 2.2 | Lu_SQL_H520, EB_cells, PC3_cells |
| 112881 T03593 | Hs.182814 | ESTs | 2.19 | A549_cells, OVCAR_cells, 293T_cells |
| 116902 H70739 | yu69f11.s1 Weizmann Olfactory Epithelium IMAGE:239085 3' similar to contains LTR | | | |
| 105621 AA280865 | Hs.6375 | H.sapiens mRNA; cDNA DKFZp564K0222 (from | 2.19 | LNCaP_cells, DU145_cells, PC3_cells |
| 126991 R31652 | Hs.821 | bigrlycan | 2.19 | 2.19 HMEC, Caco2, HMEC (total RNA) |
| 125466 R08234 | Hs.180461 | ESTs | 2.19 | Fibroblasts 2, Lu_SC_H69, HS578T_cells |
| 108491 AA082973 | Lu_AD_358, Lu_SC_H23, Lu_SQL_H520 | | | |
| 109978 H09356 | Hs.22528 | ESTs | 2.19 | 2.19 Lu_AD_358, RPWE_2, Lu_LC_H460 |
| 106990 AA521354 | Hs.24758 | ESTs | 2.19 | PRSC_log, Lu_SC_H345, Lu_SC_H69 |
| 122362 AA443919 | Hs.96840 | ESTs | 2.19 | EB_cells, LNCaP_cells, OVCAR_cells |
| 125367 AI016490 | Hs.81984 | SEC24 (S. cerevisiae) related gene famil | 2.19 | EB_cells, Lu_AD_358, PRSC_con |
| 110716 H97188 | Hs.35096 | ESTs | 2.19 | HT29_cells, Lu_SC_H69, Lu_AD_H23 |
| 129297 R11257 | Hs.180570 | H.sapiens chromosome 19; cosmid F22329 | 2.19 | DU145_cells, Fibroblasts 2, PRSC_con |
| 104992 AA102652 | Hs.22753 | ESTs; Weakly similar to coded for by C. | 2.18 | 293T_cells, MB-MDA-435s, A549_cells |
| 119896 W84738 | Hs.137319 | ESTs | 2.18 | MCF7, MB-MDA-453, Lu_SQL_H520 |
| 118594 N69022 | Hs.49599 | ESTs | 2.18 | 293T_cells, 293T_cells, OVCAR_cells |
| 129786 H98977 | Hs.246109 | ESTs | 2.18 | Lu_SC_H69, Lu_AD_H23, Lu_SC_H345 |
| 104325 D81608 | Hs.150675 | polymerase (RNA) II (DNA directed) polyp | 2.18 | 293T_cells, 293T_cells, 293T_cells |
| 123022 AA480909 | PC3_cells, Lu_SC_H345, LNCaP_cells | | | |
| 133572 W94333 | Hs.7499 | Alu repetitive element;contains element | 2.18 | OVCAR_cells, DU145_cells, LNCaP_cells |
| 133363 AA479713 | Hs.71962 | translocase of inner mitochondrial membr | 2.18 | Caco2, LNCaP_cells, Lu_SQL_H520 |
| 135361 AA053319 | Hs.167700 | ESTs | 2.18 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 128319 AA080904 | Hs.115095 | ESTs; Weakly similar to RHO-RELATED GTP- | 2.18 | EB_cells, 293T_cells, Caco2 |
| DU145_cells | | | | |
| 128660 AA011597 | Hs.177398 | ESTs | 2.18 | 2.18 Lu_SC_H345, OVCAR_cells, |
| 114877 AA235618 | Hs.205125 | ESTs | 2.18 | EB_cells, Lu_AD_H23, Lu_SQL_H520 |
| 125925 H28737 | DU145_cells, 293T_cells, OVCAR_cells | | | |
| 113427 T85105 | Hs.15471 | ESTs | 2.18 | Lu_SC_H69, Lu_SC_H345, HS578T_cells |
| 117500 N31909 | Hs.44278 | ESTs | 2.18 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 131384 F13608 | Hs.26226 | ESTs | 2.18 | PRSC_con, Lu_SC_H345, PRSC_log |
| 134499 U70370 | Hs.84136 | paired-like homeodomain transcription fa | 2.18 | 293T_cells, LNCaP_cells, OVCAR_cells |
| 128154 AA922969 | Hs.127100 | ESTs | 2.17 | Caco2, BT474_cells, MB231_cells |
| 134585 T48154 | Hs.168655 | H.sapiens mRNA for H-2K binding factor-2 | 2.17 | MB-MDA-453, MB-MDA-453, Lu_SC_H345 |
| 104987 AA101723 | Hs.16683 | ESTs | 2.17 | LNCaP_cells, 293T_cells, PRSC_log |
| 132992 AA091017 | Hs.6226 | ESTs | 2.17 | EB_cells, MCF7, DU145_cells |
| 135311 M36089 | Hs.98493 | X-ray repair complementing defective rep | 2.17 | Caco2, LNCaP_cells, DU145_cells |
| 113171 T54613 | Hs.9761 | EST | 2.17 | HMEC (total RNA), Fibroblasts 2, HMEC |
| 117736 N46999 | Hs.46648 | ESTs | 2.16 | HT29_cells, PRSC_con, Lu_SQL_H520 |
| | | | | PRSC_log, OVCAR_cells, A549_cells |

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|--------|----------|-----------|---|------|--|
| 125181 | W58461 | Hs.12396 | ESTs | 2.16 | LNCaP_cells, DU145_cells, 293T_cells |
| 120187 | Z40251 | Hs.56974 | ESTs | 2.16 | LNCaP_cells, MB-MDA-453, HMEC (total RNA) |
| 100308 | D50532 | Hs.54403 | macrophage lectin 2 (calcium dependent) | 2.16 | HT29_cells, Lu_AD_H23, Lu_AD_H23 |
| 110960 | N50887 | Hs.26549 | ESTs; Weakly similar to KIAA0449 protein | 2.16 | Caco2, A549_cells, LNCaP_cells |
| 113608 | T93113 | | ESTs; Moderately similar to !!! ALU SUB | 2.16 | Lu_SC_H69, CALU6_cells, 293T_cells |
| 107538 | Z21089 | Hs.50094 | ESTs; Weakly similar to KALIRIN [R.norve | 2.16 | HS578T_cells, 293T_cells, DU145_cells |
| 128703 | S76992 | Hs.104005 | vav 2 oncogene | 2.16 | RPWE_2, Lu_SC_H69, HT29_cells |
| 126065 | A1366484 | | ESTs | 2.16 | 293T_cells, CALU6_cells, A549_cells |
| 130000 | AA465727 | Hs.124084 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.16 | DU145_cells, LNCaP_cells, OVCAR_cells |
| 120407 | AA235040 | Hs.107283 | ESTs | 2.16 | EB_cells, 293T_cells, A549_cells |
| 121199 | AA400371 | Hs.97792 | ESTs | 2.16 | Lu_AD_358, Lu_AD_H23, A549_cells |
| 114963 | AA243867 | Hs.193055 | ESTs | 2.16 | DU145_cells, PRSC_con, LNCaP_cells |
| 100343 | D63874 | Hs.189509 | high-mobility group (nonhistone chromoso | 2.15 | CALU6_cells, MB-MDA-453, Caco2 |
| 125077 | T88822 | | ye32f5.s1 Soares fetal liver spleen 1NFL | 2.15 | Lu_AD_H23, Lu_SC_H69, Lu_SC_H345 |
| 117286 | N22181 | | ye36d12.s1 Morton Fetal Cochlea H sapien | 2.15 | 293T_cells, Lu_SC_H345, Lu_SC_H69 |
| 132876 | AA130603 | Hs.169683 | ESTs; Moderately similar to !!! ALU SUB | 2.15 | EB_cells, LNCaP_cells, HS578T_cells |
| 133834 | AA147510 | Hs.154737 | serine protease; umbilical endothelium | 2.15 | DU145_cells, EB_cells, Caco2 |
| 126908 | AA169866 | | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.15 | DU145_cells, LNCaP_cells, OVCAR_cells |
| 106900 | AA490142 | Hs.6193 | ESTs | 2.15 | Fibroblasts 2, Lu_AD_H23, PRSC_con |
| 129398 | AA437374 | Hs.234573 | H sapiens mRNA for TL132 | 2.15 | MCF7, DU145_cells, LNCaP_cells |
| 114512 | AA044274 | Hs.165215 | ESTs | 2.15 | Lu_AD_358, MB-MDA-453, HS578T_cells |
| 134381 | U56637 | Hs.184270 | capping protein (actin filament) muscle | 2.15 | LNCaP_cells, EB_cells, PC3_cells |
| 118848 | N80671 | Hs.220255 | ESTs | 2.14 | EB_cells, DU145_cells, MCF7 |
| 115526 | AA342049 | Hs.69606 | ESTs | 2.14 | 293T_cells, Caco2, Lu_SC_H69 |
| 123460 | AA598981 | Hs.251122 | EST | 2.14 | Lu_SC_H345, DU145_cells, MCF7 |
| 119812 | W73951 | Hs.58348 | ESTs; Weakly similar to CORNIFIN A [H.sa | 2.14 | 293T_cells, HS578T_cells, CALU6_cells |
| 105263 | AA227926 | Hs.6682 | ESTs | 2.14 | A549_cells, HMEC (total RNA), EB_cells |
| 129242 | W81679 | Hs.5174 | ribosomal protein S17 | 2.14 | 293T_cells, CALU6_cells, HMEC (total RNA) |
| 132348 | AA037285 | Hs.170311 | heterogeneous nuclear ribonucleoprotein | 2.14 | A549_cells, HT29_cells, Lu_SC_H520 |
| 114425 | AA015763 | Hs.132812 | ESTs | 2.14 | 293T_cells, HS578T_cells, PRSC_con |
| 127759 | AI369384 | | arylsulfatase D | 2.14 | DU145_cells, LNCaP_cells, EB_cells |
| 134069 | U29607 | Hs.78935 | methionine aminopeptidase; eIF-2-associa | 2.14 | Lu_SC_H345, DU145_cells, MCF7 |
| 116158 | AA461187 | Hs.61762 | ESTs | 2.14 | Lu_SC_H69, MCF7, MB-MDA-453 |
| 125627 | R35166 | Hs.14881 | ESTs | 2.14 | HT29_cells, Fibroblasts 2, BT474_cells |
| 118684 | N71364 | Hs.109510 | ESTs | 2.14 | OVCAR_cells, PRSC_con, HS578T_cells |
| 119419 | T97977 | Hs.60260 | ESTs | 2.14 | Lu_AD_H23, Lu_SC_H520, Lu_SC_H520 |
| 133097 | N67515 | Hs.6479 | ESTs; Weakly similar to KIAA0872 protein | 2.14 | EB_cells, Lu_AD_H23, Lu_AD_358 |
| 112121 | R45445 | Hs.252723 | H sapiens mRNA; cDNA DKFZp434D115 (from | 2.14 | 2.13 Lu_AD_H23, Lu_AD_358, BT474_cells |
| 114894 | AA236019 | Hs.188803 | ESTs | 2.13 | MB-MDA-453, MCF7, Lu_SC_H520 |
| 124087 | H08773 | | yf94d5.s1 Soares infant brain 1NIB H sap | 2.13 | Lu_SC_H69, Fibroblasts 2, HMEC (total RNA) |
| 111902 | R39191 | Hs.109445 | KIAA1020 protein | 2.13 | Caco2, 293T_cells, Lu_SC_H69 |
| 119943 | W86835 | Hs.14158 | copine III | 2.13 | LNCaP_cells, PC3_cells, HS578T_cells |
| 109276 | AA196306 | Hs.86045 | ESTs | 2.13 | Lu_SC_H345, Lu_SC_H69, Lu_LC_H460 |
| 117351 | N24581 | Hs.43230 | ESTs | 2.13 | HS578T_cells, CALU6_cells, PRSC_con |
| 116046 | AA453461 | Hs.94491 | H sapiens clone 23585 mRNA seq | 2.13 | LNCaP_cells, Caco2, EB_cells |
| 112785 | R98478 | Hs.16586 | ESTs | 2.13 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 115835 | AA428576 | Hs.41371 | ESTs | 2.13 | EB_cells, Lu_SC_H345, OVCAR_cells |
| 127499 | T49891 | Hs.119252 | tumor protein; translationally-controld | 2.13 | EB_cells, PRSC_con, LNCaP_cells |
| 129951 | AA019475 | Hs.74615 | platelet-derived growth factor receptor; | 2.13 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 124270 | H79560 | Hs.107840 | ESTs | 2.13 | OVCAR_cells, 293T_cells, 293T_cells |
| 133766 | D52420 | Hs.184326 | cell division cycle 10 (homologous to CD | 2.12 | CALU6_cells, DU145_cells, PC3_cells |
| 109248 | AA194720 | Hs.189996 | ESTs; Highly similar to sec61 homolog [H | 2.12 | HT29_cells, MB231_cells, HMEC (total RNA) |
| 106724 | AA465226 | Hs.28631 | ESTs | 2.12 | EB_cells, 293T_cells, DU145_cells |
| 100571 | HG2264-H | | Atpase, Ca2+ Transporting, Plasma Membra | 2.12 | EB_cells, Lu_AD_H23, Lu_SC_H69 |
| 133017 | AA450187 | Hs.178518 | ESTs | 2.12 | OVCAR_cells, PC3_cells, 293T_cells |
| 124313 | H94650 | Hs.108002 | ESTs | 2.12 | MB-MDA-453, Lu_SC_H345, HT29_cells |
| 113059 | T26925 | Hs.172684 | vesicle-associated membrane protein 8 (e | 2.12 | MB-MDA-453, PC3_cells, LNCaP_cells |
| 113241 | T63313 | Hs.226136 | ESTs; Moderately similar to !!! ALU SUB | 2.12 | HMEC (total RNA), BT474_cells, HMEC |
| 111952 | R40782 | Hs.21296 | ESTs | 2.12 | HT29_cells, PC3_cells, A549_cells |
| 113965 | W86519 | Hs.19631 | ESTs | 2.12 | PC3_cells, EB_cells, LNCaP_cells |
| 108059 | AA043944 | Hs.62663 | ESTs | 2.12 | EB_cells, OVCAR_cells, 293T_cells |
| 124235 | H63994 | Hs.221134 | ESTs | 2.12 | Fibroblasts 2, MB-MDA-453, PRSC_con |
| 106400 | AA447621 | Hs.31257 | ESTs | 2.12 | DU145_cells, EB_cells, Caco2 |
| 119590 | W44798 | Hs.55876 | ESTs | 2.12 | PRSC_log, Lu_SC_H69, Lu_SC_H345 |
| 112434 | R63068 | Hs.159793 | EST | 2.11 | HS578T_cells, LNCaP_cells, OVCAR_cells |
| 122731 | AA457549 | | aa92b1.s1 Stratagene fetal retina 93722 gb:X5275_ma3 LEUKOSIALIN PRECURSOR (HU | 2.11 | 2.11 MB-MDA-453, RPWE_2, MCF7 |
| 115348 | AA281562 | Hs.88860 | ESTs | 2.11 | EB_cells, Lu_AD_H23, Fibroblasts 2 |
| 128873 | AA226768 | Hs.109463 | ESTs; Weakly similar to predicted using | 2.11 | MB-MDA-453s, EB_cells, LNCaP_cells |
| 133742 | T54301 | Hs.75844 | ESTs | 2.11 | EB_cells, CALU6_cells, DU145_cells |
| 102099 | U11870 | Hs.194778 | interleukin 8 receptor; alpha | 2.11 | Lu_AD_358, PC3_cells, PRSC_con |
| 125840 | H05787 | Hs.12064 | ubiquitin specific protease 22 | 2.11 | EB_cells, LNCaP_cells, Caco2 |
| 105501 | AA255604 | Hs.31930 | ESTs | 2.1 | Fibroblasts 2, HS578T_cells, MB-MDA-453s |
| 111576 | R10334 | Hs.15489 | ESTs | 2.1 | Lu_SC_H69, PRSC_log, Lu_SC_H345 |
| 104275 | C02170 | Hs.39387 | ESTs; Weakly similar to weak similarity | 2.1 | HT29_cells, MB231_cells, Lu_SC_H69 |
| 117803 | N48620 | Hs.28483 | pregnancy specific beta-1-glycoprotein 9 | 2.1 | HT29_cells, HMEC, RPWE_2 |

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|--------|----------|-----------|---|------|--|
| 122725 | AA457407 | Hs.152204 | transmembrane protease; serine 2 | 2.1 | |
| 120987 | AA398233 | Hs.111894 | KIAA0108 gene product | 2.1 | |
| 105932 | AA403305 | Hs.12185 | ESTs; Weakly similar to myosin phosphata | 2.1 | |
| 118398 | N64706 | Hs.137282 | ESTs | 2.1 | |
| 103679 | ZB60000 | | Human DNA seq from PAC 151B14 on chromosome 10 | | |
| 130303 | L40392 | Hs.180789 | receptor subtype 3 (SSTR3), tRNA, ESTs, H. sapiens (clone S164) mRNA; 3' end of c | 2.1 | |
| 122815 | AA461080 | Hs.139446 | ESTs | 2.1 | |
| 105598 | AA279439 | Hs.20594 | ESTs; Weakly similar to misato [D.melanogaster] | 2.1 | |
| 124869 | R69088 | Hs.28728 | ESTs; Weakly similar to F55A12.9 [C.elegans] | 2.1 | |
| 129599 | F10720 | Hs.180804 | ESTs | 2.1 | |
| 110338 | H40359 | Hs.177256 | ESTs | 2.09 | |
| 134092 | H17490 | Hs.7905 | ESTs; Highly similar to sorting nexin 9 | 2.09 | |
| 133002 | AF006082 | Hs.62461 | ARP2 (actin-related protein 2; yeast) homolog | 2.09 | |
| 115570 | AA398343 | Hs.94943 | ESTs | 2.09 | |
| 120055 | W93299 | Hs.59363 | ESTs; Weakly similar to cytokeratin 20 [H.sapiens] | 2.09 | |
| 116332 | AA491208 | Hs.62620 | ESTs | 2.09 | |
| 105415 | AA243768 | Hs.4232 | ESTs; Highly similar to match to ESTs Z4 | 2.09 | |
| 116607 | D80354 | Hs.256321 | EST | 2.09 | |
| 126731 | AA593973 | Hs.232217 | ESTs; Weakly similar to !!!! ALU SUBFAMILY 1 | 2.09 | |
| 102276 | U30999 | Hs.10247 | activated leucocyte cell adhesion molecule | 2.09 | |
| 113666 | T96077 | Hs.17738 | EST | 2.09 | |
| 101183 | L19779 | Hs.795 | H2A histone family; member O | 2.09 | |
| 112177 | R49025 | Hs.22996 | ESTs | 2.09 | |
| 115038 | AA252360 | Hs.87968 | ESTs | 2.08 | |
| 109638 | F04432 | Hs.17904 | ESTs | 2.08 | |
| 109592 | W02475 | Hs.26370 | ESTs | 2.08 | |
| 133740 | U68142 | Hs.170160 | RAB2; member RAS oncogene family-like | 2.08 | |
| 126716 | AA031700 | Hs.251962 | ESTs | 2.08 | |
| 124055 | F10904 | Hs.100516 | H.sapiens clone 23605 mRNA seq | 2.08 | |
| 112823 | T66813 | Hs.12947 | EST | 2.08 | |
| 120097 | W95068 | Hs.59621 | ESTs | 2.08 | |
| 102066 | U08471 | Hs.352 | folate receptor 3 (gamma) | 2.08 | |
| 108712 | AA121993 | | zm24d11.s1 Stratagene pancreas (#93728) similar to gb:Y433 GLUTATHIONE PEROXIDASE | | |
| 134453 | X70683 | Hs.83484 | SRY (sex determining region Y)-box 4 | 2.08 | |
| 103883 | AA232836 | Hs.87363 | ESTs | 2.08 | |
| 105313 | AA233856 | Hs.16930 | ESTs | 2.08 | |
| 113669 | T96148 | Hs.17762 | ESTs | 2.08 | |
| 120380 | AA227904 | Hs.104223 | ESTs | 2.08 | |
| 121045 | AA398554 | Hs.181012 | double-stranded RNA-binding zinc finger | 2.08 | |
| 104949 | AA070735 | Hs.146090 | ESTs | 2.08 | |
| 118751 | N74210 | Hs.50454 | EST | 2.08 | |
| 112399 | R60920 | Hs.26419 | H.sapiens clone 24510 mRNA seq | 2.08 | |
| 129994 | AA599943 | Hs.38194 | ESTs; Moderately similar to !!!! ALU SUB | 2.08 | |
| 116402 | AA600054 | Hs.65302 | ESTs | 2.08 | |
| 125307 | Z40583 | Hs.101259 | ESTs | 2.08 | |
| 105047 | AA132453 | Hs.15396 | ESTs | 2.08 | |
| 128659 | T95280 | Hs.103315 | trinucleotide repeat containing 1 | 2.08 | |
| 122301 | AA437378 | Hs.98791 | ESTs | 2.08 | |
| 121974 | AA428804 | Hs.229675 | EST | 2.08 | |
| 116905 | H71420 | | y83c12.s1 Soares fatal liver spleen 1NFL | | |
| | | | 3' similar to contains Alu repetitive e | | |
| | | | KIAA0782 protein | | |
| 106703 | AA463979 | Hs.21264 | ESTs | 2.08 | |
| 121908 | AA427858 | Hs.98534 | EST | 2.07 | |
| 135119 | T23992 | Hs.94769 | ESTs; Moderately similar to RAS-RELATED | 2.07 | |
| 103558 | Z19574 | Hs.2785 | keratin 17 | 2.07 | |
| 124209 | H57317 | Hs.193433 | ESTs | 2.07 | |
| 133936 | AA045083 | Hs.77719 | gamma-glutamyl carboxylase | 2.07 | |
| 116246 | AA479961 | Hs.42913 | ESTs; Highly similar to ubiquitin-conjug | 2.07 | |
| 123230 | AA490134 | Hs.105308 | EST | 2.07 | |
| 127378 | AA452696 | | z39b05.1 Soares_total_fetus_Nb2HF8_9w | | |
| | | | to contains Alu repetitive elementcont | | |
| 110464 | H53013 | Hs.221901 | ESTs | 2.07 | |
| 135191 | X07619 | Hs.169876 | cytochrome P450; subfamily IID (debrisoq polypeptide 7a (pseudogene)) | 2.07 | |
| 101267 | L36818 | Hs.75339 | inositol polyphosphate phosphatase-like | 2.07 | |
| 105185 | AA191495 | Hs.189937 | ESTs | 2.07 | |
| 125366 | H60192 | Hs.76853 | ESTs; Weakly similar to human homolog of | 2.07 | |
| 117472 | N30131 | Hs.93738 | DKFZP434M098 protein | 2.07 | |
| 114235 | Z39710 | Hs.25341 | ESTs | 2.07 | |
| 109081 | AA165268 | Hs.72488 | ESTs | 2.07 | |
| 112596 | R78212 | Hs.163705 | ESTs | 2.07 | |
| 109254 | AA194940 | Hs.85956 | ESTs; Weakly similar to line-1 protein O | 2.07 | |
| 105898 | AA401144 | Hs.27354 | ESTs | 2.07 | |
| 116280 | AA488691 | Hs.57969 | phenylalanine-tRNA synthetase | 2.06 | |

| | | | | | |
|--------|----------|-----------|--|------|--|
| 122529 | AA449828 | Hs.99229 | ESTs | 2.06 | |
| 104612 | R99199 | Hs.173063 | transducin-like enhancer of split 2; hom | 2.06 | |
| 116465 | AA621650 | Hs.41045 | ESTs; Weakly similar to KIAA0734 protein | 2.06 | |
| 123155 | AA488414 | Hs.76127 | hcd (homologous to the E6-AP (UBE3A) ca domain (RLD) 1 | 2.06 | |
| 126752 | AI073373 | Hs.183275 | ESTs | 2.06 | |
| 126455 | N80749 | Hs.111515 | ESTs; Weakly similar to predicted using | 2.06 | |
| 129339 | R77869 | Hs.28506 | ESTs | 2.06 | |
| 115021 | AA252028 | Hs.39168 | ESTs | 2.06 | |
| 129054 | T67231 | Hs.168289 | succinate dehydrogenase complex; subunit | 2.06 | |
| 101261 | L35545 | Hs.82353 | endothelial cell protein C/activated pro | 2.06 | |
| 132697 | AA281851 | Hs.5518 | H sapiens mRNA; cDNA DKFZp566J2146 (from | | |
| 124380 | N26536 | Hs.84999 | ATPase; Cu++ transporting; beta polypept | 2.06 | |
| 103967 | AA303711 | Hs.144700 | ephrin-B1 | 2.06 | |
| 119403 | T92935 | Hs.119908 | ESTs; Highly similar to nucleolar protel | 2.06 | |
| 125755 | R66080 | Hs.191268 | H sapiens mRNA; cDNA DKFZp34N174 (from | | |
| 101843 | M93405 | Hs.170008 | methylnalnate-semialdehyde dehydrogenas | 2.05 | |
| 113032 | T24024 | Hs.7387 | DKFZP564B116 protein | 2.05 | |
| 112563 | R72632 | Hs.29282 | ESTs | 2.05 | |
| 126432 | AA583825 | Hs.235860 | ESTs | 2.05 | |
| 101636 | M57763 | Hs.89474 | ADP-ribosylation factor 6 | 2.05 | |
| 125174 | W51835 | Hs.231082 | EST | 2.05 | |
| 106168 | AA425943 | Hs.82208 | acyl-Coenzyme A dehydrogenase; very long | 2.05 | |
| 135343 | AA236796 | Hs.9914 | follistatin | 2.05 | |
| 105267 | AA227956 | Hs.25348 | follistatin-like 3 (secreted glycoprotei | 2.05 | |
| 134331 | AA452020 | Hs.234155 | ESTs; Weakly similar to CGI-128 protein | 2.05 | |
| 121634 | AA417012 | Hs.28921 | ESTs | 2.05 | |
| 131394 | R72637 | Hs.26343 | ESTs | 2.05 | |
| 111526 | R08260 | Hs.20131 | ESTs | 2.05 | |
| 125049 | T79840 | Hs.111788 | ESTs | 2.05 | |
| 120433 | AA237077 | Hs.180777 | H sapiens mRNA; cDNA DKFZp564M0264 (from | | |
| 129498 | AA449789 | Hs.75511 | connective tissue growth factor | 2.05 | |
| 127805 | AA740921 | Hs.1197 | heat shock 10kD protein 1 (chaperonin 10 | 2.05 | |
| 109275 | AA195287 | Hs.20303 | ESTs; Moderately similar to !!! ALU SUB | 2.05 | |
| 120683 | AA290987 | Hs.49657 | ESTs; Weakly simila to contains simila | 2.04 | |
| 135415 | X60655 | Hs.99967 | even-skipped homeo box 1 (homolog of Dro | 2.04 | |
| 132925 | AA252759 | Hs.238296 | DKFZP434A033 protein | 2.04 | |
| 101875 | M97287 | Hs.74592 | special AT-rich seq binding protein 1 (b | 2.04 | |
| 101463 | M22490 | Hs.68879 | bone morphogenetic protein 4 | 2.04 | |
| 129177 | T95005 | Hs.209587 | ESTs | 2.04 | |
| 130726 | W88946 | Hs.18508 | putative glycine-N-acyltransferase | 2.04 | |
| 105549 | AA262417 | Hs.5415 | ESTs | 2.04 | |
| 124543 | NG3705 | Hs.104573 | ESTs | 2.04 | |
| 123062 | AA482069 | Hs.100847 | ESTs | 2.04 | |
| 109464 | AA232857 | Hs.87100 | ESTs | 2.04 | |
| 129619 | AA610116 | Hs.11663 | tetraspan NET-6 protein | 2.04 | |
| 127545 | AA935809 | Hs.115899 | ESTs | 2.04 | |
| 133068 | R73427 | Hs.235712 | ESTs | 2.04 | |
| 113609 | T93263 | Hs.16875 | ESTs; Weakly similar to hypothetical pro | 2.04 | |
| 106645 | AA460270 | Hs.27695 | midline 1 (Optz/BBB syndrome) | 2.04 | |
| 126256 | Z21124 | | HSAAADNVTE TEST1, Human adult Testis tiss | 2.04 | |
| 129697 | R00841 | Hs.172069 | DKFZP434C212 protein | 2.04 | |
| 126730 | T19477 | | A1426R Heart H sapiens cDNA clone A1426, | 2.04 | |
| 125244 | W86466 | Hs.132756 | ESTs; Weakly similar to KIAA0591 protein | 2.04 | |
| 134762 | M91036 | Hs.242985 | hemoglobin; gamma G | 2.04 | |
| 119564 | W38206 | | Accession not listed in Genbank | 2.04 | |
| 132523 | AB002332 | Hs.50722 | clock (mouse) homolog | 2.04 | |
| 127758 | AI337031 | Hs.180195 | ESTs | 2.04 | |
| 126471 | AA158755 | Hs.175652 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.04 | |
| 110911 | N45120 | Hs.22305 | ESTs | 2.03 | |
| 122317 | AA442742 | Hs.8693 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.03 | |
| 100253 | D38024 | Hs.247951 | Hmn facioscapulohumeral muscular dystro | 2.03 | |
| 120431 | AA236884 | Hs.247323 | H sapiens mRNA for G4 protein (G4 gene; | 2.03 | |
| 122449 | AA447638 | Hs.104977 | ESTs | 2.03 | |
| 100961 | J00148 | | Accession not listed in Genbank | 2.03 | |
| 130908 | W86389 | Hs.21122 | ESTs; Moderately similar to KIAA0438 [H. | 2.03 | |
| 102643 | U67849 | | Human beta-galactoside alpha2,6-sialyltr | 2.03 | |
| 127932 | AA398510 | Hs.133148 | ESTs | 2.03 | |
| 109207 | AA190906 | Hs.204692 | ESTs | 2.03 | |
| 102598 | U62962 | Hs.106673 | eukaryotic translation initiation factor | 2.03 | |
| 124470 | N51702 | Hs.101392 | ESTs | 2.03 | |
| 104961 | AA076672 | Hs.33905 | ESTs | 2.03 | |
| 124164 | H30667 | Hs.7535 | ESTs; Highly similar to COBW-like placen | 2.03 | |
| 126468 | AA242853 | Hs.237856 | ESTs; Moderately similar to cAMP inducib | 2.03 | |
| 129683 | W05348 | Hs.158186 | DKFZP434B103 protein | 2.03 | |
| 105350 | AA235737 | Hs.186571 | ATPase; Na+/K+ transporting; alpha 3 pol | 2.03 | |

| | | | | | |
|--------|------------|--|---|------|--|
| 129794 | AA447772 | Hs.14520 | eukaryotic translation initiation factor | 2.03 | |
| 115664 | AA405974 | Hs.54673 | tumor necrosis factor (ligand) superfamily | 2.03 | |
| 119096 | R41672 | Hs.91471 | ATPase type IV; phospholipid transportin | 2.03 | |
| 133866 | L38151 | Hs.171625 | phosphatidylinositol 4-kinase; catalytic | 2.03 | |
| 132055 | N69440 | Hs.38132 | ESTs | 2.03 | |
| 125691 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 2.03 | |
| 121376 | AA405699 | Hs.166232 | ESTs; Moderately similar to SODIUM-AND TRANSPORTER 2 [H.sapiens] | 2.03 | |
| 105289 | AA233178 | Hs.103000 | KIAA0831 protein | 2.02 | |
| 100967 | J02621 | Hs.251064 | high-mobility group (nonhistone chromoso | 2.02 | |
| 124430 | N38913 | Hs.221575 | ESTs | 2.02 | |
| 128322 | AI306331 | Hs.133296 | ESTs | 2.02 | |
| 131077 | X91809 | Hs.22698 | G alpha interacting protein | 2.02 | |
| 108033 | AA404923 | Hs.92200 | KIAA0480 gene product | 2.02 | |
| 107550 | AA01045 | Hs.46783 | ESTs | 2.02 | |
| 109475 | AA233159 | Hs.87131 | ESTs | 2.02 | |
| 111400 | R00144 | Hs.189771 | ESTs | 2.02 | |
| 117516 | N32495 | Hs.151560 | ESTs | 2.02 | |
| 120506 | AA257955 | Hs.173705 | ESTs; Weakly similar to !!! ALU CLASS C | 2.02 | |
| 130850 | N39306 | Hs.20237 | DKFZP566C134 protein | 2.02 | |
| 123118 | AA486571 | Hs.105696 | ESTs; Moderately similar to !!! ALU SUB | 2.02 | |
| 111285 | N71704 | Hs.4310 | eukaryotic translation initiation factor | 2.02 | |
| 119106 | R42362 | Hs.91785 | ESTs | 2.02 | |
| 111370 | N92915 | Hs.94631 | brefeldin A-inhibited guanine nucleotide | 2.02 | |
| 125013 | T67261 | Hs.154431 | ESTs; Weakly similar to neuronal thread | 2.02 | |
| 129762 | AA460273 | Hs.12372 | KIAA0517 protein | 2.02 | |
| 120704 | AA291970 | Hs.107054 | KIAA0821 protein | 2.01 | |
| 105355 | AA235985 | Hs.26938 | Human DNA seq from clone 126A5 on chromo genes (one with DnaJ domains); the gene family member HKR3. Contains ESTs; STSs; | 2.01 | |
| 125952 | AA017723 | | small inducible cytokine A5 (RANTES) | 2.01 | |
| 103478 | Y07755 | Hs.38991 | S100 calcium-binding protein A2 | 2.01 | |
| 133544 | T33873 | Hs.74624 | protein tyrosine phosphatase; receptor t | 2.01 | |
| 112746 | R93237 | | yq11e10.s1 Scores fetal liver spleen 1NF IMAGE:196650 3; mRNA seq. | 2.01 | |
| 118513 | N67504 | Hs.40061 | ESTs | 2.01 | |
| 123423 | AA598484 | Hs.238476 | EST | 2.01 | |
| 127654 | AA769520 | | ESTs; Weakly similar to REGULATOR OF MIT | | |
| | Lu_SQ_H520 | | | | |
| 111843 | R36969 | Hs.18888 | ESTs | 2.01 | |
| 100221 | D28383 | | Human mRNA for ATP synthase B chain, 5U | 2.01 | |
| 129966 | AA452237 | Hs.194443 | ESTs; Weakly similar to BC37295_2 [H.sap | 2.01 | |
| 106798 | AA478968 | Hs.20558 | ESTs | 2.01 | |
| 114636 | AA085374 | | zn13d5.s1 Stratagene hNT neuron (#937233 gb:18441 CYTOCHROME C OXIDASE POLYPEPTI | | |
| 125348 | H21585 | Hs.191277 | ESTs; Moderately similar to ATP binding | 2.01 | |
| 130620 | AA233245 | Hs.16773 | ESTs | 2.01 | |
| 105471 | AA450118 | Hs.25722 | ESTs; Weakly similar to ZINC FINGER PROT | 2.01 | |
| 134175 | T33128 | Hs.7966 | ESTs | 2 | |
| 117291 | N22289 | yw36g08.s1 Morton Fetal Cochlea H sapien | 2 | | |
| 134199 | U47635 | Hs.79877 | myotubularin related protein 6 | 2 | |
| 128758 | AA129545 | Hs.181165 | eukaryotic translation elongation factor | 2 | |
| 112005 | R42569 | Hs.22444 | ESTs | 2 | |
| 122521 | AA449433 | Hs.149227 | ESTs; Weakly similar to PROLINE-RICH PRO2 | | |
| 130356 | X84373 | Hs.155017 | nuclear receptor interacting protein 1 | 2 | |
| 114057 | Z38153 | Hs.26921 | ESTs | 2 | |
| 107136 | AA620795 | Hs.8207 | ESTs | 2 | |

Table 3

Pkey: Unique Eas probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UG_ID | Complete_Title | Ratio BS/Met | Top 3 expressing cell lines |
|--------|----------|-------------------------------|--|--------------|------------------------------------|
| 302347 | AF039400 | Hs.194659 | chloride channel; calcium activated; fam | 19.71 | EB, NCI-H520, NCI-H23 |
| 316304 | AI936587 | Hs.221599 | ESTs | 14.49 | PRSC_con, RPWE-2, OVCA-R |
| 339196 | | CH22_FF113D11.GENSCAN.3-1 | | 10.37 | NCI-H69, PRSC_con, NCI-H345 |
| 336171 | | CH22_FGENES.708_3 | | 9.45 | NCI-H69, NCI-H460, NCI-H23 |
| 338895 | | CH22_DJ32110.GENSCAN.9-2 | | 9.31 | PC3, BT474, OVCA-R |
| 333625 | | CH22_FGENES.223_2 | | 8.96 | NCI-H69, PRSC_con, NCI-H345 |
| 333730 | | CH22_FGENES.258_1 | | 8.82 | NCI-H69, BT474, MB-MDA-231 |
| 320244 | AA296922 | Hs.129778 | gastrointestinal peptide | 8.22 | BT474, CALU6, DU145 |
| 333643 | | CH22_FGENES.232_2 | | 7.66 | MCF7, NCI-H69, LnCap |
| 333423 | | CH22_FGENES.147_3 | | 7.57 | HT29, MB-MDA-231, EB |
| 302332 | AI833168 | Hs.184507 | H sapiens Chromosome 16 BAC clone C1T987 | 7.55 | MB-MDA-231, HT29, MB-MDA-453 |
| 333588 | | CH22_FGENES.206_2 | | 7.46 | HT29, OVCA-R, BT474 |
| 322033 | AL137507 | | EST cluster (not in UniGene) | 7.35 | PRSC_con, PRSC_log, NCI-H345 |
| 308601 | AI719930 | | EST singleton (not in UniGene) with exon | 6.83 | PC3, DU145, DU145 |
| 339044 | | CH22_DA59H18.GENSCAN.27-5 | | 6.46 | NCI-H69, NCI-H345, PRSC_log |
| 314516 | AA371513 | Hs.231748 | ESTs | 6.41 | EB, OVCA-R, Caco2 |
| 327805 | | CH.05_hs g 5867968 | | 6.28 | NCI-H69, NCI-H345, PRSC_con |
| 334239 | | CH22_FGENES.364_2 | | 6.09 | NCI-H520, MB-MDA-435s, MB-MDA-453 |
| 332958 | | CH22_FGENES.48_15 | | 6.04 | NCI-H69, PRSC_con, PRSC_log |
| 313386 | W85772 | Hs.173924 | ESTs | 5.88 | MB-MDA-231, OVCA-R, BT474 |
| 314350 | AL037927 | Hs.190675 | ESTs; Moderately similar to !!! ALU SUB | 5.84 | OVCA-R, CALU6, EB |
| 337170 | | CH22_FGENES.564-1 | | 5.67 | LnCap, CALU6, NCI-H69 |
| 337503 | | CH22_FGENES.803-1 | | 5.66 | NCI-H345, PRSC_con, RPWE-2 |
| 337562 | | CH22_C65E1.GENSCAN.1-2 | | 5.53 | HT29, MB-MDA-453, BT474 |
| 337219 | | CH22_FGENES.614-3 | | 5.45 | NCI-H69, NCI-H345, PRSC_log |
| 311331 | AI679622 | Hs.32225 | immunoglobulin alpha 1 | 5.43 | NCI-H69, NCI-H23, NCI-H345 |
| 314251 | AA713589 | | EST cluster (not in UniGene) | 5.41 | PC3, EB, LnCap |
| 336246 | | CH22_FGENES.746_5 | | 5.34 | NCI-H69, NCI-H345, PRSC_log |
| 335009 | | CH22_FGENES.472_13 | | 5.31 | EB, EB, NCI-H69 |
| 339365 | | CH22_BA354112.GENSCAN.34-1 | | 5.25 | PRSC_con, NCI-H69, PRSC_log |
| 336088 | | CH22_FGENES.688_17 | | 5.21 | PRSC_con, Caco2, PRSC_log |
| 334966 | | CH22_FGENES.465_36 | | 5.16 | DU145, BT474, MB-MDA-231 |
| 334666 | | CH22_FGENES.418_18 | | 5.15 | NCI-H69, NCI-H345, PRSC_log |
| 316830 | AW182106 | Hs.127821 | ESTs | 5.12 | NCI-H345, PRSC_con, PRSC_log |
| 339413 | | CH22_DJ579N16.GENSCAN.5-8 | | 5.06 | NCI-H69, NCI-H345, PRSC_log |
| 337951 | | CH22_EM:AC005500.GENSCAN.94-1 | | 5.01 | NCI-H345, NCI-H69, PRSC_con |
| 330153 | | CH.21_p2_g 4325335 | | 5 | PRSC_con, PRSC_log, NCI-H69 |
| 333987 | | CH22_FGENES.310_11 | | 4.96 | MB-MDA-231, MB-MDA-453, MB-MDA-453 |
| 334304 | | CH22_FGENES.373_7 | | 4.96 | OVCA-R, CALU6, NCI-H23 |
| 338990 | | CH22_DA59H18.GENSCAN.6-6 | | 4.95 | PRSC_log, PRSC_con, NCI-H69 |
| 333152 | | CH22_FGENES.89_1 | | 4.89 | MB-MDA-435s, OVCA-R, A549 |
| 327049 | | CH.21_hs g 6531965 | | 4.87 | PRSC_con, NCI-H345, PRSC_log |
| 337225 | | CH22_FGENES.626-3 | | 4.83 | DU145, CALU6, EB |
| 333496 | | CH22_FGENES.168_6 | | 4.81 | NCI-H69, NCI-H345, PRSC_con |
| 334451 | | CH22_FGENES.387_11 | | 4.79 | RPWE-2, PRSC_con, NCI-H69 |
| 333594 | | CH22_FGENES.210_3 | | 4.78 | OVCA-R, PC3, HT29 |
| 333635 | | CH22_FGENES.228_2 | | 4.78 | NCI-H69, PRSC_log, PRSC_con |
| 336796 | | CH22_FGENES.176-6 | | 4.73 | NCI-H69, NCI-H345, PRSC_log |
| 333313 | | CH22_FGENES.138_5 | | 4.72 | NCI-H69, NCI-H345, PRSC_log |
| 336833 | | CH22_FGENES.242-2 | | 4.7 | NCI-H345, NCI-H69, PRSC_con |
| 336090 | | CH22_FGENES.689_2 | | 4.7 | NCI-H69, PRSC_con, PRSC_log |
| 336645 | | CH22_FGENES.26-1 | | 4.63 | HT29, OVCA-R, DU145 |
| 334565 | | CH22_FGENES.405_5 | | 4.62 | NCI-H345, PRSC_log, RPWE-2 |
| 333242 | | CH22_FGENES.111_6 | | 4.56 | NCI-H345, PRSC_log, PRSC_con |
| 326304 | | CH.17_hs g 5867277 | | 4.48 | OVCA-R, EB, DU145 |
| 337445 | | CH22_FGENES.769-4 | | 4.47 | RPWE-2, NCI-H69, PRSC_log |
| 327413 | | CH.02_hs g 5867750 | | 4.46 | NCI-H69, PRSC_log, NCI-H345 |
| 327990 | | CH.06_hs g 5868218 | | 4.44 | PRSC_con, PRSC_log, RPWE-2 |
| 325038 | H38304 | Hs.21782 | ESTs | 4.43 | PRSC_con, MB-MDA-231, HT29 |
| 314923 | AI732489 | Hs.138370 | ESTs | 4.4 | HT29, MB-MDA-231, NCI-358 |
| 328859 | | CH.07_hs g 6381928 | | 4.4 | OVCA-R, BT474, A549 |
| 334476 | | CH22_FGENES.394_7 | | 4.38 | OVCA-R, PC3, EB |
| 336092 | | CH22_FGENES.689_6 | | 4.35 | PRSC_con, Caco2, PRSC_log |
| 333965 | | CH22_FGENES.305_3 | | 4.35 | NCI-H69, NCI-H345, PRSC_log |

| | | | | | |
|--------|----------|---------------------------------|--|------------------------------|---------------------------------|
| 336402 | | CH22_FGENES.823_17 | 4.34 | RPWE-2, HT29, OVCA-R | |
| 337947 | | CH22_EM:AC005500.GENSCAN.90-5 | 4.33 | OVCA-R, DU145, PC3 | |
| 337504 | | CH22_FGENES.803-2 | 4.33 | NCI-H345, PRSC_con, PRSC_log | |
| 336813 | | CH22_FGENES.213-6 | 4.33 | DU145, HT29, OVCA-R | |
| 338069 | | CH22_EM:AC005500.GENSCAN.166-14 | 4.33 | NCI-H69, PRSC_con, NCI-H345 | |
| 318538 | N28625 | Hs.74034 | caveolin 1; caveolae protein; 22kD | 4.31 | PC3, A549, BT474 |
| 333631 | | CH22_FGENES.227_2 | 4.3 | OVCA-R, PRSC_con, LnCap | |
| 302646 | M14268 | EST | | PRSC_con, PRSC_log, RPWE-2 | |
| 336049 | | CH22_FGENES.681_2 | 4.26 | HT29, DU145, DU145 | |
| 335667 | | CH22_FGENES.590_18 | 4.25 | NCI-H520, Caco2, MB-MDA-453 | |
| 320352 | Y13323 | Hs.145296 | disintegrin protease | 4.25 | MB-MDA-231, DU145, BT474 |
| 304480 | AA430373 | | EST singleton (not in UniGene) with exon | 4.22 | NCI-358, NCI-H460, NCI-H23 |
| 327273 | | CH.01_hs gl 5867466 | | NCI-H69, NCI-H345, PRSC_con | |
| 334540 | | CH22_FGENES.403_5 | 4.17 | NCI-H69, NCI-H345, PRSC_log | |
| 334719 | | CH22_FGENES.421_30 | 4.17 | NCI-H69, NCI-H345, RPWE-2 | |
| 327827 | | CH.05_hs gl 5867968 | 4.17 | OVCA-R, NCI-H69, CALU6 | |
| 333599 | | CH22_FGENES.212_2 | 4.17 | PRSC_log, NCI-H69, PRSC_con | |
| 329638 | | CH.12_p2 gl 3779004 | 4.16 | DU145, MB-MDA-231, HT29 | |
| 307556 | AI281651 | | EST singleton (not in UniGene) with exon | 4.16 | BT474, HT29, CALU6 |
| 336836 | | CH22_FGENES.247-11 | 4.15 | PRSC_con, NCI-H345, NCH-H69 | |
| 323187 | AL121180 | Hs.240038 | ESTs | 4.14 | NCI-H345, MB-MDA-435s, RPWE-2 |
| 336397 | | CH22_FGENES.823_12 | 4.13 | NCI-H345, PRSC_con, RPWE-2 | |
| 325007 | AA736429 | | EST cluster (not in UniGene) | 4.13 | NCI-H69, PRSC_con, NCI-H345 |
| 300199 | AI304386 | Hs.150836 | ESTs | 4.11 | NCI-H345, PRSC_con, PRSC_log |
| 335832 | | CH22_FGENES.620_6 | 4.08 | NCI-H69, NCI-H345, PRSC_log | |
| 312778 | AI631655 | Hs.197919 | ESTs | 4.07 | NCI-358, NCI-H23, PRSC_con |
| 323164 | AA765301 | Hs.151858 | ESTs | 4.06 | NCI-H23, A549, HT29 |
| 315871 | AW135312 | Hs.117237 | ESTs | 4.05 | MB-MDA-231, EB, MCF7 |
| 337452 | | CH22_FGENES.775-1 | 4.02 | PRSC_con, PRSC_log, NCH-H345 | |
| 335265 | | CH22_FGENES.521_1 | 4.01 | NCI-H69, MCF7, RPWE-2 | |
| 335200 | | CH22_FGENES.508_9 | 4.01 | NCI-H69, PRSC_log, PRSC_con | |
| 336917 | | CH22_FGENES.346-4 | 3.99 | PRSC_con, NCI-H345, PRSC_log | |
| 336584 | | CH22_FGENES.847_1 | 3.98 | PRSC_log, PRSC_con, RPWE-2 | |
| 333382 | | CH22_FGENES.143_21 | 3.97 | EB, A549, HT29 | |
| 329436 | | CH.Y_hs gl 5868883 | 3.97 | BT474, PC3, HT29 | |
| 336929 | | CH22_FGENES.349-3 | 3.94 | NCI-H69, NCI-H345, PRSC_log | |
| 337238 | | CH22_FGENES.641-3 | 3.92 | NCI-H69, NCI-H345, PRSC_log | |
| 333875 | | CH22_FGENES.291_11 | 3.92 | PRSC_con, RPWE-2, PRSC_log | |
| 337059 | | CH22_FGENES.448-2 | 3.9 | NCI-H69, LnCap, RPWE-2 | |
| 332491 | M24470 | Hs.1435 | guanosine monophosphate reductase | 3.86 | OVCA-R, MB-MDA-435s, CALU6 |
| 304623 | AA521331 | | EST singleton (not in UniGene) with exon | 3.86 | OVCA-R, DU145, PC3 |
| 335348 | | CH22_FGENES.537_4 | 3.85 | HT29, MB-MDA-231, PC3 | |
| 334568 | | CH22_FGENES.405_9 | 3.85 | NCI-H69, NCI-H345, PRSC_log | |
| 336924 | | CH22_FGENES.347-9 | 3.84 | NCI-H345, PRSC_log, RPWE-2 | |
| 301654 | H81795 | | EST | 3.84 | NCI-H520, LnCap, NCI-358 |
| 334677 | | CH22_FGENES.418_30 | 3.83 | PRSC_con, NCI-H345, NCI-H69 | |
| 326688 | | CH.20_hs gl 5867582 | 3.83 | NCI-H345, PRSC_con, PRSC_log | |
| 327790 | | CH.05_hs gl 5867977 | 3.8 | PRSC_con, PRSC_log, NCH-H345 | |
| 334591 | | CH22_FGENES.408_1 | 3.8 | NCI-H69, PRSC_log, NCI-H345 | |
| 337974 | | CH22_EM:AC005500.GENSCAN.106-3 | 3.78 | PRSC_log, PRSC_con, NCI-H345 | |
| 311274 | AW293128 | Hs.197101 | ESTs | 3.78 | NCI-H345, PRSC_con, RPWE-2 |
| 326668 | | CH.20_hs gl 6552455 | 3.78 | NCI-H345, NCI-H69, PRSC_log | |
| 304195 | N35382 | | EST singleton (not in UniGene) with exon | 3.77 | NCI-H69, RPWE-2, PRSC_con |
| 336294 | | CH22_FGENES.786_4 | 3.77 | PRSC_con, PRSC_log, NCI-H69 | |
| 311613 | AL046311 | Hs.252443 | ESTs; Weakly similar to III ALU SUBFAMI | 3.76 | HT29, BT474, MB-MDA-231 |
| 338123 | | CH22_EM:AC005500.GENSCAN.195-5 | 3.75 | MB-MDA-231, HT29, BT474 | |
| 318230 | AA558125 | | EST cluster (not in UniGene) | 3.74 | RPWE-2, PRSC_con, NCI-H345 |
| 303985 | AW514501 | Hs.156110 | immunoglobulin kappa variable 1D-8 | 3.73 | MB-MDA-231, BT474, PRSC_con |
| 336502 | | CH22_FGENES.833_8 | 3.72 | NCI-H345, RPWE-2, PRSC_con | |
| 334063 | | CH22_FGENES.327_17 | 3.71 | NCI-H69, NCI-H345, PRSC_con | |
| 333600 | | CH22_FGENES.213_2 | 3.7 | NCI-H69, OVCA-R, PC3 | |
| 339424 | | CH22_DJ579N16.GENSCAN.14-3 | 3.69 | NCI-H69, NCI-H345, PRSC_con | |
| 336862 | | CH22_FGENES.297-2 | 3.67 | NCI-H345, PRSC_con, PRSC_log | |
| 334823 | | CH22_FGENES.437_5 | 3.67 | RPWE-2, PRSC_log, PRSC_con | |
| 329940 | | CH.16_p2 gl 5165199 | 3.66 | CALU6, EB, MCF7 | |
| 300275 | AI632123 | Hs.231521 | ESTs | 3.66 | PRSC_con, NCI-H69, RPWE-2 |
| 328820 | | CH.07_hs gl 5868330 | 3.66 | NCI-H69, NCI-H345, PRSC_con | |
| 332398 | AA446446 | Hs.104788 | H sapiens clone 24554 unknown mRNA | 3.66 | PRSC_con, PRSC_log, NCI-H345 |
| 325791 | | CH.14_hs gl 6682476 | 3.65 | NCI-H345, BT474, LnCap | |
| 300672 | R14469 | Hs.256573 | ESTs | 3.65 | MCF7, MB-MDA-453, MB-MDA-435s |
| 338344 | | CH22_EM:AC005500.GENSCAN.312-8 | 3.65 | NCI-H345, PRSC_log, PRSC_con | |
| 333257 | | CH22_FGENES.118_5 | 3.65 | DU145, EB, OVCA-R | |
| 332140 | AA620724 | Hs.112890 | ESTs | 3.65 | MB-MDA-453, DU145, MCF7 |
| 337489 | | CH22_FGENES.799-2 | 3.63 | NCI-H345, NCI-H69, PRSC_log | |
| 305167 | AA663080 | | EST singleton (not in UniGene) with exon | 3.63 | OVCA-R, MB-MDA-231, MB-MDA-435s |
| 336200 | | CH22_FGENES.719_4 | 3.61 | NCI-H69, PRSC_log, NCI-H345 | |

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| 339208 | | CH22_FF113D11.GENSCAN.6-3 | 3.59 | PRSC_con, NCI-H69, PRSC_log |
| 320090 AB002058 | Hs.113275 | purinergic receptor P2X-like 1; orphan r | 3.58 | OVCA-R, LnCap, NCI-H69 |
| 335999 | | CH22_FGENES.657_1 | 3.57 | NCI-H345, NCI-H69, PRSC_con |
| 332909 | | CH22_FGENES.36_13 | 3.57 | NCI-H345, PRSC_con, PRSC_log |
| 306531 AA991423 | | EST singleton (not in UniGene) with exon | 3.56 | BT474, MB-MDA-453, MB-MDA-435s |
| 333261 | | CH22_FGENES.119_1 | 3.55 | HT29, CALU6, MB-MDA-231 |
| 303883 AA176396 | Hs.169624 | ESTs | 3.54 | NCI-H69, NCI-H345, RPWE-2 |
| 335831 | | CH22_FGENES.620_5 | 3.53 | MCF7, BT474, OVCA-R |
| 333983 | | CH22_FGENES.310_7 | 3.52 | NCI-H345, PRSC_con, PRSC_log |
| 333623 | | CH22_FGENES.222_2 | 3.51 | NCI-H69, PRSC_con, PRSC_log |
| 333997 | | CH22_FGENES.310_22 | 3.5 | NCI-H345, PRSC_con, PRSC_log |
| 325623 | | CH.14_hs gj 5867000 | 3.5 | CALU6, HT29, BT474 |
| 309151 AI935829 | Hs.140 | immunglobulin gamma 3 (Gm marker) | 3.49 | EB, MCF7, MB-MDA-453 |
| 305080 AA641485 | | EST singleton (not in UniGene) with exon | 3.49 | NCI-H23, NCI-H460, NCI-358 |
| 339268 | | CH22_BA354112.GENSCAN.10-6 | 3.47 | NCI-H69, NCI-H345, PRSC_con |
| 310048 AI198352 | Hs.105077 | ESTs | 3.47 | Caco2, PRSC_con, NCI-H69 |
| 314758 AA521458 | Hs.192738 | ESTs | 3.46 | NCI-H23, NCI-H23, NCI-H520 |
| 334664 | | CH22_FGENES.418_15 | 3.45 | NCI-H69, PRSC_log, PRSC_con |
| 334661 | | CH22_FGENES.418_9 | 3.45 | NCI-H69, PRSC_con, PRSC_log |
| 330984 H38678 | Hs.32766 | H sapiens clone 24803 mRNA seq | 3.44 | OVCA-R, MCF7, PC3 |
| 333464 | | CH22_FGENES.160_1 | 3.44 | NCI-H69, MB-MDA-231, MCF7 |
| 333580 | | CH22_FGENES.199_2 | 3.42 | PRSC_con, NCI-H69, PRSC_log |
| 313356 AI266254 | Hs.132929 | ESTs | 3.42 | RPWE-2, PRSC_con, NCI-H345 |
| 334518 | | CH22_FGENES.400_1 | 3.41 | PRSC_log, PRSC_con, RPWE-2 |
| 333627 | | CH22_FGENES.225_2 | 3.4 | HT29, BT474, BT474 |
| 309641 AW194230 | Hs.253100 | EST | 3.4 | HT29, MB-MDA-453, MCF7 |
| 338221 | | CH22_EMAC005500.GENSCAN.246-10 | 3.4 | NCI-H69, PRSC_log, NCI-H345 |
| 312993 AI392673 | Hs.125230 | ESTs | 3.4 | PRSC_log, NCI-H345, NCI-H345 |
| 318336 AI971806 | Hs.164158 | ESTs | 3.38 | OVCA-R, EB, CALU6 |
| 326218 | | CH.17_hs gj 5867226 | 3.38 | NCI-H460, NCI-H69, NCI-H345 |
| 336231 | | CH22_FGENES.736_3 | 3.38 | NCI-H69, NCI-H345, PRSC_log |
| 307912 AI382224 | | EST singleton (not in UniGene) with exon | 3.37 | NCI-H345, PRSC_con, RPWE-2 |
| 336161 | | CH22_FGENES.707_6 | 3.37 | NCI-H69, NCI-H345, RPWE-2 |
| 300875 AW134756 | Hs.192477 | ESTs | 3.37 | RPWE-2, PRSC_log, PRSC_con |
| 336593 | | CH22_FGENES.135_1 | 3.37 | PRSC_con, NCI-H69, RPWE-2 |
| 310696 AI431620 | Hs.160875 | ESTs | 3.36 | HT29, OVCA-R, BT474 |
| 304745 AA577771 | | EST singleton (not in UniGene) with exon | 3.36 | NCI-H345, RPWE-2, PRSC_con |
| 308911 AI860287 | Hs.156110 | immunglobulin kappa variable 1D-8 | 3.36 | EB, DU145, CALU6 |
| 336347 | | CH22_FGENES.815_3 | 3.36 | NCI-H69, PRSC_log, PRSC_con |
| 334906 | | CH22_FGENES.452_21 | 3.33 | Caco2, CALU6, MB-MDA-453 |
| 334548 | | CH22_FGENES.403_13 | 3.33 | NCI-H345, PRSC_con, NCI-H69 |
| 336695 | | CH22_FGENES.48-4 | 3.32 | NCI-H69, PRSC_log, PRSC_con |
| 316684 AA807187 | Hs.220783 | ESTs; Weakly similar to WNT-1 PROTO-ONCO | 3.31 | DU145, EB, MB-MDA-231 |
| 315901 AI521558 | Hs.179718 | v-myb avian myeloblastosis viral oncogen | 3.3 | Caco2, LnCap, NCI-H69 |
| 320115 T93574 | | EST cluster (not in UniGene) | 3.3 | DU145, HT29, CALU6 |
| 307847 AI363993 | Hs.157273 | EST | 3.3 | NCI-H345, PRSC_con, PRSC_log |
| 327899 | | CH.06_hs gj 5868156 | 3.28 | BT474, MB-MDA-231, A549 |
| 304612 AA514207 | | EST singleton (not in UniGene) with exon | 3.28 | DU145, CALU6, LnCap |
| 330021 | | CH.16_p2_gj 6671889 | 3.27 | A549, HT29, EB |
| 338132 | | CH22_EMAC005500.GENSCAN.200-2 | 3.27 | MB-MDA-231, CALU6, EB |
| 323690 AA317497 | Hs.188897 | ESTs | 3.27 | RPWE-2, NCI-H345, MCF7 |
| 327362 | | CH.01_hs gj 58552412 | 3.26 | NCI-H69, RPWE-2, PRSC_log |
| 333488 | | CH22_FGENES.167_3 | 3.26 | NCI-H69, NCI-H345, PRSC_log |
| 334106 | | CH22_FGENES.330_5 | 3.26 | NCI-H69, PRSC_con, PRSC_log |
| 306990 AI129298 | Hs.146491 | EST; Weakly similar to FERRITIN HEAVY CH | 3.26 | NCI-H345, PRSC_log, PRSC_con |
| 328420 | | CH.07_hs gj 5868411 | 3.26 | NCI-H69, NCI-H345, PRSC_log |
| 336214 | | CH22_FGENES.722_8 | 3.26 | MCF7, EB, OVCA-R |
| 330565 U51095 | Hs.1545 | caudal type homeo box transcription fact | 3.25 | EB, DU145, HT29 |
| 333879 | | CH22_FGENES.291_15 | 3.25 | PRSC_con, PRSC_log, NCI-H69 |
| 300145 AI240850 | Hs.232016 | ESTs | 3.25 | NCI-H345, PRSC_con, PRSC_log |
| 327581 | | CH.03_hs gj 5867825 | 3.25 | EB, DU145, MB-MDA-453 |
| 308153 AI500429 | Hs.1103 | transforming growth factor, beta 1 | 3.24 | MCF7, EB, EB |
| 308337 AI608947 | | EST singleton (not in UniGene) with exon | 3.24 | PRSC_log, PRSC_con, NCI-H345 |
| 329406 | | CH.X_hs gj 6682547 | 3.23 | DU145, HT29, MB-MDA-231 |
| 325482 | | CH.12_hs gj 5866957 | 3.23 | NCI-H69, NCI-H345, PRSC_con |
| 337544 | | CH22_FGENES.833-7 | 3.22 | NCI-H69, NCI-H345, PRSC_con |
| 337204 | | CH22_FGENES.595-1 | 3.22 | NCI-H69, PRSC_con, PRSC_log |
| 309451 AW105128 | Hs.246687 | EST | 3.22 | PRSC_con, RPWE-2, NCI-H345 |
| 337259 | | CH22_FGENES.649-3 | 3.2 | PRSC_con, NCI-H345, NCI-H69 |
| 336489 | | CH22_FGENES.831_10 | 3.2 | CALU6, MB-MDA-435s, Caco2 |
| 334804 | | CH22_FGENES.435_4 | 3.18 | PRSC_log, PRSC_con, RPWE-2 |
| 335739 | | CH22_FGENES.601_10 | 3.18 | NCI-H69, RPWE-2, PRSC_con |
| 306264 AA935305 | Hs.179779 | ribosomal protein L37 | 3.17 | LnCap, NCI-H69, EB |
| 329386 | | CH.X_hs gj 6004484 | 3.17 | RPWE-2, NCI-H345, PRSC_log |
| 323479 AA278246 | | EST cluster (not in UniGene) | 3.16 | PRSC_con, NCI-H345, RPWE-2 |
| 304731 AA576085 | | EST singleton (not in UniGene) with exon | 3.16 | NCI-H69, LnCap, DU145 |

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| 339419 | | CH22_DJ579N16.GENSCAN.11-11 | 3.15 | NCI-H69, PRSC_log, RPWE-2 |
| 301202 | AI536797 | Hs.173155 ESTs | 3.15 | LnCap, NCI-H69, Caco2 |
| 333608 | | CH22_FGENES.216_3 | 3.15 | NCI-H345, PRSC_con, PRSC_log |
| 339193 | | CH22_FF113D11.GENSCAN.1-5 | 3.14 | NCI-H69, NCI-H345, PRSC_con |
| 310527 | AW293404 | Hs.211986 ESTs | 3.14 | PRSC_log, PRSC_con, RPWE-2 |
| 321146 | AA707443 | Hs.183983 ESTs | 3.14 | PRSC_con, NCI-H69, PRSC_log |
| 333271 | | CH22_FGENES.121_2 | 3.13 | NCI-H345, NCI-H69, RPWE-2 |
| 330280 | | CH.05_p2 gli6671910 | 3.13 | NCI-H69, NCI-H345, PRSC_log |
| 309977 | AW451663 | EST singleton (not in UniGene) with exon | 3.13 | PRSC_con, PRSC_log, RPWE-2 |
| 307588 | AI285535 | EST singleton (not in UniGene) with exon | 3.13 | MB-MDA-231, BT474, BT474 |
| 330551 | U39840 | Hs.105440 hepatocyte nuclear factor 3; alpha | 3.13 | MB-MDA-453, LnCap, Caco2 |
| 314404 | AW104203 | Hs.157505 ESTs | 3.13 | DU145, EB, OVCA-R |
| 334030 | | CH22_FGENES.320_2 | 3.13 | NCI-H69, NCI-H345, PRSC_con |
| 309108 | AI925949 | EST singleton (not in UniGene) with exon | 3.13 | BT474, MCF7, EB |
| 317516 | AI733250 | Hs.192262 ESTs | 3.12 | OVCA-R, EB, MB-MDA-453 |
| 304161 | H71886 | EST singleton (not in UniGene) with exon | 3.12 | PRSC_con, NCI-H69, RPWE-2 |
| 334590 | | CH22_FGENES.407_13 | 3.12 | NCI-H69, NCI-H345, PRSC_con |
| 333408 | | CH22_FGENES.145_6 | 3.11 | PRSC_log, RPWE-2, PRSC_con |
| 330387 | H14624 | Hs.31386 ESTs; Highly similar to secreted apoptosis | 3.11 | DU145, OVCA-R, PC3 |
| 332567 | N23730 | Hs.25647 v-fos FBJ murine osteosarcoma viral onco | 3.11 | EB, MB-MDA-453, MCF7 |
| 333682 | | CH22_FGENES.247_10 | 3.1 | PRSC_con, PRSC_log, RPWE-2 |
| 323152 | AI680562 | Hs.246192 ESTs; Weakly similar to REGULATOR OF MIT | 3.1 | 3.1 PC3, MB-MDA-453, DU145 |
| 311142 | AI638441 | Hs.195649 ESTs | 3.1 | PRSC_con, RPWE-2, PRSC_log |
| 333441 | | CH22_FGENES.151_5 | 3.1 | RPWE-2, NCI-H345, PRSC_log |
| 326459 | | CH.19_hs gli5867400 | 3.09 | EB, CALU6, PC3 |
| 313493 | AA910339 | Hs.126868 ESTs | 3.09 | NCI-H345, PRSC_con, RPWE-2 |
| 339356 | | CH22_BA354112.GENSCAN.31-1 | 3.08 | NCI-H69, NCI-H345, PRSC_log |
| 333629 | | CH22_FGENES.226_5 | 3.08 | NCI-H69, NCI-H345, PRSC_log |
| 304127 | H42981 | EST singleton (not in UniGene) with exon | 3.07 | LnCap, PRSC_con, DU145 |
| 325691 | | CH.14_hs gli5867021 | 3.07 | NCI-H345, PRSC_con, NCI-H69 |
| 333014 | | CH22_FGENES.61_6 | 3.07 | PRSC_con, PRSC_log, NCI-H345 |
| 327379 | | CH.02_hs gli5867795 | 3.07 | PRSC_con, PRSC_log, NCI-H69 |
| 337816 | | CH22_EMAC005500.GENSCAN.13-1 | 3.06 | NCI-H69, PRSC_con, PRSC_log |
| 337954 | | CH22_EMAC005500.GENSCAN.96-3 | 3.06 | PRSC_log, NCI-H69, NCI-H345 |
| 328109 | | CH.08_hs gli5868020 | 3.05 | HT29, BT474, MB-MDA-231 |
| 338527 | | CH22_EMAC005500.GENSCAN.396-15 | 3.05 | NCI-H69, NCI-H345, PRSC_con |
| 320083 | T87761 | EST cluster (not in UniGene) | 3.05 | BT474, MB-MDA-453, MCF7 |
| 333466 | | CH22_FGENES.161_2 | 3.05 | NCI-H345, RPWE-2, PRSC_log |
| 334788 | | CH22_FGENES.432_13 | 3.04 | EB, A549, CALU6 |
| 302681 | X97550 | EST | 3.04 | OVCA-R, EB, MB-MDA-453 |
| 336238 | | CH22_FGENES.743_3 | 3.03 | NCI-H69, PRSC_log, PRSC_con |
| 337606 | | CH22_C20H12.GENSCAN.17-2 | 3.02 | HT29, BT474, MB-MDA-231 |
| 333545 | | CH22_FGENES.180_1 | 3.02 | NCI-H69, NCI-H345, RPWE-2 |
| 309782 | AW275156 | Hs.156110 immunoglobulin kappa variable 1D-8 | 3.02 | PRSC_log, PRSC_con, RPWE-2 |
| 324277 | AA429440 | Hs.207285 ESTs | 3.02 | BT474, MB-MDA-231, HT29 |
| 321074 | H38098 | Hs.32756 ESTs | 3.02 | PC3, BT474, MB-MDA-231 |
| 337094 | | CH22_FGENES.465-19 | 3.01 | PRSC_con, PRSC_log, RPWE-2 |
| 313913 | AW391342 | EST cluster (not in UniGene) | 3 | NCI-H345, RPWE-2, PRSC_log |
| 329140 | | CH.X_hs gli6017060 | 3 | EB, DU145, PC3 |
| 335331 | | CH22_FGENES.535_4 | 3 | MB-MDA-453, HT29, BT474 |
| 334627 | | CH22_FGENES.437_9 | 2.99 | CALU6, EB, DU145 |
| 326029 | | CH.17_hs gli5867176 | 2.99 | NCI-H345, RPWE-2, PRSC_con |
| 303100 | T09353 | EST | 2.99 | MB-MDA-453, NCI-H345, RPWE-2 |
| 328768 | | CH.07_hs gli6017031 | 2.99 | NCI-H345, PRSC_con, NCI-H69 |
| 329392 | | CH.X_hs gli5478815 | 2.98 | NCI-H69, NCI-H345, PRSC_con |
| 305168 | AA663105 | EST singleton (not in UniGene) with exon | 2.98 | LnCap, NCI-H345, MCF7 |
| 300992 | AA601213 | Hs.191798 ESTs | 2.98 | Caco2, HT29, NCI-358 |
| 334474 | | CH22_FGENES.394_5 | 2.98 | NCI-H69, PRSC_con, RPWE-2 |
| 322647 | AA007534 | Hs.125062 ESTs | 2.98 | HT29, OVCA-R, A549 |
| 310620 | AI341328 | Hs.178953 ESTs | 2.97 | PRSC_con, RPWE-2, PRSC_log |
| 328276 | | CH.07_hs gli6004471 | 2.97 | NCI-H345, NCI-H69, RPWE-2 |
| 331018 | N26904 | Hs.24048 ESTs; Weakly similar to FK506/rapamycin- | 2.96 | Caco2, NCI-H460, A549 |
| 321523 | H78472 | Hs.191325 ESTs; Weakly similar to cDNA EST yk414c9 | 2.96 | PRSC_con, PRSC_log, NCI-H345 |
| 339280 | | CH22_BA354112.GENSCAN.14-12 | 2.96 | NCI-H69, PRSC_log, NCI-H345 |
| 305867 | AAB86428 | EST singleton (not in UniGene) with exon | 2.96 | NCI-H520, NCI-358, MB-MDA-453 |
| 335755 | | CH22_FGENES.604_4 | 2.95 | EB, A549, MB-MDA-453 |
| 323907 | AI043098 | Hs.165387 ESTs | 2.95 | PRSC_con, NCI-H345, PRSC_log |
| 330370 | | CH.X_p2 gli6580495 | 2.95 | EB, DU145, MB-MDA-453 |
| 334529 | | CH22_FGENES.402_9 | 2.94 | EB, MCF7, DU145 |
| 339256 | | CH22_BA354112.GENSCAN.7-11 | 2.94 | NCI-H69, NCI-H345, PRSC_con |
| 334783 | | CH22_FGENES.432_8 | 2.94 | A549, Caco2, PC3 |
| 335266 | | CH22_FGENES.521_2 | 2.94 | NCI-H69, PRSC_con, PRSC_con |
| 323707 | AA845957 | Hs.128385 ESTs | 2.94 | NCI-H345, PRSC_con, PRSC_log |
| 336199 | | CH22_FGENES.719_3 | 2.93 | NCI-H69, NCI-H345, PRSC_log |
| 338326 | | CH22_EMAC005500.GENSCAN.308-2 | 2.93 | NCI-H69, NCI-H345, NCI-358 |
| 333652 | | CH22_FGENES.239_1 | 2.93 | PC3, OVCA-R, BT474 |

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| 336479 | | CH22_FGENES.829_39 | 2.92 | NCI-H69, PRSC_con, PRSC_log |
| 336086 | | CH22_FGENES.688_15 | 2.92 | PRSC_con, Caco2, CALU6 |
| 338516 | | CH22_EM:AC005500.GENSCAN.392-6 | 2.92 | NCI-H69, NCI-H345, PRSC_con |
| 320121 | T93657 | EST cluster (not in UniGene) | 2.92 | EB, BT474, HT29 |
| 305782 | AAB44730 | EST singleton (not in UniGene) with exon | 2.92 | MB-MDA-453, MCF7, DU145 |
| 339304 | | CH22_BA35412.GENSCAN.20-16 | 2.91 | PRSC_con, PRSC_log, NCI-H69 |
| 327472 | | CH.02_hs gj 5867775 | 2.91 | PRSC_log, PRSC_con, RPWE-2 |
| 311458 | AW139426 | Hs.244718 ESTs | 2.91 | PRSC_con, PRSC_log, RPWE-2 |
| 338431 | | CH22_EM:AC005500.GENSCAN.351-4 | 2.9 | BT474, MCF7, MB-MDA-453 |
| 339230 | | CH22_BA35412.GENSCAN.1-6 | 2.89 | NCI-H69, NCI-H345, PRSC_log |
| 320586 | NM_00365 | EST cluster (not in UniGene) | 2.89 | OVCA-R, HT29, MB-MDA-231 |
| 304777 | AA581692 | Hs.2186 eukaryotic translation elongation factor | 2.89 | OVCA-R, EB, MCF7 |
| 337768 | | CH22_EM:AC000097.GENSCAN.119-6 | 2.88 | NCI-H69, LnCap, DU145 |
| 319465 | AA319115 | Hs.191558 ESTs | 2.88 | NCI-H460, NCI-H520, NCI-358 |
| 318058 | W93011 | Hs.110155 ESTs | 2.87 | BT474, MB-MDA-453, MB-MDA-435s |
| 330958 | H08815 | Hs.159824 EST | 2.87 | OVCA-R, PC3, A549 |
| 334215 | | CH22_FGENES.357_7 | 2.87 | NCI-H69, PRSC_con, PRSC_log |
| 333568 | | CH22_FGENES.185_1 | 2.87 | PRSC_con, PRSC_log, NCI-H69 |
| 333142 | | CH22_FGENES.85_5 | 2.87 | NCI-H69, HT29, MB-MDA-453 |
| 330239 | | CH.05_p2 gj 6671857 | 2.87 | MB-MDA-453, MB-MDA-453, EB |
| 302120 | R55140 | Hs.31075 ESTs; Weakly similar to Weak similarity | 2.87 | CALU6, MB-MDA-435s, BT474 |
| 338679 | | CH22_EM:AC005500.GENSCAN.470-1 | 2.86 | NCI-H345, PRSC_log, PRSC_con |
| 329041 | | CH.X_hs gj 5868584 | 2.86 | LnCap, PRSC_con, RPWE-2 |
| 333541 | | CH22_FGENES.178_3 | 2.86 | NCI-H69, NCI-H345, PRSC_con |
| 337011 | | CH22_FGENES.427-6 | 2.86 | NCI-H69, PRSC_log, PRSC_con |
| 324031 | AA375646 | EST cluster (not in UniGene) | 2.86 | NCI-H345, PRSC_log, LnCap |
| 331842 | AA416586 | Hs.98232 ESTs | 2.86 | DU145, OVCA-R, HT29 |
| 338599 | | CH22_FGENES.350_3 | 2.85 | LnCap, NCI-H69, NCI-H345 |
| 337586 | | CH22_C20H12.GENSCAN.5-4 | 2.85 | NCI-H345, NCI-H69, PRSC_con |
| 336177 | | CH22_FGENES.712_2 | 2.85 | NCI-H69, PRSC_log, RPWE-2 |
| 337522 | | CH22_FGENES.819-1 | 2.85 | CALU6, OVCA-R, HT29 |
| 338596 | | CH22_EM:AC005500.GENSCAN.437-2 | 2.85 | NCI-H69, PRSC_con, NCI-H345 |
| 309522 | AW150044 | Hs.252259 ribosomal protein S3 | 2.85 | MB-MDA-453, MB-MDA-435s, MB-MDA-435s |
| 336981 | | CH22_FGENES.397-7 | 2.85 | NCI-H69, PRSC_con, PRSC_log |
| 330286 | | CH.05_p2 gj 6671913 | 2.84 | NCI-H345, PRSC_log, NCI-H69 |
| 333713 | | CH22_FGENES.251_2 | 2.84 | RPWE-2, PRSC_con, NCI-H69 |
| 335068 | | CH22_FGENES.483_5 | 2.83 | MB-MDA-231, NCI-H345, RPWE-2 |
| 305075 | AA641288 | Hs.181165 eukaryotic translation elongation factor | 2.83 | EB, LnCap, DU145 |
| 326380 | | CH.19_hs gj 5867327 | 2.82 | NCI-H69, PRSC_con, PRSC_log |
| 334970 | | CH22_FGENES.466_3 | 2.82 | PRSC_con, NCI-H69, RPWE-2 |
| 337097 | | CH22_FGENES.471-1 | 2.82 | NCI-H345, NCI-H69, PRSC_log |
| 323676 | A1702835 | EST cluster (not in UniGene) | 2.82 | LnCap, A549, CALU6 |
| 333785 | | CH22_FGENES.274_4 | 2.82 | OVCA-R, Caco2, MB-MDA-453 |
| 334175 | | CH22_FGENES.349_10 | 2.81 | RPWE-2, BT474, MCF7 |
| 337865 | | CH22_EM:AC005500.GENSCAN.46-5 | 2.81 | Caco2, NCI-H23, BT474 |
| 302585 | AA083564 | Hs.249220 H sapiens mRNA for hTbx2; complete cds | 2.81 | EB, DU145, MB-MDA-453 |
| 336623 | | CH22_FGENES.4-5 | 2.81 | NCI-H345, PRSC_con, NCI-H69 |
| 332854 | | CH22_FGENES.22_1 | 2.8 | RPWE-2, PRSC_log, PRSC_con |
| 336978 | | CH22_FGENES.384-10 | 2.8 | PRSC_con, NCI-H345, RPWE-2 |
| 326874 | | CH.20_hs gj 6682507 | 2.8 | RPWE-2, NCI-H345, PRSC_log |
| 315121 | AA565011 | Hs.105902 ESTs | 2.8 | NCI-H345, PRSC_log, RPWE-2 |
| 311185 | A1638294 | Hs.224665 ESTs | 2.8 | NCI-H69, NCI-H345, PRSC_log |
| 334682 | | CH22_FGENES.419_4 | 2.8 | NCI-H69, PRSC_log, RPWE-2 |
| 316845 | AW418715 | Hs.250388 ESTs | 2.79 | RPWE-2, NCI-H345, PRSC_log |
| 331599 | N74626 | Hs.50535 ESTs | 2.79 | A549, MB-MDA-453, MB-MDA-435s |
| 315681 | AW022054 | Hs.136591 ESTs | 2.78 | NCI-H460, MB-MDA-453, MCF7 |
| 313012 | A1207390 | Hs.143929 ESTs | 2.78 | DU145, MB-MDA-453, MCF7 |
| 313476 | AA010267 | EST cluster (not in UniGene) | 2.78 | NCI-H520, NCI-H460, HT29 |
| 327277 | | CH.01_hs gj 5867473 | 2.78 | DU145, CALU6, EB |
| 310981 | A1494514 | Hs.171380 ESTs | 2.78 | LnCap, RPWE-2, NCI-H460 |
| 335090 | | CH22_FGENES.490_1' | 2.77 | NCI-H69, PRSC_log, PRSC_con |
| 328581 | | CH.07_hs gj 6006033 | 2.77 | HT29, MB-MDA-453, MCF7 |
| 333219 | | CH22_FGENES.104_11 | 2.77 | NCI-H69, PRSC_log, NCI-H345 |
| 308311 | A1581855 | EST singleton (not in UniGene) with exon | 2.77 | MB-MDA-231, HT29, CALU6 |
| 329760 | | CH.14_p2 gj 6048280 | 2.77 | CALU6, DU145, EB |
| 303925 | AW469999 | Hs.258523 ESTs | 2.77 | NCI-H69, LnCap, MB-MDA-231 |
| 337628 | | CH22_C20H12.GENSCAN.28-31 | 2.77 | NCI-H69, LnCap, MB-MDA-453 |
| 333520 | | CH22_FGENES.174_3 | 2.77 | NCI-H69, NCI-H345, PRSC_con |
| 303168 | AA872479 | Hs.197770 ESTs; Weakly similar to estrogen-respons | 2.76 | DU145, OVCA-R, MB-MDA-453 |
| 313451 | AW138189 | Hs.122672 ESTs | 2.76 | OVCA-R, EB, DU145 |
| 328474 | | CH.07_hs gj 5868446 | 2.76 | NCI-H69, NCI-H345, RPWE-2 |
| 331988 | AA477414 | Hs.9242 purine-rich element binding protein B | 2.76 | MB-MDA-435s, A549, OVCA-R |
| 306180 | AA922503 | EST singleton (not in UniGene) with exon | 2.76 | NCI-H69, DU145, LnCap |
| 321071 | AA013011 | Hs.241502 Cdc42 effector protein 4 | 2.76 | PRSC_log, PRSC_con, NCI-H345 |
| 302972 | W73400 | EST | 2.76 | NCI-H345, RPWE-2, NCI-H69 |
| 305185 | AA663985 | Hs.248038 major histocompatibility complex; class | 2.75 | DU145, A549, BT474 |

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| 335998 | | | CH22_FGENES.656_16 | 2.75 | NCI-H69, PRSC_con, RPWE-2 |
| 319138 | R11699 | Hs.73818 | ubiquinol-cytochrome c reductase hinge p | 2.75 | NCI-H345, NCI-H69, PRSC_con |
| 336387 | | | CH22_FGENES.822_7 | 2.75 | PRSC_con, RPWE-2, PRSC_log |
| 338054 | | | CH22_EM:AC005500.GENSCAN.158-2 | 2.75 | OVCA-R, EB, DU145 |
| 316041 | AA719183 | | EST cluster (not in UniGene) | 2.74 | DU145, MCF7, MB-MDA-453 |
| 336863 | | | CH22_FGENES.297-4 | 2.74 | MB-MDA-453, MCF7, OVCA-R |
| 335975 | | | CH22_FGENES.652_9 | 2.74 | CALU6, EB, A549 |
| 302952 | AF103179 | | EST | 2.74 | CALU6, MB-MDA-435s, BT474 |
| 326122 | | | CH.17_hs g 5867194 | 2.74 | HT29, Caco2, PC3 |
| 337427 | | | CH22_FGENES.761-4 | 2.74 | RPWE-2, NCI-H69, PRSC_log |
| 308053 | AI469244 | Hs.119252 | tumor protein; translationally-controlled | 2.74 | NCI-358, NCI-H23, Caco2 |
| 325433 | | | CH.12_hs g 5866936 | 2.74 | NCI-H345, PRSC_con, RPWE-2 |
| 316252 | AI572633 | Hs.190406 | ESTs | 2.74 | OVCA-R, MCF7, A549 |
| 310837 | AI418688 | Hs.170301 | ESTs | 2.74 | NCI-H345, PRSC_con, RPWE-2 |
| 313562 | AW467335 | Hs.257676 | ESTs | 2.74 | HT29, MCF7, MB-MDA-231 |
| 335455 | | | CH22_FGENES.562_15 | 2.74 | NCI-H69, LnCap, PRSC_con |
| 304792 | AA583101 | Hs.29797 | ribosomal protein L10 | 2.73 | EB, OVCA-R, MB-MDA-453 |
| 331979 | AA469937 | Hs.105322 | EST | 2.73 | MCF7, BT474, NCI-H460 |
| 336198 | | | CH22_FGENES.719_2 | 2.73 | NCI-H69, PRSC_con, PRSC_log |
| 314698 | AI680452 | Hs.187127 | ESTs | 2.73 | MB-MDA-231, LnCap, BT474 |
| 307954 | AI419692 | | EST singleton (not in UniGene) with exon | 2.73 | HT29, HT29, EB |
| 318288 | AI088590 | Hs.134702 | ESTs | 2.73 | PRSC_log, NCI-H345, PRSC_con |
| 327833 | | | CH.05_hs g 5867968 | 2.73 | BT474, PC3, MB-MDA-231 |
| 300221 | AW449602 | Hs.217953 | ESTs; Highly similar to NK-TUMOR RECOGNI | 2.73 | 2.73 NCI-H520, NCI-358, MB-MDA-453 |
| 326039 | | | CH.17_hs g 5867179 | 2.73 | MB-MDA-453, EB, EB |
| 318457 | AI149578 | Hs.143952 | ESTs | 2.72 | PRSC_con, PRSC_log, NCI-H345 |
| 336753 | | | CH22_FGENES.128-9 | 2.72 | MB-MDA-435s, NCI-H520, MCF7 |
| 330086 | | | CH.19_d2_g 5015293 | 2.72 | HT29, MB-MDA-453, MCF7 |
| 333566 | | | CH22_FGENES.183_2 | 2.72 | HT29, BT474, OVCA-R |
| 339384 | | | CH22_BA232E17.GENSCAN.3-22 | 2.71 | NCI-H69, NCI-H345, PRSC_log |
| 338668 | | | CH22_EM:AC005500.GENSCAN.465-1 | 2.71 | NCI-H69, RPWE-2, PRSC_con |
| 300798 | AI382618 | Hs.194613 | ESTs | 2.71 | PRSC_con, NCI-H345, PRSC_log |
| 303745 | AI142379 | | EST | 2.71 | PRSC_log, PRSC_con, RPWE-2 |
| 305197 | AA566301 | | EST singleton (not in UniGene) with exon | 2.71 | EB, NCI-H520, OVCA-R |
| 338725 | | | CH22_EM:AC005500.GENSCAN.499-1 | 2.7 | CALU6, MB-MDA-453, PC3 |
| 307799 | AI351112 | | EST singleton (not in UniGene) with exon | 2.7 | HT29, BT474, MCF7 |
| 309598 | AW173642 | Hs.250106 | EST | 2.69 | NCI-358, NCI-H69, NCI-H23 |
| 302727 | L10141 | | EST | 2.69 | OVCA-R, BT474, PC3 |
| 308544 | AI695133 | | EST singleton (not in UniGene) with exon | 2.69 | HT29, CALU6, MB-MDA-435s |
| 322877 | AA079727 | | EST cluster (not in UniGene) | 2.69 | NCI-H345, NCI-H69, PRSC_con |
| 325695 | | | CH.14_hs g 58552446 | 2.69 | NCI-H69, NCI-H460, NCI-H460 |
| 307728 | AI335557 | | EST singleton (not in UniGene) with exon | 2.68 | NCI-H69, PRSC_log, NCI-358 |
| 302399 | N79624 | | EST | 2.68 | NCI-H69, PRSC_con, NCI-H345 |
| 309343 | AW028652 | | EST singleton (not in UniGene) with exon | 2.68 | HT29, MB-MDA-231, MB-MDA-231 |
| 339360 | | | CH22_BA254112.GENSCAN.32-2 | 2.68 | NCI-H69, PRSC_log, PRSC_con |
| 337821 | | | CH22_EM:AC005500.GENSCAN.13-11 | 2.68 | PRSC_con, PRSC_log, PRSC_log |
| 337338 | | | CH22_FGENES.717-7 | 2.68 | NCI-H69, PRSC_con, PRSC_log |
| 334510 | | | CH22_FGENES.398_8 | 2.68 | NCI-H460, NCI-H23, NCI-358 |
| 300918 | AA491286 | Hs.128792 | ESTs | 2.68 | MB-MDA-435s, CALU6, DU145 |
| 335536 | | | CH22_FGENES.574_2 | 2.67 | NCI-H69, NCI-H345, PRSC_log |
| 335311 | | | CH22_FGENES.532_4 | 2.67 | MB-MDA-435s, Caco2, A549 |
| 338959 | | | CH22_DJ32H10.GENSCAN.23-31 | 2.67 | NCI-H345, PRSC_con, NCI-H69 |
| 339081 | | | CH22_DA59H18.GENSCAN.37-10 | 2.67 | NCI-H345, RPWE-2, NCI-H69 |
| 334068 | | | CH22_FGENES.327_23 | 2.67 | PRSC_con, RPWE-2, PRSC_log |
| 338976 | | | CH22_DA59H18.GENSCAN.1-3 | 2.66 | PRSC_con, PRSC_log, RPWE-2 |
| 325524 | | | CH.12_hs g 5866981 | 2.66 | NCI-H345, RPWE-2, PRSC_con |
| 333069 | | | CH22_FGENES.76_5 | 2.66 | NCI-H69, NCI-H345, PRSC_con |
| 336203 | | | CH22_FGENES.719_7 | 2.66 | OVCA-R, PC3, A549 |
| 333133 | | | CH22_FGENES.83_9 | 2.66 | HT29, OVCA-R, A549 |
| 304074 | T77842 | Hs.142528 | ESTs | 2.65 | DU145, CALU6, EB |
| 330919 | AA224594 | Hs.86941 | ESTs | 2.65 | PRSC_con, RPWE-2, LnCap |
| 333248 | | | CH22_FGENES.115_5 | 2.65 | NCI-H345, PRSC_con, MB-MDA-231 |
| 336665 | | | CH22_FGENES.42-2 | 2.65 | NCI-H69, PRSC_log, PRSC_con |
| 315322 | AA770599 | | EST cluster (not in UniGene) | 2.65 | A549, MB-MDA-453, MB-MDA-435s |
| 307474 | AI264023 | | EST singleton (not in UniGene) with exon | 2.65 | NCI-H69, NCI-H345, RPWE-2 |
| 320221 | AL050020 | Hs.127384 | DKFZP564C196 protein | 2.65 | MB-MDA-453, MCF7, HT29 |
| 301767 | AW361892 | | EST | 2.65 | NCI-H345, PRSC_con, PRSC_log |
| 327246 | | | CH.01_hs g 5867547 | 2.65 | EB, OVCA-R, DU145 |
| 337403 | | | CH22_FGENES.752-2 | 2.65 | PRSC_con, PRSC_log, RPWE-2 |
| 328221 | | | CH.06_hs g 5868099 | 2.64 | MCF7, MB-MDA-231, BT474 |
| 336759 | | | CH22_FGENES.133-2 | 2.64 | NCI-H69, PRSC_log, PRSC_con |
| 327532 | | | CH.02_hs g 58669818 | 2.64 | PC3, CALU6, A549 |
| 305621 | AA789095 | | EST singleton (not in UniGene) with exon | 2.64 | HT29, MB-MDA-231, MB-MDA-453 |
| 322931 | AA099329 | Hs.151764 | ESTs | 2.64 | PRSC_con, RPWE-2, NCI-H345 |
| 327278 | | | CH.01_hs g 5867473 | 2.64 | EB, NCI-H460, NCI-H69 |
| 332235 | N51413 | Hs.109284 | ESTs | 2.64 | DU145, EB, OVCA-R |

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| 332792 | | CH22_FGENES.3_2 | 2.63 | HT29, Caco2, A549 |
| 312340 | AI862568 | Hs.176333 ESTs | 2.63 | NCI-358, NCI-358, HT29 |
| 337484 | | CH22_FGENES.795_8 | 2.63 | NCI-H69, NCI-H345, PRSC_con |
| 325783 | | CH.14_hs gi 6456780 | 2.63 | EB, OVCA-R, PC3 |
| 303672 | AW502380 | Hs.210527 ESTs | 2.63 | PRSC_log, NCI-H345, NCI-H69 |
| 306009 | AA894560 | EST singleton (not in UniGene) with exon | 2.63 | HT29, MB-MDA-231, CALU6 |
| 308548 | AI695484 | EST singleton (not in UniGene) with exon | 2.63 | PC3, A549, NCI-358 |
| 337930 | | CH22_EM:AC005500.GENSCAN.81-3 | 2.62 | PC3, OVCA-R, MCF7 |
| 327791 | | CH.05_hs gi 5867977 | 2.62 | PRSC_log, PRSC_con, NCI-H345 |
| 330925 | AA232678 | Hs.67073 ESTs | 2.62 | OVCA-R, MCF7, LnCap |
| 327259 | | CH.01_hs gi 5867454 | 2.62 | NCI-H345, PRSC_con, RPWE-2 |
| 302150 | AF061756 | Hs.152531 heart and neural crest derivatives expre | 2.61 | OVCA-R, PC3, A549 |
| 304881 | AA598501 | Hs.195188 glyceraldehyde-3-phosphate dehydrogenase | 2.61 | MB-MDA-435s, NCI-H23, MCF7 |
| 335956 | | CH22_FGENES.647_3 | 2.61 | DU145, PRSC_con, PC3 |
| 326506 | | CH.19_hs gi 5867435 | 2.61 | RPWE-2, NCI-H460, NCI-358 |
| 335863 | | CH22_FGENES.629_8 | 2.61 | PC3, HT29, NCI-358 |
| 334752 | | CH22_FGENES.428_1 | 2.61 | PRSC_con, NCI-H69, PRSC_log |
| 333288 | | CH22_FGENES.128_19 | 2.61 | HT29, NCI-358, Caco2 |
| 305709 | AI024215 | Hs.131477 EST | 2.61 | MB-MDA-435s, MCF7, BT474 |
| 305816 | AA854776 | EST singleton (not in UniGene) with exon | 2.6 | MB-MDA-453, MCF7, MB-MDA-435s |
| 327264 | | CH.01_hs gi 5867461 | 2.6 | MB-MDA-435s, MB-MDA-435s, MB-MDA-453 |
| 310905 | AW075527 | Hs.252259 ribosomal protein S3 | 2.6 | OVCA-R, EB, DU145 |
| 324492 | AA479507 | Hs.135179 ESTs | 2.6 | DU145, EB, OVCA-R |
| 322649 | AA526549 | EST cluster (not in UniGene) | 2.6 | PRSC_con, RPWE-2, PRSC_log |
| 329384 | | CH.X_hs gi 5868869 | 2.6 | NCI-H69, NCI-H345, PRSC_con |
| 321240 | M62378 | EST cluster (not in UniGene) | 2.6 | BT474, CALU6, MB-MDA-231 |
| 302751 | AA299576 | Hs.156110 Immunoglobulin kappa variable 1D-8 | 2.59 | MCF7, MB-MDA-453, OVCA-R |
| 305841 | AA860348 | EST singleton (not in UniGene) with exon | 2.59 | NCI-H345, PRSC_log, PRSC_con |
| 324180 | AA402242 | Hs.122799 ESTs | 2.58 | EB, PC3, HT29 |
| 334196 | | CH22_FGENES.353_4 | 2.58 | NCI-H345, NCI-H69, PRSC_con |
| 338451 | | CH22_EM:AC005500.GENSCAN.359-39 | 2.58 | MB-MDA-435s, NCI-H23, MCF7 |
| 300333 | AW297396 | Hs.227052 ESTs | 2.58 | PRSC_con, PRSC_log, NCI-H69 |
| 305046 | AA632201 | EST singleton (not in UniGene) with exon | 2.58 | NCI-H460, MB-MDA-453, MB-MDA-435s |
| 305648 | AA807652 | Hs.156110 Immunoglobulin kappa variable 1D-8 | 2.57 | PRSC_con, RPWE-2, NCI-H345 |
| 301744 | W22230 | EST | 2.57 | PRSC_con, PRSC_log, NCI-H345 |
| 329182 | | CH.X_hs gi 6056331 | 2.57 | PRSC_con, RPWE-2, NCI-H345 |
| 318178 | AW137425 | Hs.158401 ESTs | 2.57 | MB-MDA-231, PRSC_con, BT474 |
| 330057 | | CH.17_p2 gi 6478962 | 2.57 | NCI-H345, RPWE-2, PRSC_con |
| 326552 | | CH.19_hs gi 5867308 | 2.57 | NCI-H345, PRSC_con, RPWE-2 |
| 311956 | T67085 | Hs.188464 ESTs | 2.57 | HT29, MB-MDA-453, NCI-H460 |
| 327185 | | CH.01_hs gi 6117805 | 2.57 | CALU6, HT29, EB |
| 302183 | NM_00224 | EST | 2.57 | MCF7, PC3, OVCA-R |
| 327263 | | CH.01_hs gi 6525274 | 2.56 | PRSC_con, NCI-H69, PRSC_log |
| 339164 | | CH22_DA59H18.GENSCAN.69-4 | 2.56 | NCI-H69, PRSC_con, NCI-H345 |
| 332763 | AA063554 | Hs.90959 ESTs | 2.56 | RPWE-2, NCI-H345, PRSC_con |
| 330579 | U67733 | Hs.154437 phosphodiesterase 2A; cGMP-stimulated | 2.55 | HT29, CALU6, PC3 |
| 329948 | | CH.16_p2 gi 5540101 | 2.55 | NCI-H460, MCF7, MB-MDA-453 |
| 300282 | AW044305 | Hs.236131 ESTs; Highly similar to homeodomain-inte | 2.55 | NCI-H460, NCI-H23, NCI-H23 |
| 335448 | | CH22_FGENES.562_5 | 2.55 | MB-MDA-453, BT474, MCF7 |
| 330959 | H09174 | Hs.26484 HIRA-Interacting protein 3 | 2.55 | MB-MDA-453, HT29, MCF7 |
| 307262 | AI202100 | EST singleton (not in UniGene) with exon | 2.55 | MCF7, DU145, MB-MDA-435s |
| 335806 | | CH22_FGENES.616_8 | 2.55 | NCI-H345, NCI-H69, PRSC_con |
| 335782 | | CH22_FGENES.609_4 | 2.55 | Caco2, MB-MDA-453, MB-MDA-435s |
| 301703 | AW301478 | EST | 2.55 | PC3, MCF7, MB-MDA-453 |
| 329018 | | CH.X_hs gi 6249620 | 2.54 | NCI-H69, PRSC_log, PRSC_con |
| 328970 | | CH.14_p2 gi 6706435 | 2.54 | NCI-H23, NCI-H460, NCI-358 |
| 334504 | | CH22_FGENES.398_2 | 2.54 | HT29, BT474, MB-MDA-231 |
| 304707 | AA564846 | EST singleton (not in UniGene) with exon | 2.53 | NCI-H520, EB, NCI-H460 |
| 329326 | | CH.X_hs gi 5868806 | 2.53 | MB-MDA-231, NCI-H345, NCI-H69 |
| 334418 | | CH22_FGENES.384_5 | 2.53 | NCI-H23, NCI-358, NCI-H460 |
| 338124 | | CH22_EM:AC005500.GENSCAN.196-2 | 2.53 | NCI-H69, PRSC_con, PRSC_log |
| 318423 | AI362671 | Hs.214491 ESTs | 2.53 | OVCA-R, EB, DU145 |
| 333006 | | CH22_FGENES.60_3 | 2.53 | NCI-H69, PRSC_con, PRSC_log |
| 333668 | | CH22_FGENES.245_2 | 2.53 | NCI-H69, PRSC_log, PRSC_con |
| 333567 | | CH22_FGENES.184_2 | 2.53 | NCI-H69, NCI-H345, PRSC_con |
| 309592 | AW172384 | EST singleton (not in UniGene) with exon | 2.52 | LnCap, NCI-H69, DU145 |
| 328989 | | CH.09_hs gi 5868535 | 2.52 | MB-MDA-435s, OVCA-R, EB |
| 326725 | | CH.20_hs gi 6552456 | 2.52 | PRSC_con, NCI-H345, NCI-H69 |
| 302995 | AF054663 | EST | 2.52 | HT29, BT474, CALU6 |
| 335733 | | CH22_FGENES.601_3 | 2.52 | NCI-H69, PRSC_log, NCI-H345 |
| 336000 | | CH22_FGENES.658_1 | 2.52 | LnCap, OVCA-R, DU145 |
| 327774 | | CH.05_hs gi 5867954 | 2.52 | DU145, CALU6, HT29 |
| 328557 | | CH.07_hs gi 5868489 | 2.52 | MB-MDA-453, MB-MDA-435s, MCF7 |
| 328228 | | CH.06_hs gi 5868105 | 2.52 | NCI-H69, NCI-H345, PRSC_con |
| 328305 | | CH.07_hs gi 6004478 | 2.52 | NCI-H69, NCI-H460, PRSC_log |
| 334010 | | CH22_FGENES.313_1 | 2.51 | NCI-H69, PRSC_log, PRSC_con |

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| 339033 | CH22_DA59H18.GENSCAN.26-1 | 2.51 | NCI-H69, NCI-H345, PRSC_con |
| 335340 | CH22_FGENES.535_17 | 2.51 | NCI-H69, PRSC_con, PRSC_log |
| 300156 | AI245582 Hs.233395 ESTs | 2.51 | PRSC_con, PRSC_log, NCI-H345 |
| 305880 | AA866065 Hs.156110 Immunoglobulin kappa variable 1D-8 | 2.5 | EB, OVCA-R, DU145 |
| 310841 | AI958009 Hs.232024 ESTs | 2.5 | LnCap, NCI-358, CALU6 |
| 336908 | CH22_FGENES.343-2 | 2.5 | NCI-H345, RPWE-2, PRSC_log |
| 304674 | AA541735 EST singleton (not in UniGene) with exon | 2.5 | RPWE-2, NCI-H69, MCF7 |
| 314521 | AW503939 Hs.107149 ESTs; Weakly similar to PTB-ASSOCIATED S2.5 | 2.5 | NCI-H460, EB, Caco2 |
| 307592 | AI285739 EST singleton (not in UniGene) with exon | 2.5 | PRSC_con, NCI-H345, PRSC_log |
| 331476 | N26190 Hs.43768 ESTs | 2.5 | NCI-H345, NCI-H69, PRSC_con |
| 325803 | CH.14_hs g 6552451 | 2.5 | NCI-H345, RPWE-2, PRSC_con |
| 306549 | AA993796 EST singleton (not in UniGene) with exon | 2.49 | A549, OVCA-R, CALU6 |
| 304833 | AA586504 EST singleton (not in UniGene) with exon | 2.49 | MCF7, DU145, LnCap |
| 336333 | CH22_FGENES.813_1 | 2.49 | NCI-H345, PRSC_con, PRSC_log |
| 332320 | T71134 Hs.100551 EST | 2.49 | NCI-H345, LnCap, RPWE-2 |
| 328236 | CH.06_hs g 5868117 | 2.49 | PRSC_con, NCI-H345, PRSC_log |
| 317335 | AI656979 Hs.130210 ESTs | 2.49 | MCF7, MB-MDA-453, PC3 |
| 339188 | CH22_DA59H18.GENSCAN.72-16 | 2.48 | NCI-H69, PRSC_con, PRSC_log |
| 334235 | CH22_FGENES.361_19 | 2.48 | NCI-H520, MB-MDA-453, A549 |
| 301214 | AW450950 Hs.157034 ESTs; Weakly similar to Unknown [H.sapiens] | 2.48 | HT29, A549, A549 |
| 332843 | CH22_FGENES.19_1 | 2.48 | DU145, CALU6, EB |
| 337431 | CH22_FGENES.763-7 | 2.48 | PRSC_con, RPWE-2, NCI-H69 |
| 336757 | CH22_FGENES.131-1 | 2.48 | NCI-H69, PRSC_log, PRSC_con |
| 305403 | AA723748 EST singleton (not in UniGene) with exon | 2.48 | NCI-H23, DU145, OVCA-R |
| 330065 | CH.19_p2 g 6165044 | 2.48 | PRSC_con, PRSC_log, NCI-H69 |
| 309245 | AI972447 EST singleton (not in UniGene) with exon | 2.48 | MB-MDA-231, NCI-H69, HT29 |
| 328876 | CH.07_hs g 6525286 | 2.47 | MB-MDA-231, CALU6, PC3 |
| 333944 | CH22_FGENES.302_2 | 2.47 | NCI-H69, RPWE-2, PRSC_log |
| 328504 | CH.07_hs g 5868471 | 2.47 | LnCap, MB-MDA-453, MB-MDA-435s |
| 338120 | CH22_EM:AC005500.GENSCAN.195-1 | 2.47 | MB-MDA-231, NCI-H69, PRSC_con |
| 306710 | AI024221 EST singleton (not in UniGene) with exon | 2.47 | OVCA-R, EB, LnCap |
| 305064 | AA636012 EST singleton (not in UniGene) with exon | 2.47 | NCI-H69, RPWE-2, PRSC_con |
| 329995 | CH.16_p2 g 4567166 | 2.47 | OVCA-R, DU145, MB-MDA-453 |
| 315694 | AI821743 Hs.168418 ESTs; Moderately similar to !!! ALU SUB | 2.46 | EB, A549, LnCap |
| 331004 | H64622 Hs.32748 ESTs | 2.46 | EB, MCF7, MB-MDA-435s |
| 305259 | AA679225 EST singleton (not in UniGene) with exon | 2.46 | PRSC_con, NCI-H345, RPWE-2 |
| 304576 | AA496563 EST singleton (not in UniGene) with exon | 2.46 | PRSC_con, RPWE-2, PRSC_log |
| 318887 | R60487 Hs.21065 ESTs | 2.46 | NCI-H345, Caco2, Caco2 |
| 308954 | AI868958 EST singleton (not in UniGene) with exon | 2.46 | PRSC_con, PRSC_log, RPWE-2 |
| 301140 | AI807692 Hs.207128 ESTs | 2.46 | OVCA-R, MB-MDA-231, HT29 |
| 322085 | AA088500 Hs.170298 ESTs | 2.46 | PRSC_log, PRSC_con, NCI-H345 |
| 339130 | CH22_DA59H18.GENSCAN.56-3 | 2.46 | NCI-H345, PRSC_con, RPWE-2 |
| 337612 | CH22_C20H12.GENSCAN.22-5 | 2.46 | EB, A549, Caco2 |
| 313765 | AW206181 Hs.185981 ESTs; Weakly similar to gag [H.sapiens] | 2.45 | RPWE-2, PRSC_log, PRSC_con |
| 311665 | AW294254 Hs.223742 ESTs | 2.45 | PRSC_log, RPWE-2, PRSC_con |
| 328820 | CH.07_hs g 5868241 | 2.45 | MB-MDA-453, MCF7, MB-MDA-435s |
| 305361 | AA708902 EST singleton (not in UniGene) with exon | 2.45 | HT29, MB-MDA-435s, A549 |
| 336243 | CH22_FGENES.746_1 | 2.44 | OVCA-R, MB-MDA-453, MB-MDA-435s |
| 320299 | H08323 Hs.177181 ESTs | 2.44 | PRSC_con, RPWE-2, NCI-H345 |
| 302535 | H48676 EST | 2.44 | MB-MDA-453, EB, DU145 |
| 333465 | CH22_FGENES.160_2 | 2.44 | NCI-H69, PRSC_con, PRSC_log |
| 334109 | CH22_FGENES.330_8 | 2.44 | NCI-H69, NCI-H345, PRSC_log |
| 301749 | F12998 Hs.90790 ESTs | 2.44 | NCI-H345, RPWE-2, PRSC_log |
| 324575 | AW502257 EST cluster (not in UniGene) | 2.44 | NCI-H345, PRSC_con, RPWE-2 |
| 337114 | CH22_FGENES.494-17 | 2.44 | NCI-H69, PRSC_log, PRSC_con |
| 336087 | CH22_FGENES.688_16 | 2.44 | PRSC_con, Caco2, PRSC_log |
| 315678 | AI657119 Hs.120036 ESTs | 2.44 | NCI-358, PC3, NCI-H23 |
| 333258 | CH22_FGENES.118_6 | 2.44 | MB-MDA-231, HT29, CALU6 |
| 303798 | V00505 Hs.36977 hemoglobin; delta | 2.44 | MB-MDA-435s, MCF7, MB-MDA-453 |
| 309759 | AW268822 EST singleton (not in UniGene) with exon | 2.44 | MB-MDA-453, EB, MCF7 |
| 318946 | AI122843 EST cluster (not in UniGene) | 2.44 | PC3, OVCA-R, DU145 |
| 321986 | AL133656 EST cluster (not in UniGene) | 2.44 | DU145, CALU6, CALU6 |
| 338151 | CH22_EM:AC005500.GENSCAN.207-5 | 2.44 | PRSC_con, PRSC_log, RPWE-2 |
| 327056 | CH.21_hs g 6531965 | 2.44 | PRSC_con, NCI-H345, RPWE-2 |
| 309605 | AW182800 EST singleton (not in UniGene) with exon | 2.43 | NCI-358, NCI-H23, NCI-H520 |
| 335783 | CH22_FGENES.610_3 | 2.43 | PRSC_con, PRSC_log, NCI-H345 |
| 325790 | CH.14_hs g 6381957 | 2.43 | MB-MDA-435s, MB-MDA-453, MB-MDA-453 |
| 339342 | CH22_BA354112.GENSCAN.27-10 | 2.43 | BT474, MB-MDA-231, MB-MDA-453 |
| 335777 | CH22_FGENES.607_13 | 2.43 | DU145, EB, BT474 |
| 309972 | AW450350 Hs.257283 ESTs | 2.43 | MCF7, MB-MDA-453, OVCA-R |
| 308718 | AI798009 EST singleton (not in UniGene) with exon | 2.43 | NCI-H345, PRSC_con, PRSC_log |
| 338087 | CH22_EM:AC005500.GENSCAN.174-16 | 2.43 | DU145, PC3, CALU6 |
| 305930 | AI124518 EST singleton (not in UniGene) with exon | 2.43 | NCI-H69, MCF7, BT474 |
| 319032 | AW409728 Hs.80449 ESTs; Weakly similar to cytoplasmic dyne | 2.43 | RPWE-2, A549, NCI-H69 |
| 304330 | AA157834 EST singleton (not in UniGene) with exon | 2.43 | MB-MDA-453, PC3, OVCA-R |
| 320538 | R54766 Hs.101120 ESTs | 2.43 | MCF7, MB-MDA-435s, MB-MDA-453 |

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| 335281 | | CH22_FGENES.524_4 | 2.43 | PC3, LnCap, A549 |
| 317431 | AI675780 | Hs.132453 ESTs | 2.43 | NCI-H345, RPWE-2, PRSC_log |
| 306511 | AA988891 | EST singleton (not in UniGene) with exon | 2.43 | OVCA-R, EB, DU145 |
| 333298 | | CH22_FGENES.133_4 | 2.43 | EB, DU145, PC3 |
| 328436 | | CH.07_hs gij5868417 | 2.43 | EB, LnCap, A549 |
| 333420 | | CH22_FGENES.146_11 | 2.43 | NCI-H345, NCI-H69, PRSC_log |
| 338113 | | CH22_EM:AC005500.GENSCAN.188-13 | 2.42 | DU145, EB, CALU6 |
| 335188 | | CH22_FGENES.507_3 | 2.42 | EB, A549, BT474 |
| 329164 | | CH.X_hs gij5868691 | 2.42 | RPWE-2, PRSC_con, PRSC_log |
| 336316 | | CH22_FGENES.799_11 | 2.42 | MB-MDA-435s, MCF7, NCI-H69 |
| 310831 | AI927594 | Hs.161142 ESTs | 2.42 | NCI-H345, PRSC_con, PRSC_log |
| 327334 | | CH.01_hs gij5902477 | 2.42 | MB-MDA-453, MB-MDA-435s, MCF7 |
| 334017 | | CH22_FGENES.315_2 | 2.42 | PRSC_con, PRSC_log, RPWE-2 |
| 308138 | AI494446 | EST singleton (not in UniGene) with exon | 2.42 | DU145, LnCap, EB |
| 333074 | | CH22_FGENES.76_10 | 2.42 | NCI-H69, RPWE-2, PRSC_log |
| 306546 | AA993109 | EST singleton (not in UniGene) with exon | 2.42 | HT29, CALU6, LnCap |
| 336516 | | CH22_FGENES.836_1 | 2.42 | NCI-H69, PRSC_con, PRSC_log |
| 305791 | AI042387 | EST singleton (not in UniGene) with exon | 2.42 | CALU6, DU145, EB |
| 329411 | | CH.X_hs gij5862549 | 2.42 | OVCA-R, EB, LnCap |
| 308659 | AI750091 | EST singleton (not in UniGene) with exon | 2.41 | EB, DU145, CALU6 |
| 313504 | AI190405 | Hs.143127 ESTs | 2.41 | DU145, EB, CALU6 |
| 326073 | | CH.17_hs gij6682495 | 2.41 | DU145, A549, MB-MDA-435s |
| 334047 | | CH22_FGENES.326_5 | 2.41 | PRSC_con, PRSC_log, NCI-H345 |
| 325464 | | CH.12_hs gij5866947 | 2.41 | NCI-358, NCI-H23, NCI-H450 |
| 334764 | | CH22_FGENES.428_13 | 2.41 | NCI-H69, NCI-H345, RPWE-2 |
| 312737 | AI033500 | Hs.132895 ESTs | 2.41 | OVCA-R, DU145, CALU6 |
| 306591 | AI000248 | EST singleton (not in UniGene) with exon | 2.41 | MB-MDA-231, MCF7, DU145 |
| 333582 | | CH22_FGENES.201_2 | 2.41 | NCI-H69, PRSC_con, PRSC_log |
| 337843 | | CH22_EM:AC005500.GENSCAN.30-8 | 2.4 | EB, LnCap, A549 |
| 335284 | | CH22_FGENES.526_6 | 2.4 | NCI-H69, NCI-H345, PRSC_log |
| 305134 | AA653159 | EST singleton (not in UniGene) with exon | 2.4 | DU145, HT29, MB-MDA-453 |
| 335527 | | CH22_FGENES.572_7 | 2.4 | DU145, OVCA-R, EB |
| 336795 | | CH22_FGENES.176-5 | 2.4 | NCI-H69, NCI-H345, PRSC_log |
| 303144 | AF202889 | EST | 2.4 | PRSC_con, PRSC_log, NCI-H69 |
| 334948 | | CH22_FGENES.465_15 | 2.4 | PRSC_con, PRSC_log, RPWE-2 |
| 328860 | | CH.07_hs gij5381928 | 2.4 | PRSC_con, PRSC_log, NCI-H345 |
| 322929 | AI365585 | Hs.146246 ESTs | 2.4 | NCI-H460, A549, HT29 |
| 333561 | | CH22_FGENES.180_18 | 2.4 | OVCA-R, EB, DU145 |
| 338239 | | CH22_EM:AC005500.GENSCAN.264-5 | 2.4 | NCI-H69, NCI-H345, PRSC_con |
| 323670 | AI040411 | Hs.161763 ESTs; Weakly similar to KIAA0738 protein | 2.4 | DU145, MB-MDA-453, EB |
| 305903 | AA873085 | EST singleton (not in UniGene) with exon | 2.4 | MCF7, A549, NCI-H520 |
| 312573 | AW297673 | Hs.190526 ESTs | 2.4 | LnCap, NCI-H460, NCI-H23 |
| 334470 | | CH22_FGENES.394_1 | 2.4 | NCI-H520, HT29, NCI-H23 |
| 333272 | | CH22_FGENES.122_1 | 2.39 | NCI-H345, PRSC_con, RPWE-2 |
| 304010 | AW518383 | Hs.177592 ribosomal protein; large; P1 | 2.39 | DU145, CALU6, EB |
| 337316 | | CH22_FGENES.692-1 | 2.39 | MCF7, BT474, OVCA-R |
| 316769 | AI914939 | Hs.212184 ESTs | 2.39 | PRSC_con, NCI-H345, RPWE-2 |
| 336280 | | CH22_FGENES.763_4 | 2.39 | NCI-H345, PRSC_log, PRSC_con |
| 331223 | T98872 | Hs.194181 ESTs | 2.39 | DU145, HT29, PC3 |
| 337172 | | CH22_FGENES.565-2 | 2.39 | EB, OVCA-R, DU145 |
| 300625 | AI671992 | Hs.143631 ESTs; Weakly similar to WASP-family prot | 2.39 | EB, NCI-H520, LnCap |
| 337092 | | CH22_FGENES.465-12 | 2.39 | PRSC_con, PRSC_log, NCI-H69 |
| 334528 | | CH22_FGENES.402_8 | 2.39 | NCI-H345, PRSC_con, NCI-H69 |
| 338411 | | CH22_EM:AC005500.GENSCAN.341-7 | 2.39 | NCI-H345, NCI-H69, PRSC_con |
| 331344 | AA357927 | Hs.70208 ESTs | 2.39 | PC3, EB, A549 |
| 334044 | | CH22_FGENES.323_2 | 2.38 | MB-MDA-231, MCF7, LnCap |
| 333918 | | CH22_FGENES.296_7 | 2.38 | RPWE-2, NCI-H345, EB |
| 317168 | AI042614 | Hs.125910 ESTs | 2.38 | NCI-H345, PRSC_con, RPWE-2 |
| 333424 | | CH22_FGENES.147_4 | 2.38 | DU145, MCF7, OVCA-R |
| 317779 | AW450515 | Hs.128381 ESTs | 2.38 | EB, DU145, OVCA-R |
| 315142 | AI380577 | Hs.190219 ESTs | 2.38 | OVCA-R, EB, CALU6 |
| 310471 | AW270515 | Hs.149596 ESTs | 2.38 | NCI-H460, NCI-H23, NCI-H23 |
| 325049 | AW410339 | Hs.256310 ESTs; Weakly similar to centaurin beta2 | 2.38 | PRSC_con, RPWE-2, NCI-H345 |
| 305234 | AA670431 | EST singleton (not in UniGene) with exon | 2.38 | MB-MDA-453, MB-MDA-231, A549 |
| 337760 | | CH22_EM:AC000097.GENSCAN.116-8 | 2.38 | PRSC_con, PRSC_log, RPWE-2 |
| 311502 | AW204380 | Hs.208662 ESTs | 2.38 | NCI-H345, NCI-H69, LnCap |
| 337548 | | CH22_FGENES.844-5 | 2.38 | MB-MDA-453, MCF7, CALU6 |
| 328981 | | CH.21_hs gij5868016 | 2.38 | NCI-H345, NCI-H69, PRSC_con |
| 309600 | AW182066 | EST singleton (not in UniGene) with exon | 2.37 | RPWE-2, NCI-358, NCI-H69 |
| 328936 | | CH.06_hs gij5868500 | 2.37 | OVCA-R, MB-MDA-453, CALU6 |
| 327937 | | CH.06_hs gij5868192 | 2.37 | BT474, EB, OVCA-R |
| 328282 | | CH.07_hs gij5868353 | 2.37 | DU145, CALU6, CALU6 |
| 303607 | AI046388 | Hs.208206 ESTs; Weakly similar to Naf1 alpha prote | 2.37 | LnCap, PRSC_log, NCI-H345 |
| 304227 | N94974 | Hs.75344 ribosomal protein S4; X-linked | 2.37 | EB, PC3, OVCA-R |
| 314101 | AW452279 | Hs.257542 ESTs | 2.37 | OVCA-R, CALU6, CALU6 |
| 325026 | AI671168 | Hs.12285 ESTs | 2.37 | NCI-H345, PRSC_con, PRSC_log |

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| 315015 | AI659989 | Hs.132625 | ESTs | 2.37 | MB-MDA-453, MB-MDA-231, LnCap |
| 328662 | | CH.07_hs gl 6004473 | | 2.37 | NCI-H345, RPWE-2, PRSC_con |
| 305867 | AA864572 | EST singleton (not in UniGene) with exon | | 2.37 | MCF7, MB-MDA-453, MB-MDA-231 |
| 333296 | | CH22_FGENES.132_3 | | 2.37 | EB, PC3, CALU6 |
| 331070 | R01116 | Hs.182059 | ESTs | 2.36 | OVCA-R, MB-MDA-453, A549 |
| 333698 | | CH22_FGENES.250_12 | | 2.36 | HT29, OVCA-R, Caco2 |
| 316423 | AA758756 | Hs.121380 | ESTs | 2.36 | HT29, MCF7, MB-MDA-435s |
| 323189 | AL121194 | Hs.120589 | ESTs | 2.36 | PC3, NCI-H460, DU145 |
| 318889 | Z43296 | Hs.18720 | programmed cell death 8 (apoptosis-induc- | 2.36 | OVCA-R, A549, MB-MDA-453 |
| 334237 | | CH22_FGENES.362_1 | | 2.36 | NCI-H345, NCI-H69, LnCap |
| 315931 | AI700148 | Hs.117328 | ESTs | 2.36 | MCF7, NCI-H345, DU145 |
| 326884 | | CH.20_hs gl 6682511 | | 2.36 | A549, EB, PC3 |
| 333132 | | CH22_FGENES.83_8 | | 2.36 | NCI-H69, HT29, EB |
| 306574 | AA995719 | Hs.76067 | heat shock 27kD protein 1 | 2.36 | RPWE-2, PRSC_log, PRSC_con |
| 324416 | AI669524 | Hs.194115 | ESTs | 2.36 | NCI-H345, RPWE-2, PRSC_con |
| 329496 | | CH.10_p2 gl 3983518 | | 2.35 | HT29, MCF7, MB-MDA-231 |
| 320994 | H22381 | | EST cluster (not in UniGene) | 2.35 | NCI-H23, A549, CALU6 |
| 320481 | AA461139 | Hs.24372 | ESTs; Weakly similar to dJ207H1.1 [H.sap- | 2.35 | PRSC_con, RPWE-2, PRSC_log |
| 309958 | AW444488 | | EST singleton (not in UniGene) with exon | 2.35 | NCI-H345, PRSC_con, PRSC_log |
| 327009 | | CH.21_hs gl 5867664 | | 2.35 | HT29, BT474, MCF7 |
| 309594 | AW172821 | Hs.181165 | eukaryotic translation elongation factor | 2.35 | HT29, DU145, EB |
| 335468 | | CH22_FGENES.567_4 | | 2.35 | NCI-H69, PRSC_con, NCI-H345 |
| 304269 | AA069029 | | EST singleton (not in UniGene) with exon | 2.35 | PRSC_con, PRSC_log, RPWE-2 |
| 305877 | AA865649 | | EST singleton (not in UniGene) with exon | 2.35 | A549, MCF7, OVCA-R |
| 305700 | AA815428 | | EST singleton (not in UniGene) with exon | 2.35 | PRSC_con, NCI-H345, PRSC_log |
| 326423 | | CH.19_hs gl 5867369 | | 2.34 | PC3, MCF7, LnCap |
| 334560 | | CH22_FGENES.404_3 | | 2.34 | HT29, NCI-H460, MB-MDA-435s |
| 337100 | | CH22_FGENES.472-3 | | 2.34 | PRSC_log, PRSC_con, RPWE-2 |
| 301505 | AW014374 | Hs.144849 | ESTs | 2.34 | CALU6, MB-MDA-231, DU145 |
| 312142 | AW298359 | Hs.221069 | ESTs | 2.34 | PRSC_con, RPWE-2, PRSC_log |
| 305787 | AA845035 | | EST singleton (not in UniGene) with exon | 2.34 | NCI-H23, NCI-H520, NCI-H460 |
| 338686 | | CH22_EM:AC005500.GENSCAN.472-5 | | 2.33 | BT474, MB-MDA-231, MB-MDA-453 |
| 331977 | AA465207 | Hs.125887 | ESTs | 2.33 | OVCA-R, A549, MB-MDA-435s |
| 314687 | M79114 | Hs.135177 | ESTs | 2.33 | NCI-H69, PRSC_con, NCI-H345 |
| 336089 | | CH22_FGENES.688_18 | | 2.33 | PRSC_con, Caco2, PRSC_log |
| 338952 | | CH22_DJ32110.GENSCAN.23-22 | | 2.33 | PC3, OVCA-R, HT29 |
| 334612 | | CH22_FGENES.411_11 | | 2.33 | OVCA-R, MB-MDA-453, EB |
| 338223 | | CH22_EM:AC005500.GENSCAN.250-10 | | 2.33 | DU145, MB-MDA-453, MCF7 |
| 327845 | | CH.05_hs gl 5631962 | | 2.32 | OVCA-R, MB-MDA-453, PC3 |
| 308187 | AI538108 | Hs.156110 | immunoglobulin kappa variable 1D-8 | 2.32 | NCI-H69, NCI-358, PRSC_con |
| 317767 | AW294164 | Hs.128340 | ESTs; Weakly similar to Cdc42 GTPase-act | 2.32 | BT474, CALU6, MB-MDA-231 |
| 330468 | L10343 | Hs.112341 | protease inhibitor 3; skin-derived (SKAL | 2.32 | PC3, Caco2, HT29 |
| 319003 | R17712 | | EST cluster (not in UniGene) | 2.32 | MCF7, PC3, MB-MDA-453 |
| 323022 | AI066733 | Hs.133865 | ESTs | 2.32 | CALU6, MB-MDA-231, DU145 |
| 303148 | R73167 | Hs.127317 | ESTs; Weakly similar to CYTOCHROME P450 | 2.32 | 2.32 NCI-H345, PRSC_con, RPWE-2 |
| 303215 | AW250314 | | EST | 2.32 | NCI-H345, PRSC_con, PRSC_log |
| 318891 | H10477 | Hs.195208 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.32 | NCI-H69, LnCap, NCI-H345 |
| 336653 | | CH22_FGENES.33-4 | | 2.32 | DU145, EB, LnCap |
| 333329 | | CH22_FGENES.138_22 | | 2.32 | DU145, BT474, MB-MDA-231 |
| 301980 | U69962 | Hs.121498 | potassium voltage-gated channel; Shab-re | 2.31 | NCI-H345, MB-MDA-231, LnCap |
| 336968 | | CH22_FGENES.375-28 | | 2.31 | HT29, BT474, EB |
| 308539 | AI694191 | | EST singleton (not in UniGene) with exon | 2.31 | NCI-H345, NCI-H69, PRSC_log |
| 326417 | | CH.19_hs gl 5867362 | | 2.31 | HT29, MCF7, BT474 |
| 328851 | | CH.07_hs gl 56381923 | | 2.31 | NCI-H520, NCI-H460, NCI-H23 |
| 329254 | | CH.X_hs gl 5868733 | | 2.31 | RPWE-2, NCI-H345, PRSC_con |
| 303075 | W88779 | Hs.59125 | ESTs | 2.3 | DU145, OVCA-R, EB |
| 335131 | | CH22_FGENES.497_15 | | 2.3 | NCI-H69, NCI-H345, PRSC_log |
| 303129 | AA308334 | Hs.172210 | MUF1 protein | 2.3 | LnCap, DU145, HT29 |
| 327067 | | CH.21_hs gl 5631965 | | 2.3 | NCI-H345, NCI-H69, MB-MDA-435s |
| 324064 | AW137650 | | EST cluster (not in UniGene) | 2.3 | DU145, HT29, EB |
| 325965 | | CH.16_hs gl 5867147 | | 2.3 | NCI-H69, NCI-H345, RPWE-2 |
| 334525 | | CH22_FGENES.402_4 | | 2.3 | NCI-H345, PRSC_con, NCI-H69 |
| 336654 | | CH22_FGENES.34-2 | | 2.3 | BT474, PC3, MB-MDA-453 |
| 302348 | AF100779 | Hs.194680 | WNT1 inducible signaling pathway protein | 2.3 | LnCap, CALU6, DU145 |
| 309275 | AI989570 | | EST singleton (not in UniGene) with exon | 2.3 | NCI-H460, NCI-H23, NCI-H520 |
| 329246 | | CH.X_hs gl 5868732 | | 2.3 | NCI-H69, NCI-H345, PRSC_log |
| 305557 | AA774834 | | EST singleton (not in UniGene) with exon | 2.3 | CALU6, CALU6, MCF7 |
| 322907 | AA084941 | | EST cluster (not in UniGene) | 2.3 | MB-MDA-231, CALU6, EB |
| 318683 | AI703241 | Hs.202653 | ESTs; Weakly similar to Xin [M.musculus] | 2.29 | NCI-H345, PRSC_con, RPWE-2 |
| 309233 | AI971416 | | EST singleton (not in UniGene) with exon | 2.29 | CALU6, OVCA-R, EB |
| 308913 | AI860692 | Hs.119122 | ribosomal protein L13a | 2.29 | MB-MDA-435s, MCF7, HT29 |
| 335827 | | CH22_FGENES.620_1 | | 2.29 | PRSC_con, PRSC_log, RPWE-2 |
| 334066 | | CH22_FGENES.327_21 | | 2.29 | PRSC_con, PRSC_log, NCI-H345 |
| 302656 | AW293005 | Hs.220905 | ESTs | 2.29 | NCI-H23, Caco2, CALU6 |
| 308974 | AI872290 | Hs.140 | immunoglobulin gamma 3 (Gm marker) | 2.29 | CALU6, A549, NCI-H69 |
| 333607 | | CH22_FGENES.216_2 | | 2.29 | OVCA-R, MCF7, A549 |

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| 335174 | | CH22_FGENES.504_4 | 2.29 | HT29, A549, MB-MDA-453 |
| 332028 | AA489680 | Hs.134406 ESTs; Weakly similar to Dm1p homolog [H] | 2.29 | EB, A549, DU145 |
| 336417 | | CH22_FGENES.823_39 | 2.29 | NCI-H69, NCI-H345, PRSC_log |
| 323426 | AA251401 | EST cluster (not in UniGene) | 2.29 | HT29, MB-MDA-231, BT474 |
| 336618 | | CH22_FGENES.2-1 | 2.29 | NCI-358, NCI-H460, NCI-H69 |
| 310017 | AI188739 | Hs.148488 ESTs | 2.29 | NCI-H345, PRSC_log, PRSC_con |
| 334055 | | CH22_FGENES.327_6 | 2.28 | DU145, OVCA-R, MB-MDA-453 |
| 337168 | | CH22_FGENES.562-28 | 2.28 | NCI-H69, PRSC_log, NCI-H345 |
| 329824 | | CH.14_p2 gij6630758 | 2.28 | NCI-H23, CALU6, RPWE-2 |
| 333891 | | CH22_FGENES.292_13 | 2.28 | NCI-H69, MB-MDA-231, RPWE-2 |
| 339127 | | CH22_DA59H18.GENSCAN.55-1 | 2.28 | PRSC_con, NCI-H345, RPWE-2 |
| 305686 | AA812726 | EST singleton (not in UniGene) with exon | 2.28 | NCI-H520, NCI-H23, NCI-H460 |
| 329782 | | CH.14_p2 gij5912597 | 2.28 | NCI-H69, NCI-H345, PRSC_log |
| 311059 | AI810001 | Hs.175346 ESTs | 2.28 | MCF7, BT474, MB-MDA-435s |
| 336934 | | CH22_FGENES.351-1 | 2.28 | BT474, HT29, MB-MDA-435s |
| 314893 | AA761093 | EST cluster (not in UniGene) | 2.28 | OVCA-R, HT29, DU145 |
| 331596 | N72574 | Hs.50220 ESTs | 2.28 | A549, MCF7, NCI-358 |
| 330729 | AA258559 | Hs.3736 ESTs; Weakly similar to DELTA-LIKE PROTE | 2.28 | MB-MDA-231, CALU6, MCF7 |
| 338285 | | CH22_EM:AC005500.GENSCAN.293-3 | 2.27 | NCI-H69, PRSC_log, PRSC_con |
| 300154 | AI245127 | Hs.179331 ESTs | 2.27 | NCI-H23, NCI-H520, NCI-358 |
| 306383 | AA969078 | Hs.183698 ribosomal protein L29 | 2.27 | RPWE-2, NCI-H345, PRSC_log |
| 309005 | AI884454 | EST singleton (not in UniGene) with exon | 2.27 | A549, MCF7, BT474 |
| 332995 | | CH22_FGENES.58_2 | 2.27 | RPWE-2, NCI-H345, PRSC_log |
| 337426 | | CH22_FGENES.761-3 | 2.27 | DU145, EB, CALU6 |
| 337778 | | CH22_EM:AC000097.GENSCAN.119-20 | 2.27 | NCI-H69, PRSC_con, PRSC_log |
| 329705 | | CH.14_p2 gij6065790 | 2.27 | PRSC_con, PRSC_log, RPWE-2 |
| 335971 | | CH22_FGENES.652_4 | 2.27 | PRSC_log, MB-MDA-231, NCI-H23 |
| 315862 | AI075846 | Hs.133998 ESTs | 2.27 | HT29, MB-MDA-435s, OVCA-R |
| 316466 | AI911204 | Hs.126365 ESTs | 2.27 | NCI-H460, NCI-358, BT474 |
| 334430 | | CH22_FGENES.385_3 | 2.27 | NCI-H345, NCI-H69, PRSC_con |
| 331941 | AA452257 | Hs.99272 ESTs | 2.26 | PRSC_con, LnCap, PRSC_log |
| 301230 | AW269804 | Hs.153019 ESTs | 2.26 | NCI-H345, PRSC_log, NCI-H520 |
| 317394 | AI935024 | Hs.190518 ESTs | 2.26 | NCI-H345, PRSC_con, PRSC_log |
| 306220 | AA928363 | EST singleton (not in UniGene) with exon | 2.26 | NCI-H345, PRSC_con, PRSC_log |
| 304134 | H54627 | EST singleton (not in UniGene) with exon | 2.26 | DU145, CALU6, PC3 |
| 335421 | | CH22_FGENES.551_1 | 2.26 | NCI-H69, PRSC_con, PRSC_log |
| 305260 | AA679280 | Hs.156110 Immunoglobulin kappa variable 1D-8 | 2.26 | NCI-H345, NCI-H69, PRSC_con |
| 303592 | AA421129 | EST | 2.26 | CALU6, OVCA-R, DU145 |
| 317982 | AI004985 | Hs.130607 ESTs | 2.26 | PC3, MB-MDA-435s, A549 |
| 325304 | | CH.11_hs gij5866910 | 2.26 | MCF7, CALU6, A549 |
| 334118 | | CH22_FGENES.330_19 | 2.26 | PRSC_con, NCI-H69, PRSC_log |
| 335687 | | CH22_FGENES.596_2 | 2.26 | A549, CALU6, LnCap |
| 334035 | | CH22_FGENES.322_3 | 2.26 | NCI-H345, PRSC_con, RPWE-2 |
| 305454 | AA738413 | EST singleton (not in UniGene) with exon | 2.25 | EB, HT29, CALU6 |
| 335902 | | CH22_FGENES.635_10 | 2.25 | EB, DU145, HT29 |
| 339215 | | CH22_FF113D11.GENSCAN.6-10 | 2.25 | PRSC_con, PRSC_log, RPWE-2 |
| 328810 | | CH.07_hs gij5868327 | 2.25 | PC3, OVCA-R, MB-MDA-453 |
| 337396 | | CH22_FGENES.749-1 | 2.25 | EB, A549, DU145 |
| 336808 | | CH22_FGENES.205-3 | 2.25 | NCI-H345, NCI-H69, PRSC_con |
| 305808 | AA853958 | EST singleton (not in UniGene) with exon | 2.24 | MB-MDA-453, DU145, EB |
| 333571 | | CH22_FGENES.188_2 | 2.24 | MCF7, MB-MDA-453, PC3 |
| 323023 | AA225188 | Hs.258539 ESTs | 2.24 | EB, DU145, CALU6 |
| 334626 | | CH22_FGENES.416_2 | 2.24 | NCI-H69, NCI-H345, PRSC_log |
| 333593 | | CH22_FGENES.210_2 | 2.24 | NCI-H69, NCI-H345, PRSC_con |
| 326708 | | CH.20_hs gij5867593 | 2.24 | NCI-H460, NCI-H23, NCI-H520 |
| 314502 | AI041717 | Hs.132141 ESTs | 2.23 | NCI-H345, RPWE-2, PRSC_con |
| 309181 | AI951727 | EST singleton (not in UniGene) with exon | 2.23 | PRSC_con, PC3, MB-MDA-231 |
| 324926 | H56196 | Hs.117798 ESTs | 2.23 | EB, EB, DU145 |
| 333532 | | CH22_FGENES.227_3 | 2.23 | CALU6, CALU6, MB-MDA-453 |
| 328243 | | CH.06_hs gij6056292 | 2.23 | PC3, LnCap, LnCap |
| 327037 | | CH.21_hs gij5531965 | 2.23 | LnCap, DU145, EB |
| 307380 | AI222985 | EST singleton (not in UniGene) with exon | 2.23 | NCI-H345, PRSC_con, PRSC_log |
| 334766 | | CH22_FGENES.428_15 | 2.23 | PRSC_log, NCI-H345, RPWE-2 |
| 335236 | | CH22_FGENES.515_8 | 2.23 | OVCA-R, MCF7, BT474 |
| 336615 | | CH22_FGENES.613_5 | 2.23 | NCI-H69, PRSC_log, PRSC_con |
| 307558 | AI281998 | EST singleton (not in UniGene) with exon | 2.23 | DU145, OVCA-R, CALU6 |
| 308029 | AI457115 | Hs.62954 ferritin; heavy polypeptide 1 | 2.23 | EB, OVCA-R, MB-MDA-453 |
| 331508 | N47559 | Hs.46732 EST | 2.23 | MB-MDA-453, MCF7, BT474 |
| 320980 | AJ237672 | Hs.214142 5,10-methylenetetrahydrofolate reductase | 2.23 | OVCA-R, EB, EB |
| 304241 | AA010976 | EST singleton (not in UniGene) with exon | 2.23 | BT474, MB-MDA-453s, MB-MDA-231 |
| 314682 | AI190864 | Hs.178226 ESTs; Weakly similar to III ALU SUBFAMI | 2.23 | MB-MDA-231, MCF7, OVCA-R |
| 308382 | AI624301 | EST singleton (not in UniGene) with exon | 2.22 | OVCA-R, BT474, CALU6 |
| 314476 | AW207857 | Hs.169604 ESTs | 2.22 | DU145, EB, A549 |
| 327884 | | CH.06_hs gij5868130 | 2.22 | NCI-H69, PRSC_log, PRSC_con |
| 337279 | | CH22_FGENES.665-2 | 2.22 | NCI-H345, NCI-H69, PRSC_con |
| 302263 | AA325517 | EST | 2.22 | BT474, NCI-H520, DU145 |

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| 322840 | AA083710 | EST cluster (not in UniGene) | 2.22 | HT29, MB-MDA-453, CALU6 |
| 307574 | AI283549 | EST singleton (not in UniGene) with exon | 2.22 | OVCA-R, CALU6, BT474 |
| 319027 | AA716612 | EST cluster (not in UniGene) | 2.22 | LnCap, NCI-H69, NCI-H69 |
| 305925 | AA877893 | EST singleton (not in UniGene) with exon | 2.22 | NCI-H345, NCI-H69, NCI-H345 |
| 329725 | | CH.14_p2_g 5065785 | 2.22 | NCI-H69, PRSC_con, NCI-H345 |
| 316194 | AW298529 | Hs.255774 ESTs | 2.22 | CALU6, EB, NCI-H520 |
| 301119 | AF142579 | EST | 2.22 | A549, OVCA-R, EB |
| 333815 | | CH22_FGENES.282_4 | 2.22 | MB-MDA-435s, EB, MB-MDA-435 |
| 334358 | | CH22_FGENES.378_1 | 2.22 | NCI-H345, RPWE-2, PRSC_con |
| 303763 | AF043250 | Hs.30928 DNA segment on chromosome 19 (unique) | 112.21 | Caco2, NCI-H23, NCI-H520 |
| 335593 | | CH22_FGENES.581_32 | 2.21 | NCI-H345, PRSC_log, RPWE-2 |
| 334026 | | CH22_FGENES.318_3 | 2.21 | NCI-H69, PRSC_con, NCI-H345 |
| 322224 | AF086064 | EST cluster (not in UniGene) | 2.21 | PRSC_con, PRSC_log, RPWE-2 |
| 309836 | AW295497 | Hs.157397 ESTs | 2.21 | NCI-H345, PRSC_con, RPWE-2 |
| 332669 | M33374 | Hs.561 NADH dehydrogenase (ubiquinone) 1 beta s | 2.21 | NCI-H520, CALU6, OVCA-R |
| 307629 | AI300246 | EST singleton (not in UniGene) with exon | 2.21 | MB-MDA-231, MB-MDA-453, HT29 |
| 300470 | T87841 | EST | 2.21 | PC3, EB, CALU6 |
| 330064 | | CH.19_p2_g 6165044 | 2.21 | NCI-H69, PRSC_con, BT474 |
| 338819 | | CH22_DJ246D7.GENSCAN.1-24 | 2.21 | NCI-H69, RPWE-2, PRSC_log |
| 337797 | | CH22_EM:AC005500.GENSCAN.34 | 2.21 | LnCap, NCI-H69, NCI-H520 |
| 328025 | | CH.05_hs_g 5902482 | 2.2 | RPWE-2, PRSC_con, PRSC_log |
| 326240 | | CH.17_hs_g 5867260 | 2.2 | EB, LnCap, MB-MDA-453 |
| 312865 | AW005376 | Hs.173280 ESTs | 2.2 | DU145, DU145, OVCA-R |
| 338450 | | CH22_EM:AC005500.GENSCAN.359-36 | 2.2 | MCF7, MB-MDA-453, MB-MDA-435s |
| 302532 | U60181 | Hs.248115 growth hormone secretagogue receptor | 2.2 | PRSC_con, PRSC_log, PRSC_log |
| 321132 | AA081495 | EST cluster (not in UniGene) | 2.2 | NCI-H23, NCI-H520, NCI-358 |
| 337787 | | CH22_EM:AC000097.GENSCAN.123-3 | 2.2 | EB, PC3, LnCap |
| 337032 | | CH22_FGENES.438-3 | 2.2 | NCI-H69, NCI-H345, RPWE-2 |
| 300026 | M11507 | AFFX control transferrin receptor | 2.2 | HT29, EB, MB-MDA-231 |
| 333139 | | CH22_FGENES.83_16 | 2.2 | HT29, MB-MDA-453, Caco2 |
| 334298 | | CH22_FGENES.372_4 | 2.2 | PRSC_con, PRSC_log, RPWE-2 |
| 335002 | | CH22_FGENES.470_7 | 2.2 | PRSC_con, NCI-H345, NCI-H345 |
| 335000 | | CH22_FGENES.470_5 | 2.2 | EB, PC3, A549 |
| 337298 | | CH22_FGENES.678-3 | 2.2 | NCI-H69, A549, HT29 |
| 302461 | AF104253 | Hs.241381 cofactor required for Sp1 transcriptional | 2.2 | EB, CALU6, LnCap |
| 334819 | | CH22_FGENES.436_15 | 2.19 | CALU6, BT474, Caco2 |
| 300426 | AW452660 | Hs.253296 ESTs | 2.19 | DU145, CALU6, HT29 |
| 302569 | AC004472 | multiple UniGene matches | 2.19 | RPWE-2, PRSC_log, PRSC_con |
| 339401 | | CH22_BA232E17.GENSCAN.7-7 | 2.19 | NCI-H345, NCI-H69, PRSC_log |
| 328791 | | CH.07_hs_g 5868309 | 2.19 | DU145, PC3, HT29 |
| 337333 | | CH22_FGENES.711-3 | 2.19 | NCI-H69, NCI-H345, PRSC_log |
| 339363 | | CH22_BA354112.GENSCAN.33-6 | 2.19 | NCI-H69, PRSC_log, PRSC_con |
| 329429 | | CH.Y_hs_g 5868882 | 2.19 | CALU6, HT29, OVCA-R |
| 336927 | | CH22_FGENES.348-3 | 2.19 | NCI-H69, PRSC_log, NCI-358 |
| 336351 | | CH22_FGENES.816_3 | 2.19 | DU145, EB, MB-MDA-231 |
| 313466 | AA004731 | Hs.148876 ESTs | 2.19 | CALU6, DU145, OVCA-R |
| 307433 | AI244895 | EST singleton (not in UniGene) with exon | 2.19 | NCI-H23, NCI-H23, NCI-358 |
| 336590 | | CH22_FGENES.51_2 | 2.19 | PRSC_con, NCI-H69, PRSC_log |
| 310758 | AI770001 | Hs.209445 ESTs | 2.18 | EB, MB-MDA-231, BT474 |
| 327823 | | CH.05_hs_g 5867968 | 2.18 | PRSC_con, NCI-H69, NCI-H345 |
| 313257 | N92638 | EST cluster (not in UniGene) | 2.18 | PRSC_log, RPWE-2, PRSC_con |
| 335377 | | CH22_FGENES.543_17 | 2.18 | PC3, MB-MDA-435s, CALU6 |
| 303958 | ALD42931 | EST singleton (not in UniGene) with exon | 2.18 | NCI-H345, RPWE-2, PRSC_con |
| 320153 | AF064594 | Hs.120360 phospholipase A2; group VI | 2.18 | LnCap, PC3, MB-MDA-435s |
| 335201 | | CH22_FGENES.508_10 | 2.18 | OVCA-R, DU145, HT29 |
| 338591 | | CH22_EM:AC005500.GENSCAN.434-4 | 2.18 | NCI-H69, NCI-H345, RPWE-2 |
| 331958 | AA455960 | Hs.99405 ESTs | 2.18 | MCF7, NCI-H23, NCI-H460 |
| 337218 | | CH22_FGENES.614-2 | 2.18 | CALU6, A549, MCF7 |
| 309470 | AW118833 | EST singleton (not in UniGene) with exon | 2.18 | PC3, EB, MB-MDA-435s |
| 331896 | AA435495 | Hs.97174 H sapiens mRNA; cDNA DKFZp566E164 (from | 2.18 | 2.18 RPWE-2, NCI-H69, PRSC_log |
| 330275 | | CH.05_p2_g 6671904 | 2.18 | NCI-H345, PRSC_log, PRSC_con |
| 335817 | | CH22_FGENES.618_5 | 2.18 | A549, Caco2, PC3 |
| 332896 | | CH22_FGENES.35_10 | 2.18 | NCI-H345, RPWE-2, PRSC_log |
| 303294 | AA205300 | EST | 2.17 | MB-MDA-435s, A549, MCF7 |
| 338703 | | CH22_EM:AC005500.GENSCAN.480-2 | 2.17 | HT29, BT474, NCI-H69 |
| 300115 | AI215044 | Hs.208130 ESTs | 2.17 | PC3, OVCA-R, HT29 |
| 330979 | H22466 | Hs.31795 ESTs | 2.17 | MCF7, EB, MB-MDA-435s |
| 317246 | AW105092 | Hs.155690 ESTs | 2.17 | MB-MDA-453, DU145, EB |
| 329078 | | CH.X_hs_g 5868597 | 2.17 | MB-MDA-453, MB-MDA-231, BT474 |
| 312554 | AI222630 | Hs.109390 ESTs | 2.17 | NCI-H520, OVCA-R, MCF7 |
| 323207 | AI052795 | Hs.192201 ESTs | 2.17 | NCI-H69, NCI-H345, PRSC_log |
| 301894 | AA484435 | Hs.41997 alpha-1-B glycoprotein | 2.17 | PRSC_con, LnCap, PRSC_log |
| 329097 | | CH.X_hs_g 5868624 | 2.16 | MB-MDA-231, MCF7, NCI-358 |
| 328328 | | CH.07_hs_g 5868375 | 2.16 | NCI-H345, PRSC_con, NCI-H69 |
| 302671 | AA522440 | Hs.135917 ESTs | 2.16 | BT474, DU145, A549 |
| 329201 | | CH.X_hs_g 5868718 | 2.16 | OVCA-R, PC3, MB-MDA-435s |

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| 329802 | | CH.15_p2 g 6634760 | 2.16 | PRSC_con, NCI-H69, NCI-H345 |
| 334435 | | CH22_FGENES.385_10 | 2.16 | PRSC_con, NCI-H345, RPWE-2 |
| 330742 AA400979 Hs.25691 | | calcitonin receptor-like receptor activi | 2.16 | MCF7, MB-MDA-453, PC3 |
| 328484 | | CH.07_hs g 5868454 | 2.16 | NCI-H69, PRSC_log, NCI-H345 |
| 334784 | | CH22_FGENES.432_9 | 2.16 | PRSC_log, RPWE-2, PRSC_con |
| 337771 | | CH22_EM:AC000097.GENSCAN.119-10 | 2.16 | NCI-H69, PRSC_con, RPWE-2 |
| 300181 AI284955 Hs.157568 | | ESTs: Weakly similar to ataxin-2 [M.musc | 2.16 | DU145, EB, CALU6 |
| 300268 AI539446 Hs.245450 | | ESTs | 2.16 | PRSC_con, RPWE-2, PRSC_log |
| 309575 AW168096 Hs.195188 | | glyceraldehyde-3-phosphate dehydrogenase | 2.16 | A549, NCI-H23, MB-MDA-453 |
| 336548 | | CH22_FGENES.841_5 | 2.16 | NCI-H345, NCI-H69, MB-MDA-231 |
| 328506 | | CH.07_hs g 5868471 | 2.16 | EB, A549, CALU6 |
| 330189 | | CH.05_p2 g 6165182 | 2.16 | NCI-H460, MCF7, MB-MDA-453 |
| 305480 AA746500 Hs.25911 | | HLA-B associated transcript-2 | 2.16 | EB, DU145, NCI-358 |
| 302270 R56151 | | EST | 2.16 | OVCA-R, MB-MDA-435s, PRSC_con |
| 306669 AI004899 | | EST singleton (not in UniGene) with exon | 2.16 | PRSC_log, PRSC_con, NCI-H345 |
| 325887 | | CH.16_hs g 5867087 | 2.16 | EB, CALU6, NCI-358 |
| 327015 | | CH.21_hs g 5867664 | 2.15 | EB, PC3, HT29 |
| 338576 | | CH22_EM:AC005500.GENSCAN.429-1 | 2.15 | NCI-H69, NCI-H345, PRSC_con |
| 333592 | | CH22_FGENES.209_2 | 2.15 | NCI-H69, OVCA-R, PRSC_con |
| 317253 AW071241 Hs.199685 | | ESTs | 2.15 | MB-MDA-435s, NCI-H23, MB-MDA-453 |
| 302301 R67493 Hs.127150 | | ESTs: Weakly similar to ZINC FINGER PROT | 2.15 | PC3, MCF7, MB-MDA-435s |
| 336858 | | CH22_FGENES.293-8 | 2.15 | RPWE-2, PRSC_con, NCI-H69 |
| 308417 AI640693 Hs.2186 | | eukaryotic translation elongation factor | 2.15 | EB, OVCA-R, CALU6 |
| 338177 | | CH22_EM:AC005500.GENSCAN.219-5 | 2.15 | NCI-H345, NCI-H23, NCI-H520 |
| 337592 | | CH22_C20H12.GENSCAN.6-7 | 2.15 | PC3, A549, HT29 |
| 325945 | | CH.16_hs g 5867138 | 2.15 | MB-MDA-453, MB-MDA-435s, DU145 |
| 335262 | | CH22_FGENES.520_3 | 2.15 | EB, PC3, A549 |
| 333665 | | CH22_FGENES.244_1 | 2.15 | PRSC_con, RPWE-2, PRSC_log |
| 333710 | | CH22_FGENES.250_25 | 2.14 | PRSC_log, NCI-H69, PRSC_con |
| 304927 AA604728 Hs.195188 | | glyceraldehyde-3-phosphate dehydrogenase | 2.14 | LnCap, PC3, MCF7 |
| 336999 | | CH22_FGENES.417-20 | 2.14 | NCI-H69, NCI-H345, PRSC_con |
| 313283 W32480 Hs.157099 | | ESTs | 2.14 | EB, MB-MDA-231, A549 |
| 306221 AA928686 | | EST singleton (not in UniGene) with exon | 2.14 | NCI-H460, PRSC_con, NCI-H23 |
| 333205 | | CH22_FGENES.102_5 | 2.14 | NCI-H69, PRSC_con, PRSC_log |
| 312932 AI804218 Hs.209614 | | ESTs | 2.14 | PRSC_con, NCI-H345, RPWE-2 |
| 328938 | | CH.08_hs g 5868500 | 2.14 | HT29, PC3, MB-MDA-453 |
| 326746 | | CH.20_hs g 5867611 | 2.14 | NCI-H345, NCI-H69, PRSC_con |
| 337964 | | CH22_EM:AC005500.GENSCAN.100-9 | 2.14 | RPWE-2, PRSC_con, PRSC_log |
| 337984 | | CH22_EM:AC005500.GENSCAN.110-2 | 2.14 | EB, DU145, NCI-H345 |
| 337704 | | CH22_EM:AC000097.GENSCAN.87-6 | 2.14 | NCI-H69, NCI-H460, NCI-358 |
| 302162 AF119046 | | EST | 2.14 | MB-MDA-435s, PC3, EB |
| 303192 AA081755 Hs.8059 | | ESTs: Highly similar to SYNAPTOTAGMIN IV | 2.14 | MB-MDA-435s, MB-MDA-435s, MB-MDA-453 |
| 306200 AA926816 | | EST singleton (not in UniGene) with exon | 2.14 | MB-MDA-453, CALU6, DU145 |
| 303996 AW515979 Hs.84298 | | CD74 antigen (invariant polypeptid of majo | 2.14 | LnCap, MB-MDA-231, BT474 |
| 325409 | | CH.12_hs g 58666921 | 2.14 | PRSC_log, PRSC_con, RPWE-2 |
| 308558 AI700145 Hs.172182 | | poly(A)-binding protein; cytoplasmic 1 | 2.14 | MCF7, EB, MB-MDA-435s |
| 302185 AA243837 Hs.156915 | | ESTs | 2.14 | MB-MDA-453, MCF7, EB |
| 303021 W39612 | | EST | 2.14 | PRSC_con, NCI-H69, RPWE-2 |
| 301005 AW451916 Hs.210848 | | ESTs | 2.14 | DU145, EB, HT29 |
| 336029 | | CH22_FGENES.672_4 | 2.14 | NCI-H69, PRSC_con, RPWE-2 |
| 305443 AA736653 | | EST singleton (not in UniGene) with exon | 2.14 | NCI-358, NCI-H520, NCI-H23 |
| 335485 | | CH22_FGENES.570_17 | 2.13 | NCI-H460, MB-MDA-435s, MCF7 |
| 304817 AA584712 | | EST singleton (not in UniGene) with exon | 2.13 | MCF7, MCF7, NCI-H520 |
| 309859 AW298760 | | EST singleton (not in UniGene) with exon | 2.13 | NCI-H69, PRSC_con, LnCap |
| 326206 | | CH.17_hs g 5867219 | 2.13 | EB, MB-MDA-231, LnCap |
| 303656 AA437189 Hs.122574 | | ESTs | 2.13 | LnCap, MB-MDA-435s, EB |
| 334745 | | CH22_FGENES.426_3 | 2.13 | OVCA-R, DU145, MB-MDA-453 |
| 318504 T26453 | | EST cluster (not in UniGene) | 2.13 | RPWE-2, LnCap, CALU6 |
| 306839 AI077385 | | EST singleton (not in UniGene) with exon | 2.13 | MCF7, MB-MDA-453, MB-MDA-435s |
| 303843 W94322 Hs.58094 | | melanoma inhibitory activity | 2.13 | MB-MDA-435s, NCI-H345, RPWE-2 |
| 308444 AI659388 Hs.197097 | | EST | 2.13 | MB-MDA-453, MCF7, BT474 |
| 301322 AW448965 Hs.256305 | | ESTs | 2.13 | NCI-H345, LnCap, PC3 |
| 326597 | | CH.21_hs g 5867660 | 2.13 | HT29, A549, CALU6 |
| 326793 | | CH.20_hs g 5867631 | 2.13 | PRSC_log, PRSC_con, MB-MDA-453 |
| 320360 H12405 | | EST cluster (not in UniGene) | 2.12 | MB-MDA-231, BT474, HT29 |
| 316301 AW205279 Hs.192009 | | ESTs | 2.12 | DU145, DU145, EB |
| 335371 | | CH22_FGENES.543_9 | 2.12 | PC3, MB-MDA-435s, DU145 |
| 301178 AA828385 | | EST | 2.12 | EB, OVCA-R, LnCap |
| 326136 | | CH.17_hs g 5867202 | 2.12 | RPWE-2, PRSC_log, PRSC_con |
| 339213 | | CH22_FF113D11.GENSCAN.6-8 | 2.12 | OVCA-R, PC3, MB-MDA-231 |
| 335980 | | CH22_FGENES.653_2 | 2.12 | BT474, BT474, OVCA-R |
| 314380 AA758797 Hs.192807 | | ESTs | 2.11 | PRSC_con, PRSC_log, RPWE-2 |
| 306779 AI041302 | | EST singleton (not in UniGene) with exon | 2.11 | NCI-H345, PRSC_con, PRSC_log |
| 335774 | | CH22_FGENES.607_10 | 2.11 | PC3, A549, MB-MDA-453 |
| 334914 | | CH22_FGENES.457_3 | 2.11 | PRSC_con, NCI-H345, NCI-H69 |
| 304619 AA515554 Hs.119598 | | ribosomal protein L3 | 2.11 | EB, MB-MDA-453, MB-MDA-435s |

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| 303358 | AI199714 | Hs.158149 | ESTs | 2.11 | CALU6, OVCA-R, DU145 |
| 306558 | AA994743 | | EST singleton (not in UniGene) with exon | 2.11 | HT29, MB-MDA-453, CALU6 |
| 337781 | | CH22_EM:AC000097.GENSCAN.121-3 | | 2.11 | PRSC_log, PRSC_con, RPWE-2 |
| 333140 | | CH22_FGENES.84_1 | | 2.11 | HT29, NCI-H69, OVCA-R |
| 315081 | AI247134 | Hs.155281 | ESTs | 2.11 | MB-MDA-453, MCF7, HT29 |
| 302965 | AA446441 | Hs.138842 | ESTs | 2.11 | NCI-358, NCI-H23, CALU6 |
| 302138 | N83965 | | EST | 2.11 | PRSC_log, PRSC_con, NCI-H345 |
| 320802 | D83824 | Hs.185055 | BENE protein | 2.11 | A549, PC3, HT29 |
| 322152 | AA565332 | | EST cluster (not in UniGene) | 2.11 | A549, CALU6, EB |
| 326418 | | CH.19_hs gi 5867365 | | 2.1 | EB, OVCA-R, DU145 |
| 308709 | AI783498 | Hs.181165 | eukaryotic translation elongation factor | 2.1 | MB-MDA-435s, MB-MDA-453, DU145 |
| 332737 | C01852 | Hs.84359 | hypothetical protein | 2.1 | NCI-H23, A549, DU145 |
| 333283 | | CH22_FGENES.128_13 | | 2.1 | NCI-H345, RPWE-2, PRSC_con |
| 328636 | | CH.07_hs gi 6004473 | | 2.1 | DU145, EB, MB-MDA-453 |
| 329187 | | CH.X_hs gi 5868713 | | 2.1 | NCI-358, NCI-H23, NCI-H460 |
| 305999 | AA889603 | | EST singleton (not in UniGene) with exon | 2.1 | HT29, OVCA-R, PC3 |
| 333220 | | CH22_FGENES.104_12 | | 2.1 | PRSC_con, PRSC_log, RPWE-2 |
| 335092 | | CH22_FGENES.492_2 | | 2.1 | NCI-H69, PRSC_con, NCI-H345 |
| 304887 | AA599355 | | EST singleton (not in UniGene) with exon | 2.1 | DU145, EB, MCF7 |
| 325359 | | CH.12_hs gi 5866920 | | 2.1 | MB-MDA-453, EB, MB-MDA-435s |
| 330956 | H08730 | Hs.6933 | ESTs | 2.1 | NCI-H520, PRSC_con, NCI-H345 |
| 323786 | AW449315 | Hs.165795 | ESTs | 2.1 | OVCA-R, A549, LnCap |
| 333619 | | CH22_FGENES.219_3 | | 2.1 | BT474, OVCA-R, HT29 |
| 324538 | AW502979 | | EST cluster (not in UniGene) | 2.09 | CALU6, A549, DU145 |
| 303405 | AA308601 | | EST | 2.09 | DU145, CALU6, NCI-H69 |
| 328570 | | CH.07_hs gi 5868231 | | 2.09 | LnCap, MB-MDA-231, DU145 |
| 308971 | AI871218 | Hs.224731 | EST | 2.09 | NCI-H23, NCI-H460, NCI-358 |
| 330467 | K02268 | Hs.22584 | prodorphin | 2.09 | PC3, BT474, MB-MDA-453 |
| 334793 | | CH22_FGENES.433_5 | | 2.09 | EB, DU145, LnCap |
| 300908 | AA618335 | Hs.146137 | ESTs; Weakly similar to putative [C.eleg] | 2.09 | NCI-H345, PRSC_log, PRSC_con |
| 309656 | AW197060 | Hs.195188 | glyceraldehyde-3-phosphate dehydrogenase | 2.09 | A549, NCI-H23, NCI-H460 |
| 320963 | AB029041 | Hs.209646 | KIAA1118 protein | 2.09 | PRSC_con, PRSC_log, NCI-H345 |
| 310833 | AW295351 | Hs.169136 | ESTs | 2.09 | PC3, LnCap, MB-MDA-453 |
| 335693 | | CH22_FGENES.596_8 | | 2.09 | NCI-H69, LnCap, PRSC_log |
| 325966 | | CH.16_hs gi 5867147 | | 2.09 | MCF7, CALU6, MB-MDA-453 |
| 329319 | | CH.X_hs gi 6381976 | | 2.09 | NCI-H460, EB, DU145 |
| 338526 | | CH22_EM:AC005500.GENSCAN.396-14 | | 2.09 | NCI-H69, NCI-H345, PRSC_log |
| 336751 | | CH22_FGENES.128-5 | | 2.09 | NCI-H69, NCI-H345, PRSC_log |
| 325510 | | CH.12_hs gi 5866974 | | 2.09 | HT29, OVCA-R, CALU6 |
| 323553 | AA292626 | Hs.122854 | ESTs | 2.08 | NCI-H345, RPWE-2, NCI-358 |
| 326343 | | CH.17_hs gi 5525295 | | 2.08 | EB, LnCap, DU145 |
| 335470 | | CH22_FGENES.568_3 | | 2.08 | NCI-H69, PRSC_con, PRSC_log |
| 320122 | T93681 | Hs.187515 | ESTs | 2.08 | MCF7, MB-MDA-453, BT474 |
| 335320 | | CH22_FGENES.534_7 | | 2.08 | BT474, MB-MDA-231, HT29 |
| 307120 | AI184343 | | EST singleton (not in UniGene) with exon | 2.08 | HT29, MCF7, PC3 |
| 338080 | | CH22_EM:AC005500.GENSCAN.172-11 | | 2.08 | LnCap, PC3, HT29 |
| 313113 | AI056258 | Hs.122523 | ESTs | 2.08 | MCF7, DU145, MB-MDA-453 |
| 337685 | | CH22_EM:AC000097.GENSCAN.77-1 | | 2.08 | NCI-H69, NCI-H345, PRSC_log |
| 327461 | | CH.02_hs gi 6004455 | | 2.08 | NCI-H23, BT474, NCI-358 |
| 335895 | | CH22_FGENES.635_3 | | 2.08 | HT29, MB-MDA-231, NCI-H520 |
| 303933 | AW471472 | | EST singleton (not in UniGene) with exon | 2.08 | MB-MDA-231, BT474, NCI-H345 |
| 314803 | AI935159 | Hs.166841 | ESTs; Weakly similar to MYOSIN LIGHT CHA NON-MUSCLE ISOZYMES [H.sapiens] | 2.08 | PC3, A549, BT474 |
| 302722 | U53530 | | EST | 2.08 | DU145, MB-MDA-435s, OVCA-R |
| 307703 | AI318588 | | EST singleton (not in UniGene) with exon | 2.08 | HT29, MB-MDA-435s, CALU6 |
| 310558 | AI334985 | Hs.176976 | ESTs | 2.08 | A549, LnCap, PC3 |
| 315276 | AA860090 | | EST cluster (not in UniGene) | 2.08 | PC3, MCF7, OVCA-R |
| 306443 | AA976950 | | EST singleton (not in UniGene) with exon | 2.07 | OVCA-R, PC3, EB |
| 307961 | AI421059 | | EST singleton (not in UniGene) with exon | 2.07 | HT29, OVCA-R, CALU6 |
| 329735 | | CH.14_p2 gi 5065780 | | 2.07 | EB, HT29, OVCA-R |
| 335193 | | CH22_FGENES.507_8 | | 2.07 | EB, A549, A549 |
| 320347 | R34423 | Hs.221535 | ESTs | 2.07 | CALU6, A549, EB |
| 316153 | AA724474 | Hs.147208 | ESTs | 2.07 | MB-MDA-453, PC3, HT29 |
| 300921 | AW293224 | Hs.232165 | ESTs | 2.07 | HT29, CALU6, CALU6 |
| 319264 | T65096 | | EST cluster (not in UniGene) | 2.07 | MB-MDA-453, MCF7, CALU6 |
| 330204 | | CH.05_p2 gi 6013606 | | 2.07 | OVCA-R, DU145, EB |
| 317070 | AI142037 | Hs.125379 | ESTs | 2.07 | PRSC_con, NCI-H345, OVCA-R |
| 337645 | | CH22_EM:AC000097.GENSCAN.10-8 | | 2.07 | NCI-H345, PRSC_log, NCI-H69 |
| 312501 | AW450490 | Hs.132886 | ESTs | 2.07 | NCI-H520, CALU6, MCF7 |
| 335587 | | CH22_FGENES.581_26 | | 2.07 | NCI-H69, NCI-H345, PRSC_log |
| 311482 | AI917706 | Hs.129997 | ESTs | 2.07 | NCI-H520, MCF7, MB-MDA-435s |
| 302488 | AF161441 | | EST | 2.07 | EB, DU145, CALU6 |
| 304692 | AA554202 | Hs.76057 | heat shock 27kD protein 1 | 2.07 | MCF7, MB-MDA-453, PC3 |
| 325369 | | CH.12_hs gi 5866920 | | 2.07 | DU145, DU145, MB-MDA-453 |
| 306284 | AA936835 | | EST singleton (not in UniGene) with exon | 2.07 | BT474, MB-MDA-231, HT29 |
| 337402 | | CH22_FGENES.752-1 | | 2.07 | A549, BT474, DU145 |

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| 327418 | | CH_02_hs gij5867750 | 2.07 | MCF7, MB-MDA-453, MB-MDA-435s |
| 317977 | AI004775 | Hs.205091 ESTs; Weakly similar to WW domain bindin | 2.07 | BT474, MB-MDA-453, PC3 |
| 331870 | AA428560 | Hs.161845 EST | 2.07 | MB-MDA-231, MB-MDA-435s, BT474 |
| 300750 | AA514805 | Hs.105464 ESTs | 2.07 | HT29, BT474, BT474 |
| 336657 | | CH22_FGENES.35-14 | 2.07 | MB-MDA-453, MCF7, NCI-H460 |
| 336035 | | CH22_FGENES.678_6 | 2.07 | NCI-H69, PRSC_con, RPWE-2 |
| 325320 | | CH.11_hs gij5866370 | 2.06 | NCI-H69, PRSC_log, PRSC_con |
| 306053 | AA905312 | EST singleton (not in UniGene) with exon | 2.06 | HT29, OVCA-R, MB-MDA-231 |
| 333175 | | CH22_FGENES.95_2 | 2.06 | LnCap, HT29, DU145 |
| 304491 | AA437096 | Hs.115502 EST | 2.06 | MB-MDA-435s, CALU6, CALU6 |
| 310632 | AI697536 | Hs.176991 ESTs | 2.06 | NCI-H69, PRSC_log, NCI-H345 |
| 338521 | | CH22_EM:AC005500.GENSCAN.395-35 | 2.06 | NCI-H345, PRSC_log, PRSC_log |
| 334900 | | CH22_FGENES.452_14 | 2.06 | A549, CALU6, NCI-H69 |
| 337451 | | CH22_FGENES.774-2 | 2.06 | PRSC_con, PRSC_log, RPWE-2 |
| 308792 | AI815153 | Hs.195188 glyceraldehyde-3-phosphate dehydrogenase | 2.06 | DU145, BT474, MB-MDA-453 |
| 336854 | | CH22_FGENES.280-1 | 2.06 | LnCap, EB, MB-MDA-435s |
| 304485 | AA434076 | EST singleton (not in UniGene) with exon | 2.06 | MB-MDA-231, BT474, CALU6 |
| 326458 | | CH.19_hs gij5867400 | 2.06 | EB, DU145, LnCap |
| 303506 | AA340605 | Hs.105887 ESTs | 2.06 | LnCap, MCF7, CALU6 |
| 333628 | | CH22_FGENES.226_2 | 2.06 | NCI-H520, NCI-358, NCI-358 |
| 300763 | AA180753 | EST | 2.06 | NCI-H69, NCI-H345, PRSC_con |
| 334836 | | CH22_FGENES.439_6 | 2.06 | NCI-H345, PRSC_con, RPWE-2 |
| 335217 | | CH22_FGENES.512_3 | 2.06 | PRSC_log, PRSC_con, NCI-H69 |
| 338970 | | CH22_EM:AC005500.GENSCAN.26-3 | 2.06 | A549, MB-MDA-453, LnCap |
| 334842 | | CH22_FGENES.439_21 | 2.06 | DU145, HT29, CALU6 |
| 309309 | AW006428 | Hs.232857 EST | 2.06 | EB, DU145, OVCA-R |
| 332949 | | CH22_FGENES.47_12 | 2.06 | EB, DU145, OVCA-R |
| 310530 | AW369663 | Hs.150150 ESTs | 2.06 | PRSC_con, PRSC_log, RPWE-2 |
| 329401 | | CH.X_hs gij6682544 | 2.06 | NCI-H69, PRSC_con, RPWE-2 |
| 316893 | AA837332 | EST cluster (not in UniGene) | 2.06 | OVCA-R, MCF7, MB-MDA-453 |
| 325022 | W95840 | Hs.59745 NADH dehydrogenase (ubiquinone) flavoprotein | 2.06 | Caco2, NCI-358, OVCA-R |
| 329839 | | CH.14_p2 gij6572062 | 2.05 | MB-MDA-231, RPWE-2, CALU6 |
| 306668 | AI004890 | EST singleton (not in UniGene) with exon | 2.05 | DU145, MB-MDA-453, MCF7 |
| 315604 | AW137442 | Hs.136965 ESTs | 2.05 | LnCap, EB, PC3 |
| 318551 | AI909951 | Hs.239307 tyrosyl-tRNA synthetase | 2.05 | NCI-H345, PRSC_con, RPWE-2 |
| 339344 | | CH22_BA354112.GENSCAN.28-1 | 2.05 | BT474, MB-MDA-231, A549 |
| 310621 | AI632098 | Hs.198099 ESTs | 2.05 | NCI-H69, RPWE-2, MCF7 |
| 327051 | | CH.21_hs gij6531965 | 2.05 | PRSC_con, NCI-H345, PRSC_log |
| 336827 | | CH22_FGENES.236-2 | 2.05 | NCI-H345, A549, MB-MDA-231 |
| 311846 | AI078033 | Hs.177170 ESTs; Moderately similar to !!! ALU SUB | 2.05 | OVCA-R, DU145, CALU6 |
| 335036 | | CH22_FGENES.475_14 | 2.05 | NCI-H69, PRSC_con, NCI-H345 |
| 313100 | N52880 | Hs.122817 ESTs | 2.05 | RPWE-2, NCI-H345, PRSC_log |
| 301927 | AF014459 | Hs.113250 retinoblastoma (X-linked; juvenile) 1 | 2.05 | MB-MDA-231, NCI-H345, PRSC_con |
| 326070 | | CH.17_hs gij5867175 | 2.05 | MB-MDA-435s, MB-MDA-231, BT474 |
| 338514 | | CH22_EM:AC005500.GENSCAN.392-4 | 2.05 | PRSC_con, PRSC_log, RPWE-2 |
| 328098 | | CH.06_hs gij5868020 | 2.05 | DU145, CALU6, EB |
| 301102 | AA679361 | Hs.249487 ESTs | 2.05 | NCI-H460, PRSC_con, NCI-H23 |
| 306193 | AA923457 | EST singleton (not in UniGene) with exon | 2.05 | NCI-H345, PRSC_con, RPWE-2 |
| 317027 | AA883808 | Hs.174148 ESTs | 2.05 | EB, DU145, CALU6 |
| 336102 | AI239895 | Hs.130555 CH22_FGENES.693_2 | 2.04 | LnCap, NCI-H69, PRSC_log |
| 301372 | | ESTs | 2.04 | PRSC_con, RPWE-2, PRSC_log |
| 332525 | | CH22_FGENES.116_4 | 2.04 | NCI-358, A549, HT29 |
| 322516 | AW372340 | Hs.159717 ESTs | 2.04 | HT29, MB-MDA-231, BT474 |
| 324148 | AA393624 | EST cluster (not in UniGene) | 2.04 | RPWE-2, PRSC_con, MB-MDA-231 |
| 338770 | | CH22_EM:AC005500.GENSCAN.520-1 | 2.04 | PRSC_con, NCI-H69, NCI-H460 |
| 314795 | AI798611 | Hs.157277 ESTs | 2.04 | EB, PC3, LnCap |
| 333004 | | CH22_FGENES.60_1 | 2.04 | A549, NCI-358, DU145 |
| 302405 | AW245825 | Hs.211914 NADH dehydrogenase (ubiquinone) Fe-S pro | 2.04 | NCI-H520, CALU6, Caco2 |
| 323587 | AI905527 | Hs.141901 ESTs; Moderately similar to !!! ALU SUB | 2.04 | EB, A549, HT29 |
| 300898 | AI276278 | Hs.157176 ESTs | 2.04 | PC3, MB-MDA-453, BT474 |
| 301506 | AI143978 | Hs.143519 ESTs; Weakly similar to testicular tektin | 2.04 | NCI-H69, RPWE-2, NCI-H345 |
| 325851 | | CH.16_hs gij5867067 | 2.04 | MB-MDA-231, HT29, EB |
| 323945 | AI125604 | Hs.155117 ESTs | 2.04 | MCF7, DU145, DU145 |
| 303265 | AW160951 | EST | 2.04 | LnCap, OVCA-R, DU145 |
| 334135 | | CH22_FGENES.336_2 | 2.04 | PC3, A549, MB-MDA-435s |
| 329793 | | CH.14_p2 gij6522661 | 2.04 | DU145, CALU6, HT29 |
| 332595 | AA256431 | Hs.3244 G protein pathway suppressor 2 | 2.04 | A549, CALU6, NCI-H23 |
| 316059 | AW166388 | Hs.250181 ESTs | 2.04 | MCF7, HT29, A549 |
| 324104 | AW246071 | Hs.133122 ESTs | 2.04 | Caco2, A549, MCF7 |
| 306801 | AI052653 | EST singleton (not in UniGene) with exon | 2.03 | EB, LnCap, PC3 |
| 338096 | | CH22_EM:AC005500.GENSCAN.181-14 | 2.03 | DU145, HT29, CALU6 |
| 327544 | | CH.03_hs gij5867797 | 2.03 | PRSC_con, NCI-H69, NCI-H345 |
| 318813 | F13195 | EST cluster (not in UniGene) | 2.03 | PRSC_con, RPWE-2, PRSC_log |
| 325289 | | CH.11_hs gij5866903 | 2.03 | EB, OVCA-R, A549 |
| 311099 | T56361 | Hs.182167 hemoglobin; gamma A | 2.03 | HT29, BT474, EB |
| 316079 | AA922213 | Hs.121735 ESTs | 2.03 | LnCap, OVCA-R, EB |

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| 309533 | AW151131 | EST singleton (not in UniGene) with exon | 2.03 | MB-MDA-231, BT474, LnCap |
| 338579 | | CH22_EM:AC005500.GENSCAN.431-3 | 2.03 | NCI-H69, NCI-H345, RPWE-2 |
| 326549 | | CH.19_hs gl 5867307 | 2.03 | NCI-H69, Caco2, NCI-H345 |
| 320012 | AI628384 | Hs.193745 ESTs | 2.03 | BT474, MB-MDA-453, MCF7 |
| 334111 | | CH22_FGENES.330_10 | 2.03 | NCI-H69, MB-MDA-231, BT474 |
| 327123 | | CH.21_hs gl 5631971 | 2.03 | NCI-H345, NCI-H69, RPWE-2 |
| 324568 | AW502311 | EST cluster (not in UniGene) | 2.03 | NCI-H345, NCI-H520, NCI-H460 |
| 306012 | AA896989 | EST singleton (not in UniGene) with exon | 2.03 | NCI-H69, PRSC_log, PRSC_con |
| 303105 | AA012877 | EST | 2.03 | RPWE-2, OVCA-R, EB |
| 302194 | U52219 | Hs.158329 G protein-coupled receptor 50 | 2.03 | NCI-H520, NCI-H23, PC3 |
| 326646 | | CH.20_hs gl 5867562 | 2.03 | NCI-H460, OVCA-R, HT29 |
| 304060 | T61464 | EST singleton (not in UniGene) with exon | 2.03 | NCI-H345, PRSC_con, PRSC_log |
| 304667 | AA535602 | EST singleton (not in UniGene) with exon | 2.03 | A549, DU145, EB |
| 330514 | M83652 | Hs.53155 properdin P factor, complement | 2.02 | NCI-H23, NCI-H460, NCI-358 |
| 310324 | AI473273 | Hs.159874 ESTs; Weakly similar to GLUTAMATE [H.sap | 2.02 | NCI-H345, MB-MDA-231, BT474 |
| 330327 | | CH.08_p2 gl 5919194 | 2.02 | NCI-H345, NCI-H69, PRSC_log |
| 308447 | AI659985 | EST singleton (not in UniGene) with exon | 2.02 | NCI-H345, RPWE-2, PRSC_log |
| 307778 | AI344972 | Hs.231498 EST | 2.02 | NCI-H69, CALU6, OVCA-R |
| 319459 | T87351 | Hs.194121 ESTs | 2.02 | NCI-H460, NCI-358, NCI-H520 |
| 300935 | AA513644 | Hs.222815 ESTs; Weakly similar to Wiskott-Aldrich | 2.02 | DU145, EB, OVCA-R |
| 314318 | AL037405 | Hs.176141 ESTs | 2.02 | PRSC_con, LnCap, PRSC_log |
| 334779 | | CH22_FGENES.432_1 | 2.02 | EB, HT29, DU145 |
| 336994 | | CH22_FGENES.410-2 | 2.02 | NCI-H345, PRSC_con, NCI-H69 |
| 334076 | | CH22_FGENES.327_31 | 2.02 | OVCA-R, CALU6, EB |
| 318116 | AW452865 | Hs.132339 ESTs | 2.02 | MB-MDA-231, NCI-H69, NCI-H345 |
| 326783 | | CH.20_hs gl 5525298 | 2.02 | NCI-H69, PRSC_con, RPWE-2 |
| 336142 | | CH22_FGENES.705_4 | 2.02 | NCI-H69, PRSC_log, PRSC_con |
| 320913 | AA663733 | EST cluster (not in UniGene) | 2.02 | DU145, EB, CALU6 |
| 301644 | AW239364 | EST | 2.02 | PRSC_con, RPWE-2, PRSC_log |
| 300944 | AW081072 | Hs.164624 ESTs; Weakly similar to Slit-3 protein [| 2.01 | RPWE-2, NCI-H69, NCI-H23 |
| 310080 | AW137088 | Hs.144857 ESTs | 2.01 | PRSC_con, NCI-H345, PRSC_log |
| 311248 | AI863918 | Hs.195078 ESTs | 2.01 | NCI-H345, NCI-H69, RPWE-2 |
| 319207 | R87679 | EST cluster (not in UniGene) | 2.01 | HT29, A549, NCI-H460 |
| 334760 | | CH22_FGENES.428_9 | 2.01 | NCI-358, NCI-H69, PRSC_log |
| 338368 | | CH22_EM:AC005500.GENSCAN.325-2 | 2.01 | NCI-H23, NCI-H520, NCI-H460 |
| 317300 | AI417007 | Hs.166338 ESTs | 2.01 | NCI-H460, DU145, NCI-H23 |
| 323699 | AW178750 | EST cluster (not in UniGene) | 2.01 | MCF7, MB-MDA-453, OVCA-R |
| 301366 | AA907713 | Hs.221667 ESTs | 2.01 | PRSC_con, NCI-H345, RPWE-2 |
| 333306 | | CH22_FGENES.137_3 | 2.01 | NCI-H69, NCI-H345, PRSC_con |
| 328031 | | CH.06_hs gl 5902482 | 2.01 | MB-MDA-231, NCI-H345, PRSC_con |
| 301806 | AA326007 | Hs.12056 astaglycoprotein receptor 1 | 2.01 | MB-MDA-453, DU145, EB |
| 300993 | AA584930 | Hs.191777 ESTs; Weakly similar to XAP-5-like prote | 2.01 | HT29, NCI-H23, NCI-358 |
| 320042 | T84520 | EST cluster (not in UniGene) | 2.01 | PRSC_con, NCI-H345, NCI-H69 |
| 331082 | R17059 | Hs.22100 ESTs | 2.01 | EB, DU145, MB-MDA-435s |
| 308851 | A1829820 | EST singleton (not in UniGene) with exon | 2.01 | DU145, EB, PC3 |
| 301163 | AAT32066 | EST | 2.01 | OVCA-R, PC3, MB-MDA-435s |
| 304734 | AA576428 | EST singleton (not in UniGene) with exon | 2.01 | LnCap, MB-MDA-453, DU145 |
| 334855 | | CH22_FGENES.442_6 | 2.01 | NCI-H345, RPWE-2, PRSC_log |
| 337121 | | CH22_FGENES.519-1 | 2.01 | NCI-H69, NCI-H345, PRSC_con |
| 331838 | AA412498 | Hs.104778 ESTs | 2.01 | BT474, BT474, MCF7 |
| 339181 | | CH22_DA59H18.GENSCAN.72-6 | 2.01 | NCI-H345, PRSC_con, NCI-H69 |
| 327564 | | CH.03_hs gl 5867811 | 2.01 | BT474, HT29, DU145 |
| 304108 | R63932 | Hs.28467 EST | 2 | BT474, OVCA-R, MCF7 |
| 315036 | AA534953 | Hs.163297 ESTs | 2 | MB-MDA-435s, MB-MDA-453, LnCap |
| 312777 | W92809 | Hs.138557 ESTs | 2 | PRSC_con, NCI-H345, MB-MDA-231 |
| 305888 | AA868536 | Hs.126145 EST | 2 | HT29, HT29, BT474 |
| 323185 | R52177 | EST cluster (not in UniGene) | 2 | EB, A549, BT474 |
| 308681 | AI761307 | EST singleton (not in UniGene) with exon | 2 | RPWE-2, PRSC_con, NCI-H345 |
| 325755 | | CH.14_hs gl 5682474 | 2 | NCI-H345, PRSC_con, PRSC_log |
| 324376 | AW499705 | EST cluster (not in UniGene) | 2 | DU145, BT474, PC3 |
| 331890 | AA432166 | Hs.3577 succinate dehydrogenase complex; subunit | 2 | CALU6, MB-MDA-453, A549 |

Table 4

| Pkey | Exr_Accn | UniG_ID | Complete_Title | Ratio_Met/BS | Top 3 expressing cell lines |
|--------|----------|-------------------------------|--|--------------|-------------------------------------|
| 313168 | AI801098 | Hs.151500 | ESTs | 12.23 | Caco2, EB, OVCA-R |
| 334593 | | CH22_FGENES.408_3 | | 8.06 | NCI-H69, OVCA-R, OVCA-R |
| 331084 | R20655 | Hs.81281 | Human clone 23732 mRNA; partial cds | 7.89 | LnCap, OVCA-R, EB |
| 324598 | AA502659 | Hs.163986 | ESTs | 7.77 | OVCA-R, EB, CALU6 |
| 314071 | AA192455 | Hs.188690 | ESTs | 7.76 | CALU6, EB, DU145 |
| 315178 | AW362945 | Hs.162459 | ESTs | 6.81 | OVCA-R, EB, CALU6 |
| 325519 | | CH.12_hs g 6017036 | | 6.34 | NCI-H69, NCI-H345, PRSC_con |
| 331433 | H68097 | Hs.161023 | EST | 6.16 | OVCA-R, A549, EB |
| 315021 | AA533447 | | EST cluster (not in UniGene) | 6.15 | PC3, EB, CALU6 |
| 337695 | | CH22_EM:AC000097.GENSCAN.84-1 | | 5.84 | NCI-H69, NCI-H345, DU145 |
| 324048 | AA378739 | | EST cluster (not in UniGene) | 5.77 | OVCA-R, DU145, EB |
| 300781 | AA731209 | | EST cluster (not in UniGene) with exon h | 5.72 | MB-MDA-453, MCF7, MB-MDA-435s |
| 320701 | AI093177 | Hs.134923 | ESTs | 5.68 | A549, NCI-H345, NCI-H69 |
| 332471 | AA416957 | Hs.120980 | nuclear receptor co-repressor 2 | 5.68 | LnCap, A549, OVCA-R |
| 331858 | AA421163 | Hs.163848 | ESTs | 5.66 | OVCA-R, DU145, Caco2 |
| 330987 | H40988 | Hs.131965 | ESTs5.35 | 5.31 | NCI-H345, OVCA-R, LnCap |
| 322309 | AF086372 | | EST cluster (not in UniGene) | 5.17 | OVCA-R, DU145, PC3 |
| 324733 | AA582082 | Hs.199410 | ESTs | 5.16 | PRSC_con, PRSC_log, NCI-H345 |
| 313577 | AA565051 | Hs.155029 | ESTs | 5.16 | OVCA-R, PC3, EB |
| 310956 | AW271974 | Hs.210295 | ESTs | 5.15 | NCI-H69, PRSC_log, PRSC_con |
| 311332 | AW282247 | Hs.255052 | ESTs | 5.05 | Caco2, OVCA-R, EB |
| 314522 | AI732331 | Hs.187750 | ESTs; Moderately similar to !!! ALU CLA | 5.04 | EB, DU145, HT29 |
| 330886 | AA135608 | Hs.189384 | ESTs; Weakly similar to !!! ALU SUBFAMI | 4.93 | OVCA-R, DU145, Caco2 |
| 313597 | AW162263 | Hs.249990 | ESTs | 4.84 | NCI-H460, NCI-H345, NCI-H23 |
| 314439 | AI539443 | Hs.137447 | ESTs | 4.84 | DU145, Caco2, MB-MDA-231 |
| 320807 | AA086110 | Hs.188536 | H sapiens clone 24838 mRNA seq | 4.83 | PC3, OVCA-R, DU145 |
| 311804 | AA135159 | Hs.203349 | ESTs | 4.82 | OVCA-R, PC3, Caco2 |
| 321354 | AA078493 | | EST cluster (not in UniGene) | 4.81 | DU145, EB, OVCA-R |
| 325169 | H01560 | Hs.163818 | ESTs; Weakly similar to !!! ALU SUBFAMI | 4.8 | NCI-H345, DU145, LnCap |
| 312828 | AI865455 | Hs.211818 | ESTs; Moderately similar to !!! ALU SUB | 4.78 | DU145, DU145, DU145 |
| 321226 | AA311443 | Hs.251416 | H sapiens mRNA; cDNA DKFZp586E2317 (from CH.05_hs g 5867964 | 4.75 | DU145, OVCA-R, MB-MDA-453 |
| 327772 | | | | 4.74 | HT29, MB-MDA-231, NCI-H345 |
| 315642 | AA742222 | Hs.120634 | ESTs | 4.7 | DU145, EB, MB-MDA-453 |
| 311905 | AA555215 | Hs.151913 | ESTs | 4.7 | DU145, Caco2, PRSC_con |
| 312754 | R99834 | Hs.250383 | ESTs | 4.59 | OVCA-R, PC3, EB |
| 336637 | | CH22_FGENES.13-7 | | 4.58 | NCI-H69, PRSC_log, NCI-H345 |
| 331644 | T99544 | Hs.173734 | ESTs; Weakly similar to !!! ALU CLASS B | 4.55 | OVCA-R, NCI-H345, Caco2 |
| 336984 | | CH22_FGENES.401-2 | | 4.55 | Caco2, Caco2, EB |
| 316261 | AW134485 | Hs.144957 | ESTs | 4.53 | NCI-H460, NCI-H345, Caco2 |
| 300417 | AW139492 | Hs.245887 | ESTs | 4.52 | DU145, CALU6, EB |
| 300610 | N72596 | Hs.99120 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 4.52 | OVCA-R, PC3, EB |
| 324718 | AI557019 | Hs.116467 | ESTs | 4.5 | LnCap, PC3, PRSC_con |
| 332170 | F04112 | Hs.177178 | ESTs | 4.47 | Caco2, DU145, DU145 |
| 324042 | AA377589 | | EST cluster (not in UniGene) | 4.45 | NCI-H345, PRSC_con, PRSC_log |
| 331148 | R73816 | Hs.17385 | ESTs | 4.44 | CALU6, OVCA-R, EB |
| 328981 | | CH.09_hs g 5868527 | | 4.43 | HT29, BT474, NCI-H69 |
| 321920 | N63915 | | EST cluster (not in UniGene) | 4.34 | Caco2, A549, A549 |
| 320832 | AA214584 | | EST cluster (not in UniGene) | 4.34 | NCI-H23, CALU6, OVCA-R |
| 321971 | AI680459 | Hs.201441 | ESTs | 4.33 | DU145, HT29, CALU6 |
| 308572 | AI707882 | | EST singleton (not in UniGene) with exon | 4.33 | MCF7, NCI-H345, OVCA-R |
| 302459 | AF169255 | | EST cluster (not in UniGene) with exon h | 4.28 | MB-MDA-231, OVCA-R, LnCap |
| 321847 | T08401 | | EST cluster (not in UniGene) | 4.25 | MB-MDA-453, MB-MDA-435s, MB-MDA-231 |
| 337884 | | CH22_EM:AC005500.GENSCAN.54-2 | | 4.23 | HT29, NCI-H23, MB-MDA-435s |
| 307494 | AI269188 | Hs.175656 | EST | 4.23 | NCI-H23, NCI-H520, NCI-358 |
| 314915 | AA573072 | Hs.187748 | ESTs; Weakly similar to !!! ALU SUBFAMI | 4.21 | PC3, OVCA-R, Caco2 |
| 336638 | | CH22_FGENES.14-2 | | 4.21 | NCI-H69, NCI-H345, PRSC_log |
| 319379 | T91443 | Hs.193963 | ESTs | 4.2 | PC3, OVCA-R, LnCap |
| 312332 | R33041 | Hs.106200 | ESTs | 4.19 | NCI-H69, OVCA-R, NCI-H460 |
| 331445 | H89093 | Hs.41215 | ESTs | 4.19 | EB, HT29, DU145 |
| 315841 | AW136397 | Hs.247572 | ESTs | 4.19 | Caco2, MB-MDA-453, LnCap |
| 315712 | AI950133 | Hs.120882 | ESTs; Moderately similar to !!! ALU SUB | 4.18 | LnCap, NCI-H345, OVCA-R |
| 319559 | AA773876 | Hs.251597 | ESTs | 4.15 | NCI-H345, Caco2, DU145 |
| 300791 | AI138455 | Hs.256135 | ESTs; Moderately similar to !!! ALU SUB | 4.13 | NCI-358, RPWE-2, NCI-H460 |

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|--------|----------|--|------|--------------------------------|
| 312129 | AW300867 | EST cluster (not in UniGene) | 4.12 | OVCA-R, MCF7, A549 |
| 321165 | AA411263 | Hs.128783 ESTs | 4.11 | OVCA-R, Caco2, PRSC_con |
| 313220 | AI971981 | Hs.118241 ESTs | 4.1 | OVCA-R, DU145, Caco2 |
| 314022 | AW452420 | Hs.248678 ESTs | 4.1 | OVCA-R, EB, PC3 |
| 321359 | AW474412 | EST cluster (not in UniGene) | 4.1 | DU145, OVCA-R, PC3 |
| 328841 | | CH.07_hs g 6381920 | 4.09 | NCI-H69, PRSC_log, NCI-H345 |
| 337888 | | CH22_EMAC005500.GENSCAN.56-6 | 4.09 | NCI-H345, NCI-H69, OVCA-R |
| 333245 | | CH22_FGENES.115_2 | 4.09 | PRSC_log, PRSC_con, NCI-H345 |
| 311958 | AI247472 | Hs.132865 ESTs | 4.06 | EB, DU145, CALU6 |
| 314775 | AI149880 | Hs.188809 ESTs | 4.06 | OVCA-R, PC3, EB |
| 317901 | AW150944 | Hs.250541 ESTs | 4.06 | BT474, MB-MDA-453, MB-MDA-435s |
| 309985 | AW452919 | EST singleton (not in UniGene) with exon | 4.05 | MB-MDA-453, NCI-H23, NCI-H4520 |
| 311004 | AA632846 | EST cluster (not in UniGene) | 4.05 | MB-MDA-453, OVCA-R, EB |
| 323497 | AI523613 | Hs.221544 ESTs | 4.04 | LnCap, OVCA-R, EB |
| 332347 | W60326 | Hs.221716 ESTs | 4.04 | EB, CALU6, PC3 |
| 331388 | AA456852 | Hs.43543 suppressor of white apricot homolog 2 | 4.01 | A549, EB, Caco2 |
| 313197 | AI738851 | Hs.222487 ESTs | 3.96 | OVCA-R, EB, PC3 |
| 315710 | AA931550 | Hs.192785 ESTs | 3.95 | EB, MB-MDA-231, OVCA-R |
| 316897 | AA838114 | EST cluster (not in UniGene) | 3.94 | OVCA-R, A549, MB-MDA-453 |
| 322564 | W86440 | Hs.118344 ESTs | 3.94 | NCI-H460, Caco2, EB |
| 304605 | AA513225 | EST singleton (not in UniGene) with exon | 3.9 | NCI-H345, RPWE-2, BT474 |
| 325726 | | CH.14_hs g 6552447 | 3.9 | OVCA-R, LnCap, LnCap |
| 320190 | R32047 | Hs.141012 ESTs; Weakly similar to ALU SUBFAMI | 3.89 | DU145, NCI-H23, PRSC_log |
| 331566 | N63062 | Hs.48703 EST | 3.87 | NCI-H23, NCI-H460, NCI-358 |
| 319403 | T98413 | EST cluster (not in UniGene) | 3.86 | NCI-H345, PRSC_log, LnCap |
| 324643 | AI436356 | Hs.130729 ESTs | 3.84 | OVCA-R, DU145, NCI-H345 |
| 315298 | AI969314 | Hs.211377 ESTs | 3.82 | NCI-H345, PRSC_con, PRSC_log |
| 321632 | AA419617 | EST cluster (not in UniGene) | 3.81 | EB, OVCA-R, A549 |
| 313219 | N74924 | Hs.182099 ESTs | 3.8 | EB, Caco2, OVCA-R |
| 330833 | AA046804 | ESTs; Weakly similar to ALU SUBFAMI | 3.8 | LnCap, DU145, PC3 |
| 327289 | | CH.01_hs g 5867481 | 3.79 | EB, HT29, DU145 |
| 314429 | AW300749 | EST cluster (not in UniGene) | 3.79 | OVCA-R, PC3, PRSC_con |
| 314475 | AI911160 | Hs.127505 ESTs | 3.79 | DU145, CALU6, NCI-H69 |
| 317130 | AW293995 | Hs.192277 ESTs | 3.78 | EB, PC3, Caco2 |
| 336635 | | CH22_FGENES.13-5 | 3.77 | NCI-H69, NCI-H345, PRSC_log |
| 333323 | | CH22_FGENES.138_16 | 3.76 | NCI-H460, NCI-H23, PRSC_con |
| 332135 | AA620331 | Hs.245351 EST | 3.75 | NCI-H345, A549, Caco2 |
| 316979 | AA861087 | EST cluster (not in UniGene) | 3.75 | NCI-H345, NCI-H69, RPWE-2 |
| 316435 | AI671871 | Hs.192618 ESTs; Weakly similar to ALU CLASS C | 3.74 | MB-MDA-435s, MCF7, MB-MDA-453 |
| 315422 | AW135357 | Hs.192374 ESTs | 3.73 | OVCA-R, A549, EB |
| 335616 | | CH22_FGENES.613_5 | 3.72 | NCI-H69, NCI-H345, RPWE-2 |
| 320258 | W93241 | EST cluster (not in UniGene) | 3.71 | MB-MDA-231, NCI-H69, EB |
| 300463 | N52510 | Hs.186470 ESTs | 3.69 | OVCA-R, A549, DU145 |
| 306881 | AI088695 | EST singleton (not in UniGene) with exon | 3.68 | CALU6, HT29, EB |
| 337304 | | CH22_FGENES.681-6 | 3.67 | MCF7, MB-MDA-453, LnCap |
| 323693 | AW297758 | Hs.249721 ESTs | 3.67 | OVCA-R, MB-MDA-453, DU145 |
| 331073 | R07998 | Hs.186228 ESTs; Weakly similar to ALU SUBFAMI | 3.67 | RPWE-2, NCI-H345, OVCA-R |
| 318162 | AW286277 | Hs.132171 ESTs | 3.67 | MB-MDA-231, DU145, CALU6 |
| 318042 | AW294522 | Hs.149991 ESTs | 3.66 | EB, HT29, CALU6 |
| 308069 | AI470895 | EST singleton (not in UniGene) with exon | 3.64 | Caco2, Caco2, NCI-H23 |
| 327614 | | CH.04_hs g 6525283 | 3.62 | NCI-H460, NCI-H345, NCI-H69 |
| 337514 | | CH22_FGENES.809-7 | 3.62 | NCI-358, NCI-H23, NCI-H460 |
| 332093 | AA608794 | Hs.112592 ESTs | 3.6 | EB, OVCA-R, DU145 |
| 327793 | | CH.05_hs g 5867979 | 3.59 | LnCap, OVCA-R, EB |
| 331053 | N70242 | Hs.183146 ESTs | 3.59 | OVCA-R, EB, Caco2 |
| 303769 | AA134888 | Hs.173415 ESTs | 3.58 | HT29, CALU6, CALU6 |
| 319872 | R97130 | Hs.189699 ESTs | 3.58 | PRSC_con, LnCap, RPWE-2 |
| 317902 | AI828602 | Hs.211265 ESTs | 3.57 | CALU6, NCI-H345, OVCA-R |
| 324090 | AI656531 | Hs.116070 ESTs | 3.57 | PRSC_con, NCI-H345, PRSC_log |
| 300120 | AW204314 | Hs.170784 ESTs | 3.57 | NCI-H69, NCI-H345, PRSC_con |
| 307752 | AI339447 | EST singleton (not in UniGene) with exon | 3.56 | NCI-358, HT29, MB-MDA-231 |
| 322438 | W44531 | Hs.167851 ESTs | 3.55 | NCI-H345, NCI-H69, Caco2 |
| 311275 | AI659166 | Hs.207144 ESTs | 3.55 | MB-MDA-231, PRSC_con, LnCap |
| 338830 | | CH22_DJ246D7.GENSCAN.6-7 | 3.54 | LnCap, PC3, OVCA-R |
| 315647 | AA648983 | Hs.212911 ESTs | 3.53 | OVCA-R, MB-MDA-453, CALU6 |
| 331469 | N22273 | Hs.39140 ESTs | 3.52 | EB, A549, CALU6 |
| 313445 | AI123657 | Hs.127264 ESTs | 3.51 | EB, OVCA-R, A549 |
| 330139 | | CH.21_p2_g 4210430 | 3.5 | EB, CALU6, DU145 |
| 304450 | AA404521 | Hs.10326 coatomer protein complex; subunit epsilon | 3.49 | NCI-H345, NCI-H69, NCI-H460 |
| 325763 | | CH.14_hs g 6682475 | 3.49 | PC3, BT474, OVCA-R |
| 312803 | AA677934 | Hs.117864 ESTs | 3.47 | OVCA-R, Caco2, MB-MDA-453 |
| 303654 | AA436942 | Hs.168308 ESTs | 3.46 | DU145, NCI-H460, NCI-H69 |
| 317924 | AI222324 | Hs.166306 ESTs; Weakly similar to zinc finger prot | 3.46 | PRSC_con, PRSC_log, NCI-H69 |
| 312354 | AA036955 | Hs.167040 ESTs | 3.44 | Caco2, MB-MDA-435s, NCI-H460 |
| 337517 | | CH22_FGENES.814-6 | 3.43 | NCI-H69, HT29, PC3 |
| 324865 | AA702138 | Hs.114103 ESTs | 3.42 | NCI-H23, NCI-H460, NCI-H520 |

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|--------|----------|---|------|-----------------------------------|
| 323755 | AW300094 | EST cluster (not in UniGene) | 3.42 | PRSC_con, RPWE-2, NCI-H345 |
| 314452 | AL042699 | Hs.209222 ESTs | 3.42 | NCI-H345, PRSC_con, PRSC_log |
| 337911 | | CH22_EM:AC005500.GENSCAN.59-6 | 3.42 | OVCA-R, PC3, HT29 |
| 318086 | AI025499 | Hs.132238 ESTs | 3.41 | CALU6, LnCap, OVCA-R |
| 311859 | AA704705 | Hs.181044 ESTs; Weakly similar to Chain A; Human O Complexed With L-Canaline [H.sapiens] | 3.41 | LnCap, MB-MDA-435s, A549 |
| 314409 | H15560 | Hs.131833 ESTs | 3.41 | NCI-H69, LnCap, LnCap |
| 323333 | AA228883 | EST cluster (not in UniGene) | 3.41 | Caco2, OVCA-R, NCI-H69 |
| 325690 | | CH.14_hs g 5867021 | 3.4 | HT29, CALU6, DU145 |
| 314539 | AA398216 | Hs.180092 ESTs | 3.4 | MB-MDA-231, BT474, EB |
| 310567 | AI691065 | Hs.155780 ESTs | 3.4 | PRSC_con, NCI-H345, NCI-H69 |
| 330527 | S77356 | transcript ch21=oligomycin sensitivity/c 8 stomach cancer cell lines, mRNA, 262 n | 3.39 | NCI-H23, Caco2, A549 |
| 314660 | AA436007 | Hs.188780 ESTs | 3.39 | OVCA-R, BT474, Caco2 |
| 321321 | AB033072 | EST cluster (not in UniGene) | 3.39 | NCI-358, EB, Caco2 |
| 323356 | AA234009 | Hs.188715 ESTs | 3.38 | DU145, CALU6, CALU6 |
| 328592 | | CH.07_hs g 5868227 | 3.38 | MCF7, NCI-358, MB-MDA-231 |
| 311116 | AI631195 | Hs.232193 ESTs | 3.36 | NCI-H520, NCI-H23, PRSC_log |
| 323853 | AA393460 | EST cluster (not in UniGene) | 3.36 | DU145, EB, Caco2 |
| 327740 | | CH.05_hs g 5867943 | 3.35 | EB, LnCap, OVCA-R |
| 326857 | | CH.20_hs g 5552460 | 3.33 | NCI-H69, MCF7, NCI-H345 |
| 317787 | AW339612 | Hs.249364 ESTs | 3.31 | NCI-H345, PRSC_con, PRSC_log |
| 325760 | | CH.14_hs g 5552449 | 3.3 | EB, CALU6, HT29 |
| 337513 | | CH22_FGENES.809-4 | 3.29 | LnCap, NCI-H23, NCI-H460 |
| 336606 | | CH22_FGENES.428_3 | 3.29 | NCI-H69, A549, NCI-H23 |
| 322895 | AW470295 | Hs.192152 ESTs | 3.29 | DU145, Caco2, EB |
| 314312 | AA814971 | Hs.257634 ESTs | 3.29 | RPWE-2, NCI-H69, NCI-H345 |
| 328224 | | CH.06_hs g 5868101 | 3.28 | DU145, NCI-H345, LnCap |
| 336128 | | CH22_FGENES.701_16 | 3.27 | BT474, NCI-H520, MB-MDA-231 |
| 332442 | AA281323 | Hs.4947 ESTs | 3.27 | Caco2, PC3, NCI-H345 |
| 302514 | M14269 | EST cluster (not in UniGene) with exon h | 3.27 | DU145, CALU6, NCI-H520 |
| 313749 | AW450376 | Hs.130803 ESTs | 3.26 | OVCA-R, NCI-H69, DU145 |
| 302891 | AI681578 | Hs.114164 ESTs | 3.26 | LnCap, NCI-H345, PRSC_log |
| 334690 | | CH22_FGENES.420_3 | 3.25 | NCI-H69, RPWE-2, PRSC_con |
| 308676 | AI761036 | EST singleton (not in UniGene) with exon | 3.25 | DU145, MB-MDA-231, HT29 |
| 304254 | AA046273 | Hs.111334 ferritin; light polypeptide | 3.24 | OVCA-R, DU145, A549 |
| 311994 | AA648314 | Hs.13849 ESTs | 3.24 | NCI-H60, NCI-H23, MB-MDA-453 |
| 321020 | AB023170 | Hs.227850 KIAA0953 protein | 3.24 | EB, MCF7, MB-MDA-435s |
| 316724 | AA810788 | Hs.123337 ESTs | 3.23 | DU145, OVCA-R, BT474 |
| 326942 | | CH.21_hs g 56004466 | 3.22 | HT29, BT474, NCI-H23 |
| 324824 | AI826999 | Hs.224624 ESTs | 3.21 | OVCA-R, MB-MDA-453, EB |
| 320789 | R78712 | EST cluster (not in UniGene) | 3.21 | DU145, LnCap, EB |
| 315070 | AW131368 | Hs.186736 ESTs | 3.21 | Caco2, NCI-358, NCI-H460 |
| 303794 | AW241987 | Hs.197025 ESTs | 3.19 | OVCA-R, PC3, LnCap |
| 310237 | AI884313 | Hs.158906 ESTs | 3.19 | NCI-358, NCI-H345, MCF7 |
| 313960 | AA130859 | EST cluster (not in UniGene) | 3.18 | MB-MDA-231, HT29, BT474 |
| 336634 | | CH22_FGENES.13-4 | 3.18 | NCI-H69, NCI-H345, BT474 |
| 301085 | AA779058 | Hs.190428 ESTs; Weakly similar to NG26 [H.sapiens] | 3.17 | NCI-H345, NCI-H345, NCI-358 |
| 313774 | AW136836 | Hs.144583 ESTs | 3.17 | Caco2, EB, OVCA-R |
| 307177 | AI188864 | EST singleton (not in UniGene) with exon | 3.17 | EB, CALU6, CALU6 |
| 324025 | AI174861 | Hs.190623 ESTs | 3.17 | OVCA-R, DU145, PC3 |
| 313099 | AI307359 | Hs.128064 ESTs | 3.17 | MB-MDA-231, BT474, EB |
| 305536 | AA770682 | EST singleton (not in UniGene) with exon | 3.17 | NCI-358, Caco2, HT29 |
| 331916 | AA446131 | Hs.124918 ESTs | 3.17 | EB, OVCA-R, Caco2 |
| 314912 | AI431345 | Hs.161784 ESTs | 3.17 | EB, BT474, MCF7 |
| 303388 | AL039504 | EST cluster (not in UniGene) with exon h | 3.17 | HT29, NCI-358, Caco2 |
| 332273 | R05818 | Hs.173830 ESTs | 3.16 | MCF7, DU145, EB |
| 314697 | AW088739 | Hs.243770 ESTs | 3.16 | MB-MDA-453, DU145, MCF7 |
| 335344 | | CH22_FGENES.536_3 | 3.15 | PRSC_log, NCI-H345, PRSC_con |
| 326162 | | CH.17_hs g 5867168 | 3.15 | BT474, HT29, HT29 |
| 304467 | AA424703 | EST singleton (not in UniGene) with exon | 3.15 | NCI-H23, RPWE-2, NCI-H460 |
| 339340 | | CH22_BA354112.GENSCAN.27-8 | 3.15 | LnCap, OVCA-R, MB-MDA-453 |
| 325393 | | CH.12_hs g 5866921 | 3.13 | Caco2, NCI-H23, NCI-358 |
| 315367 | AA732484 | Hs.169399 ESTs | 3.13 | OVCA-R, EB, MB-MDA-453 |
| 307085 | AI160868 | EST singleton (not in UniGene) with exon | 3.12 | RPWE-2, PRSC_con, PRSC_log |
| 313001 | N29264 | Hs.249591 ESTs; Moderately similar to III ALU SUB | 3.12 | NCI-H345, OVCA-R, Caco2 |
| 307606 | AI290006 | EST singleton (not in UniGene) with exon | 3.12 | MB-MDA-231, HT29, NCI-H23 |
| 325710 | | CH.14_hs g 5682473 | 3.09 | NCI-H69, MB-MDA-453, BT474 |
| 313810 | AA400079 | Hs.257854 ESTs | 3.09 | EB, DU145, CALU6 |
| 335482 | | CH22_FGENES.570_11 | 3.09 | NCI-H460, NCI-358, NCI-H23 |
| 326310 | | CH.17_hs g 5867277 | 3.08 | MCF7, MB-MDA-453, PC3 |
| 325742 | | CH.14_hs g 5552448 | 3.08 | NCI-H23, NCI-H460, HT29 |
| 312467 | AI241809 | Hs.75458 ribosomal protein L18 | 3.08 | NCI-358, NCI-H23, NCI-H460 |
| 327309 | | CH.01_hs g 5456757 | 3.07 | NCI-H69, MB-MDA-435s, MB-MDA-435s |
| 310583 | AW205632 | Hs.211198 ESTs | 3.07 | OVCA-R, A549, Caco2 |
| 322373 | W25673 | Hs.130829 ESTs | 3.07 | NCI-H69, PRSC_con, NCI-H345 |

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|--------|-----------|-----------|--|------|-------------------------------|
| 324497 | AW152624 | Hs.136340 | ESTs | 3.06 | NCI-H345, RPWE-2, PRSC_con |
| 315095 | AAB31815 | Hs.243788 | ESTs | 3.06 | Caco2, DU145, EB |
| 302445 | N79647 | | EST cluster (not in UniGene) with exon h | 3.05 | OVCA-R, A549, NCI-H460 |
| 302842 | AW383226 | Hs.163834 | ESTs; Highly similar to Chp [R.norvegicus] | 3.05 | A549, DU145, NCI-H23 |
| 317346 | AA952875 | Hs.221274 | ESTs | 3.04 | BT474, HT29, HT29 |
| 334650 | | | CH22_FGENES.417_17 | 3.04 | MCF7, BT474, OVCA-R |
| 306644 | AI002913 | | EST singleton (not in UniGene) with exon | 3.04 | CALU6, MCF7, BT474 |
| 322682 | AI110679 | | EST cluster (not in UniGene) | 3.03 | NCI-H345, RPWE-2, OVCA-R |
| 311065 | AW204582 | Hs.224906 | ESTs | 3.03 | PRSC_log, PRSC_con, NCI-H460 |
| 318623 | AA355439 | Hs.151547 | ESTs | 3.03 | DU145, MB-MDA-435s, HT29 |
| 304978 | AA617735 | | EST singleton (not in UniGene) with exon | 3.03 | CALU6, BT474, MB-MDA-435s |
| 305554 | AA774567 | Hs.121774 | EST | 3.03 | EB, NCI-H460, Caco2 |
| 302574 | U66199 | Hs.249165 | fibroblast growth factor 11 | 3.03 | HT29, DU145, PC3 |
| 336202 | | | CH22_FGENES.719_6 | 3.02 | NCI-H69, NCI-H23, NCI-H23 |
| 302893 | AI117539 | Hs.173515 | H sapiens mRNA; cDNA DKFZp586H021 (from | 3.02 | 3.02 EB, DU145, CALU6 |
| 315166 | AI343966 | Hs.158528 | ESTs | 3.01 | Caco2, EB, NCI-H69 |
| 335606 | | | CH22_FGENES.582_3 | 3.01 | NCI-H23, NCI-H520, NCI-H345 |
| 330058 | | | CH.17_p gl 6634847 | 3.01 | OVCA-R, HT29, LnCap |
| 303179 | AA071215 | | EST cluster (not in UniGene) with exon h | 3.01 | MCF7, RPWE-2, MB-MDA-453 |
| 307625 | AI299817 | | EST singleton (not in UniGene) with exon | 3 | MB-MDA-231, LnCap, BT474 |
| 323074 | AL119445 | Hs.203213 | ESTs | 3 | NCI-H23, NCI-H520, NCI-H460 |
| 336232 | | | CH22_FGENES.736_7 | 3 | HT29, BT474, MB-MDA-231 |
| 334915 | | | CH22_FGENES.457_4 | 3 | NCI-H345, PRSC_con, NCI-H69 |
| 329116 | | | CH.X_hs gl 5868650 | 3 | NCI-H69, PRSC_con, RPWE-2 |
| 333495 | | | CH22_FGENES.168_5 | 3 | OVCA-R, NCI-H69, NCI-H345 |
| 303756 | AI738488 | Hs.115838 | ESTs | 2.99 | HT29, PRSC_con, DU145 |
| 332134 | AA610123 | Hs.139240 | DKFZP564F1422 protein | 2.99 | EB, A549, MCF7 |
| 322916 | AW1367294 | Hs.154091 | ESTs | 2.99 | DU145, DU145, OVCA-R |
| 318050 | AI052093 | Hs.133132 | ESTs | 2.99 | NCI-H345, DU145, NCI-H520 |
| 301019 | AI1747356 | Hs.98722 | ESTs | 2.99 | NCI-358, NCI-H69, MB-MDA-435s |
| 315213 | AA587773 | Hs.136494 | ESTs | 2.98 | MB-MDA-231, BT474, LnCap |
| 339251 | | | CH22_BA354I12.GENSCAN.7-5 | 2.98 | NCI-H69, PRSC_log, HT29 |
| 303835 | T05645 | | EST cluster (not in UniGene) with exon h | 2.97 | BT474, NCI-H345, LnCap |
| 300070 | AI174603 | Hs.256832 | ESTs | 2.97 | DU145, A549, OVCA-R |
| 320954 | AB028953 | Hs.204121 | KJAA1030 protein | 2.97 | LnCap, DU145, PC3 |
| 327624 | | | CH.04_hs gl 5867871 | 2.97 | EB, DU145, LnCap |
| 329029 | | | CH.X_hs gl 6525302 | 2.96 | NCI-H69, PRSC_log, LnCap |
| 317040 | AA868584 | Hs.126154 | ESTs | 2.96 | DU145, EB, LnCap |
| 328016 | | | CH.06_hs gl 5902482 | 2.96 | NCI-H345, PRSC_con, DU145 |
| 312674 | AI762475 | Hs.151327 | ESTs; Moderately similar to III ALU SUB | 2.96 | OVCA-R, NCI-H69, NCI-H69 |
| 332301 | R70253 | Hs.127282 | ESTs | 2.96 | OVCA-R, DU145, MB-MDA-231 |
| 300951 | AI732374 | Hs.105834 | ESTs; Weakly similar to 25 kDa trypsin i | 2.95 | NCI-358, NCI-H460, Caco2 |
| 318226 | AI078446 | Hs.134125 | ESTs | 2.95 | NCI-H460, NCI-H23, NCI-358 |
| 311349 | AW292933 | Hs.254110 | ESTs | 2.94 | EB, DU145, OVCA-R |
| 312757 | AI285970 | Hs.183817 | ESTs | 2.94 | DU145, LnCap, LnCap |
| 316507 | AI381515 | Hs.158381 | ESTs | 2.94 | PRSC_con, PRSC_log, RPWE-2 |
| 302278 | AF018080 | Hs.173730 | Mediterranean fever | 2.93 | EB, NCI-H69, DU145 |
| 311016 | AW173166 | Hs.243468 | ESTs | 2.93 | NCI-H345, LnCap, LnCap |
| 323884 | AA340724 | Hs.214028 | ESTs | 2.92 | EB, Caco2, HT29 |
| 336632 | | | CH22_FGENES.13-2 | 2.92 | NCI-H69, NCI-H345, MB-MDA-231 |
| 328886 | | | CH.07_hs gl 6588003 | 2.92 | HT29, PC3, LnCap |
| 301859 | T61587 | | EST cluster (not in UniGene) with exon h | 2.92 | LnCap, EB, EB |
| 323775 | AA329856 | Hs.143022 | ESTs | 2.92 | PRSC_con, PRSC_log, RPWE-2 |
| 315426 | AI391486 | Hs.128171 | ESTs | 2.92 | CALU6, EB, A549 |
| 322264 | AF086242 | | EST cluster (not in UniGene) | 2.92 | Caco2, OVCA-R, DU145 |
| 315135 | AA627561 | Hs.192446 | ESTs | 2.91 | EB, HT29, DU145 |
| 327982 | | | CH.06_hs gl 5868216 | 2.91 | LnCap, MB-MDA-453, NCI-H69 |
| 314530 | AI052358 | Hs.131741 | ESTs | 2.91 | NCI-H460, NCI-H520, RPWE-2 |
| 315003 | AA527650 | Hs.156037 | ESTs | 2.9 | PRSC_con, RPWE-2, MB-MDA-231 |
| 339032 | | | CH22_DA59H18.GENSCAN.25-1 | 2.9 | NCI-H69, PRSC_con, RPWE-2 |
| 308379 | AI623950 | Hs.2186 | eukaryotic translation elongation factor | 2.89 | BT474, MB-MDA-231, HT29 |
| 312133 | T87714 | Hs.221665 | ESTs | 2.88 | Caco2, MB-MDA-453, MCF7 |
| 307992 | AI434168 | | EST singleton (not in UniGene) with exon | 2.88 | NCI-H520, MCF7, NCI-H23 |
| 308010 | AI439190 | Hs.181165 | eukaryotic translation elongation factor | 2.88 | Caco2, NCI-H69, NCI-H345 |
| 320154 | AA336019 | Hs.119559 | ESTs | 2.88 | MB-MDA-453, DU145, EB |
| 331496 | N34929 | Hs.171984 | ESTs | 2.86 | MB-MDA-453, PC3, MCF7 |
| 320016 | H57622 | Hs.194574 | ESTs | 2.86 | PRSC_con, RPWE-2, PRSC_log |
| 317923 | AW450544 | Hs.220751 | ESTs | 2.86 | NCI-H345, PRSC_con, PRSC_log |
| 301822 | X17033 | Hs.1142 | Integrin; alpha 2 (CD49B; alpha 2 subunit | 2.86 | PC3, BT474, CALU6 |
| 311759 | AA705075 | Hs.169536 | Rhesus blood group-associated glycoprotein | 2.85 | DU145, HT29, MB-MDA-231 |
| 315083 | AI221325 | Hs.210655 | ESTs | 2.84 | PRSC_con, RPWE-2, NCI-H345 |
| 317759 | AI908455 | Hs.202460 | ESTs; Weakly similar to hypothetical L1 | 2.83 | HT29, MB-MDA-231, BT474 |
| 313980 | AI633205 | Hs.159914 | ESTs | 2.83 | Caco2, MB-MDA-453, A549 |
| 310941 | AI453402 | Hs.173705 | ESTs; Weakly similar to III ALU CLASS C | 2.83 | NCI-H345, MCF7, Caco2 |
| 313593 | AI911488 | Hs.213724 | ESTs | 2.83 | LnCap, Caco2, NCI-H460 |
| 314973 | AW273128 | Hs.254669 | EST | 2.82 | BT474, LnCap, RPWE-2 |

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|--------|-----------|---------------------------|--|------|---------------------------------|
| 310950 | AI582758 | Hs.170561 | ESTs | 2.82 | EB, MB-MDA-453, LnCap |
| 323626 | AL039822 | Hs.207604 | ESTs | 2.82 | PC3, HT29, CALU6 |
| 325410 | | CH.12_hs gj 5866921 | | 2.81 | MB-MDA-453, PRSC_con, NCI-358 |
| 313911 | AI565458 | Hs.116385 | ESTs | 2.81 | PRSC_con, EB, RPWE-2 |
| 334244 | | CH22_FGENES.365_5 | | 2.81 | OVCA-R, PC3, MB-MDA-453 |
| 309333 | AW025709 | | EST singleton (not in UniGene) with exon | 2.81 | NCI-H460, NCI-H23, NCI-358 |
| 328467 | | CH.07_hs gj 5868434 | | 2.81 | EB, OVCA-R, HT29 |
| 318563 | AW250501 | | EST cluster (not in UniGene) | 2.81 | BT474, NCI-H23, MB-MDA-231 |
| 326412 | | CH.19_hs gj 5867362 | | 2.81 | BT474, PRSC_log, RPWE-2 |
| 303407 | AA309616 | | EST cluster (not in UniGene) with exon h | 2.8 | CALU6, NCI-H345, DU145 |
| 328462 | | CH.07_hs gj 5868433 | | 2.8 | BT474, CALU6, MCF7 |
| 335157 | | CH22_FGENES.501_7 | | 2.8 | NCI-H69, NCI-H345, PRSC_log |
| 313458 | AA007259 | Hs.255853 | ESTs | 2.79 | OVCA-R, DU145, LnCap |
| 310416 | AI695047 | Hs.202395 | ESTs | 2.79 | DU145, MB-MDA-435s, PC3 |
| 317709 | AI435973 | Hs.128056 | ESTs | 2.79 | NCI-H460, NCI-358, DU145 |
| 321415 | AI377596 | Hs.3337 | transmembrane 4 superfamily member 1 | 2.79 | A549, PC3, OVCA-R |
| 313693 | AW469180 | Hs.170651 | ESTs | 2.79 | OVCA-R, MCF7, EB |
| 309438 | AW102802 | Hs.225787 | ESTs; Moderately similar to hypothetical | 2.79 | PC3, OVCA-R, DU145 |
| 308961 | AI870248 | | EST singleton (not in UniGene) with exon | 2.78 | BT474, MB-MDA-231, EB |
| 329107 | | CH.X_hs gj 5868626 | | 2.78 | DU145, MCF7, MB-MDA-435s |
| 313975 | AW025024 | Hs.65114 | keratin 18 | 2.78 | Caco2, EB, DU145 |
| 330901 | AA157818 | Hs.238380 | Human endogenous retroviral protease mRNA | 2.78 | PC3, NCI-H520, BT474 |
| 311749 | R06249 | Hs.13911 | ESTs | 2.78 | OVCA-R, MB-MDA-453, MCF7 |
| 329853 | | CH.14_p2 gj 5682295 | | 2.78 | BT474, BT474, HT29 |
| 322340 | AF088076 | | EST cluster (not in UniGene) | 2.77 | NCI-H345, Caco2, LnCap |
| 326806 | | CH.20_hs gj 5469835 | | 2.77 | NCI-H69, NCI-H345, MB-MDA-231 |
| 314661 | AA436432 | | EST cluster (not in UniGene) | 2.77 | NCI-H460, MB-MDA-435s, CALU6 |
| 322135 | AF075082 | | EST cluster (not in UniGene) | 2.77 | NCI-358, NCI-H460, Caco2 |
| 331849 | AA417078 | Hs.193767 | ESTs | 2.77 | DU145, EB, CALU6 |
| 301056 | AI797955 | Hs.208076 | ESTs; Weakly similar to D(4) DOPAMINE RE | 2.76 | NCI-H69, RPWE-2, PRSC_con |
| 327739 | | CH.05_hs gj 5867942 | | 2.76 | EB, PC3, LnCap |
| 308016 | AI445116 | | EST singleton (not in UniGene) with exon | 2.76 | LnCap, HT29, MB-MDA-231 |
| 331549 | N56866 | Hs.237507 | EST | 2.76 | MB-MDA-453, MCF7, OVCA-R |
| 331851 | AA418599 | Hs.98303 | caveolin 3 | 2.75 | MB-MDA-231, NCI-H345, BT474 |
| 315023 | AA533505 | Hs.185844 | ESTs | 2.75 | PRSC_con, OVCA-R, EB |
| 335565 | | CH22_FGENES.579_1 | | 2.75 | OVCA-R, EB, A549 |
| 306137 | AA916176 | | EST singleton (not in UniGene) with exon | 2.74 | EB, LnCap, DU145 |
| 332240 | N54803 | | yv31d2.s1 Soares fetal liver spleen 1NFL 3' similar to contains L1.i3 L1 repeat | 2.74 | DU145, EB, CALU6 |
| 313246 | N90762 | Hs.159454 | ESTs | 2.74 | NCI-H69, NCI-H345, PRSC_log |
| 303642 | AW299459 | | EST cluster (not in UniGene) with exon h | 2.74 | EB, A549, Caco2 |
| 325513 | | CH.12_hs gj 6017035 | | 2.74 | MB-MDA-231, NCI-H345, BT474 |
| 337236 | | CH22_FGENES.639-2 | | 2.74 | MCF7, MB-MDA-453, NCI-H69 |
| 311555 | AW407892 | Hs.244807 | ESTs | 2.74 | BT474, NCI-H345, NCI-H69 |
| 339266 | | CH22_BA35412.GENSCAN.10-4 | | 2.73 | CALU6, DU145, OVCA-R |
| 300127 | AW028615 | Hs.235224 | ESTs; Weakly similar to KIAA0422 [H.sapi | 2.73 | NCI-H345, RPWE-2, PRSC_log |
| 311741 | R00099 | Hs.193642 | ESTs | 2.72 | LnCap, PC3, OVCA-R |
| 310915 | AW449673 | Hs.201893 | ESTs | 2.72 | DU145, EB, MB-MDA-435s |
| 324982 | T31689 | Hs.98518 | ESTs | 2.71 | PRSC_con, PRSC_log, RPWE-2 |
| 305030 | AA629988 | | EST singleton (not in UniGene) with exon | 2.71 | DU145, DU145, NCI-358 |
| 315396 | AW286107 | Hs.152686 | ESTs | 2.69 | OVCA-R, Caco2, EB |
| 319098 | AI908374 | | EST cluster (not in UniGene) | 2.69 | RPWE-2, LnCap, PC3 |
| 309119 | AI927384 | Hs.228499 | EST; Moderately similar to PK-120 precu | 2.69 | LnCap, NCI-H23, NCI-358 |
| 312095 | AW444937 | Hs.233482 | ESTs | 2.68 | Caco2, OVCA-R, HT29 |
| 324316 | AI291330 | | EST cluster (not in UniGene) | 2.68 | NCI-H460, Caco2, PRSC_log |
| 331367 | AA425688 | Hs.41641 | ESTs; Weakly similar to CAGH4 [H.sapiens | 2.68 | MB-MDA-435s, NCI-H520, NCI-H460 |
| 339116 | | CH22_DA59H18.GENSCAN.49-4 | | 2.68 | DU145, EB, CALU6 |
| 324297 | AI565566 | Hs.168587 | ESTs | 2.68 | PRSC_con, OVCA-R, PRSC_log |
| 318728 | Z30201 | | EST cluster (not in UniGene) | 2.68 | LnCap, Caco2, PC3 |
| 304813 | AA584540 | | EST singleton (not in UniGene) with exon | 2.68 | BT474, OVCA-R, RPWE-2 |
| 312393 | N34376 | Hs.191659 | ESTs; Weakly similar to !!! ALU CLASS E | 2.68 | NCI-H345, PRSC_con, EB |
| 330671 | AB002302 | Hs.92236 | KIAA0304 gene product | 2.67 | NCI-358, OVCA-R, Caco2 |
| 305406 | AA723860 | | EST singleton (not in UniGene) with exon | 2.66 | OVCA-R, EB, MCF7 |
| 330957 | H08778 | Hs.133521 | ESTs | 2.66 | EB, PC3, OVCA-R |
| 300350 | AI871129 | Hs.172597 | ESTs; Weakly similar to zinc finger prot | 2.66 | NCI-H23, NCI-H520, NCI-H460 |
| 322302 | W76021 | | EST cluster (not in UniGene) | 2.66 | DU145, OVCA-R, PC3 |
| 321891 | AIW157424 | Hs.165954 | ESTs | 2.66 | EB, OVCA-R, Caco2 |
| 300124 | AI217394 | Hs.242447 | ESTs | 2.65 | PRSC_con, A549, HT29 |
| 302747 | AF062275 | | EST cluster (not in UniGene) with exon h | 2.65 | NCI-H23, BT474, MCF7 |
| 308741 | AI802780 | Hs.209002 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.65 | PC3, EB, OVCA-R |
| 310802 | AI631546 | Hs.159732 | ESTs | 2.65 | PRSC_con, PRSC_log, NCI-H69 |
| 300694 | AA063406 | | EST cluster (not in UniGene) with exon h | 2.65 | BT474, EB, MCF7 |
| 311395 | R23313 | | EST cluster (not in UniGene) | 2.64 | EB, OVCA-R, DU145 |
| 336538 | | CH22_FGENES.840_2 | | 2.64 | DU145, NCI-H460, NCI-358 |
| 316473 | AA829961 | | EST cluster (not in UniGene) | 2.64 | LnCap, OVCA-R, EB |
| 328134 | | CH.06_hs gj 5868039 | | 2.64 | LnCap, EB, CALU6 |

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| 329330 | | CH.X_hs g 5868806 | 2.64 | EB, CALU6, DU145 |
| 316664 | AI042101 | EST cluster (not in UniGene) | 2.64 | NCI-H345, MB-MDA-231, PRSC_log |
| 328015 | | CH.06_hs g 5902482 | 2.63 | BT474, HT29, MB-MDA-231 |
| 308991 | AI879831 | EST singleton (not in UniGene) with exon h | 2.63 | BT474, EB, NCI-H23 |
| 323899 | AL042966 | EST cluster (not in UniGene) | 2.62 | DU145, A549, CALU6 |
| 321708 | AA476817 | EST cluster (not in UniGene) | 2.62 | EB, A549, CALU6 |
| 301752 | T75247 | EST cluster (not in UniGene) with exon h | 2.62 | HT29, BT474, NCI-H345 |
| 309351 | AW057547 | EST singleton (not in UniGene) with exon h | 2.62 | NCI-H23, PRSC_con, LnCap |
| 314412 | AI864270 | Hs.155654 ESTs | 2.62 | CALU6, MB-MDA-231, BT474 |
| 309441 | AW103055 | Hs.244230 EST | 2.62 | BT474, MB-MDA-231, MB-MDA-453 |
| 335993 | | CH22_FGENES.656_6 | 2.61 | NCI-H460, NCI-358, NCI-H520 |
| 318196 | AI056776 | Hs.133397 ESTs | 2.6 | EB, CALU6, HT29 |
| 322880 | AA310521 | Hs.50848 ESTs; Weakly similar to KIAA0862 protein | 2.6 | DU145, A549, PC3 |
| 300558 | AI540051 | Hs.122638 ESTs | 2.6 | OVCA-R, NCI-H69, MCF7 |
| 318594 | AA918320 | Hs.224581 ESTs | 2.6 | PC3, MB-MDA-453, DU145 |
| 308554 | AI698132 | Hs.201923 EST | 2.6 | LnCap, EB, NCI-H345 |
| 335108 | | CH22_FGENES.494_14 | 2.6 | NCI-H69, NCI-H345, MB-MDA-231 |
| 312483 | AI417526 | Hs.184636 ESTs | 2.59 | PC3, DU145, OVCA-R |
| 311981 | AW452773 | Hs.257612 EST | 2.59 | NCI-H460, MB-MDA-453, NCI-H23 |
| 319359 | F13458 | EST cluster (not in UniGene) | 2.59 | LnCap, NCI-H460, MB-MDA-231 |
| 300230 | AI377746 | Hs.158846 ESTs | 2.59 | HT29, NCI-358, NCI-H345 |
| 316504 | AW135854 | Hs.132458 ESTs | 2.59 | DU145, EB, CALU6 |
| 322337 | AA249804 | EST cluster (not in UniGene) | 2.59 | NCI-H69, NCI-H345, NCI-H345 |
| 301775 | AW247670 | EST cluster (not in UniGene) with exon h | 2.59 | NCI-H345, RPWE-2, PRSC_log |
| 301089 | AA666396 | Hs.220727 ESTs | 2.58 | PRSC_log, PRSC_con, RPWE-2 |
| 331213 | T88698 | Hs.163862 ESTs | 2.58 | DU145, EB, OVCA-R |
| 321121 | W23285 | EST cluster (not in UniGene) | 2.58 | NCI-H69, MB-MDA-435s, PC3 |
| 316634 | AW241910 | Hs.122254 ESTs | 2.58 | MCF7, HT29, BT474 |
| 322141 | AF075092 | EST cluster (not in UniGene) | 2.58 | PC3, OVCA-R, HT29 |
| 321208 | T82331 | Hs.127453 ESTs | 2.58 | A549, CALU6, Caco2 |
| 339071 | | CH22_DA59H18.GENSCAN.34-1 | 2.58 | CALU6, DU145, EB |
| 311666 | AW389509 | Hs.223747 ESTs | 2.57 | OVCA-R, MB-MDA-231, BT474 |
| 318662 | AI285898 | Hs.115357 ESTs | 2.57 | OVCA-R, DU145, EB |
| 317010 | AA663395 | EST cluster (not in UniGene) | 2.57 | NCI-H520, PRSC_con, NCI-358 |
| 324710 | AI742028 | Hs.120884 ESTs; Weakly similar to RAS-RELATED PROT | 2.57 | 2.57 LnCap, DU145, MB-MDA-453 |
| 327888 | | CH.06_hs g 5868149 | 2.56 | NCI-H345, MB-MDA-435s, RPWE-2 |
| 336149 | | CH22_FGENES.706_5 | 2.56 | NCI-H69, PC3, A549 |
| 312816 | H74319 | Hs.188620 ESTs | 2.56 | EB, Caco2, NCI-H460 |
| 327999 | | CH.06_hs g 5867994 | 2.56 | NCI-358, NCI-H520, NCI-H23 |
| 316761 | AI911173 | Hs.213722 ESTs | 2.55 | NCI-H345, NCI-H460, MB-MDA-231 |
| 336958 | | CH22_FGENES.367-1 | 2.55 | HT29, CALU6, CALU6 |
| 325043 | W27919 | Hs.32944 inositol polyphosphate-4-phosphatase; ty | 2.55 | NCI-H460, NCI-H23, HT29 |
| 315417 | AW452360 | Hs.186770 ESTs | 2.55 | NCI-H345, NCI-H69, PRSC_con |
| 331603 | N78656 | Hs.161535 EST | 2.55 | NCI-H345, PRSC_con, PRSC_log |
| 309403 | AW082954 | EST singleton (not in UniGene) with exon h | 2.55 | BT474, MB-MDA-231, MCF7 |
| 337289 | | CH22_FGENES.672-8 | 2.54 | BT474, HT29, MB-MDA-231 |
| 314242 | AI570943 | Hs.246280 ESTs | 2.54 | Caco2, MB-MDA-435s, MB-MDA-453 |
| 328053 | | CH.06_hs g 5902482 | 2.54 | MB-MDA-231, DU145, MB-MDA-453 |
| 307215 | AI193189 | EST singleton (not in UniGene) with exon h | 2.53 | HT29, CALL6, MB-MDA-231 |
| 327566 | | CH.03_hs g 5857811 | 2.53 | NCI-H69, NCI-H520, NCI-H345 |
| 326338 | | CH.17_hs g 6056311 | 2.53 | PC3, A549, DU145 |
| 318115 | AI384027 | Hs.159130 ESTs; Moderately similar to !!!! ALU SUB | 2.53 | DU145, EB, PC3 |
| 307437 | AI245683 | EST singleton (not in UniGene) with exon h | 2.52 | NCI-H23, NCI-H520, NCI-358 |
| 322059 | AA412371 | Hs.121344 ESTs | 2.52 | EB, DU145, OVCA-R |
| 322505 | AF147315 | EST cluster (not in UniGene) | 2.52 | PRSC_con, RPWE-2, NCI-H69 |
| 314032 | AW081897 | Hs.193211 ESTs | 2.52 | NCI-H345, LnCap, DU145 |
| 336125 | | CH22_FGENES.701_12 | 2.51 | NCI-H69, LnCap, DU145 |
| 312765 | AI692908 | Hs.181873 ESTs | 2.51 | NCI-H23, NCI-358, NCI-H520 |
| 335523 | | CH22_FGENES.572_3 | 2.51 | HT29, BT474, OVCA-R |
| 327585 | | CH.03_hs g 5857825 | 2.51 | HT29, NCI-H460, MB-MDA-453 |
| 323183 | AW393850 | EST cluster (not in UniGene) | 2.51 | MB-MDA-231, LnCap, RPWE-2 |
| 314418 | AI478722 | Hs.232275 ESTs; Moderately similar to !!!! ALU SUB | 2.51 | EB, DU145, DU145 |
| 313361 | AI359782 | Hs.137312 ESTs | 2.5 | CALU6, HT29, DU145 |
| 305632 | AA805276 | EST singleton (not in UniGene) with exon h | 2.5 | MB-MDA-453, NCI-H460, NCI-H23 |
| 331689 | W90131 | Hs.184857 ESTs | 2.5 | NCI-H69, EB, A549 |
| 323438 | AI540243 | Hs.113817 ESTs | 2.5 | NCI-H345, PRSC_con, MB-MDA-231 |
| 315742 | AI821724 | Hs.143198 H sapiens PAC clone DJ0872F07 from 7q31 | 2.5 | MCF7, MB-MDA-453, MB-MDA-435s |
| 305971 | AA868674 | EST singleton (not in UniGene) with exon h | 2.5 | NCI-358, NCI-H23, NCI-H520 |
| 336633 | | CH22_FGENES.13-3 | 2.5 | NCI-H69, NCI-H345, PRSC_log |
| 304746 | AA577793 | EST singleton (not in UniGene) with exon h | 2.49 | NCI-H69, BT474, MB-MDA-231 |
| 327925 | | CH.06_hs g 5868172 | 2.49 | NCI-358, NCI-358, NCI-H460 |
| 336055 | | CH22_FGENES.683_4 | 2.49 | EB, HT29, MB-MDA-231 |
| 328888 | | CH.07_hs g 6588003 | 2.48 | MB-MDA-435s, MB-MDA-453, PRSC_log |
| 311244 | AW016694 | Hs.197689 ESTs | 2.48 | NCI-H345, MCF7, PC3 |
| 327155 | | CH.01_hs g 5867549 | 2.48 | NCI-H69, MB-MDA-231, NCI-H345 |
| 334907 | | CH22_FGENES.453_2 | 2.48 | DU145, NCI-H345, MB-MDA-231 |

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| 314887 | AA910236 | Hs.139469 | ESTs | 2.48 | DU145, A549, A549 |
| 339435 | | CH22_DJ579N16.GENSCAN.18-10 | | 2.48 | NCI-H69, MCF7, BT474 |
| 334172 | | CH22_FGENES.349_5 | | 2.48 | NCI-H69, NCI-H345, PRSC_log |
| 320767 | AA299525 | EST cluster (not in UniGene) | | 2.48 | NCI-358, NCI-H23, NCI-H460 |
| 335772 | | CH22_FGENES.156-1 | | 2.47 | NCI-358, NCI-358, NCI-H23 |
| 326957 | | CH.21_hs g 6469836 | | 2.47 | BT474, RPWE-2, PRSC_con |
| 308505 | AI686615 | Hs.200778 | EST; Weakly similar to SALIVARY PROLINE- | 2.47 | MCF7, MB-MDA-453, MB-MDA-435s |
| 321325 | AB033100 | | EST cluster (not in UniGene) | 2.47 | EB, CALU6, A549 |
| 313149 | AW291092 | Hs.201058 | ESTs | 2.47 | NCI-H345, PRSC_con, RPWE-2 |
| 338325 | | CH22_EM:AC005500.GENSCAN.307-7 | | 2.46 | BT474, LnCap, EB |
| 307877 | AI368880 | | EST singleton (not in UniGene) with exon | 2.46 | NCI-H23, PRSC_log, NCI-H520 |
| 311525 | AI799444 | Hs.247095 | ESTs; Moderately similar to !!! ALU SUB | 2.46 | PRSC_con, PRSC_log, NCI-H345 |
| 337023 | | CH22_FGENES.433-12 | | 2.46 | OVCA-R, CALU6, PRSC_con |
| 300916 | AI361798 | Hs.164675 | ESTs | 2.45 | LnCap, DU145, CALU6 |
| 302919 | AI137382 | | EST cluster (not in UniGene) with exon h | 2.45 | LnCap, MB-MDA-231, CALU6 |
| 320303 | AI079289 | Hs.137154 | H sapiens mRNA full length insert cDNA c | 2.45 | BT474, MB-MDA-231, MB-MDA-453 |
| 318359 | AI097439 | Hs.135548 | ESTs | 2.45 | NCI-H460, MB-MDA-453, NCI-H345 |
| 314384 | AA535840 | Hs.162203 | ESTs; Weakly similar to alternatively sp | 2.45 | OVCA-R, PC3, EB |
| 326763 | | CH.20_hs g 6598307 | | 2.45 | NCI-H69, NCI-H345, RPWE-2 |
| 319900 | AW408392 | | EST cluster (not in UniGene) | 2.45 | Caco2, NCI-H460, NCI-H23 |
| 314451 | AA586368 | Hs.190232 | ESTs | 2.45 | PRSC_con, NCI-H345, MB-MDA-231 |
| 300641 | AW237699 | Hs.118346 | ESTs | 2.44 | NCI-H345, PRSC_log, PRSC_con |
| 324368 | AW299374 | | EST cluster (not in UniGene) | 2.44 | PC3, DU145, OVCA-R |
| 336510 | | CH22_FGENES.834_5 | | 2.44 | NCI-H69, RPWE-2, PRSC_con |
| 326876 | | CH.20_hs g 65682507 | | 2.44 | NCI-H23, NCI-H460, NCI-H520 |
| 307753 | AI340509 | Hs.182426 | ribosomal protein S2 | 2.44 | NCI-H23, NCI-H460, Caco2 |
| 317071 | M78728 | Hs.132694 | ESTs | 2.44 | NCI-H345, NCI-H69, RPWE-2 |
| 313877 | AA767669 | Hs.250113 | ESTs; Moderately similar to thyroid horm component TRAP150 [H.sapiens] | 2.44 | DU145, LnCap, CALU6 |
| 315974 | AW029203 | Hs.191952 | ESTs | 2.43 | EB, DU145, OVCA-R |
| 322970 | AI885052 | Hs.142287 | ESTs; Weakly similar to !!! ALU CLASS F | 2.43 | NCI-H345, RPWE-2, EB |
| 317733 | AI028257 | Hs.132317 | ESTs | 2.43 | CALU6, RPWE-2, OVCA-R |
| 313599 | AA748749 | Hs.136742 | ESTs | 2.42 | NCI-H460, NCI-358, NCI-H520 |
| 323014 | AA305198 | | EST cluster (not in UniGene) | 2.42 | PRSC_con, NCI-H460, RPWE-2 |
| 324980 | AA969121 | Hs.254296 | ESTs | 2.41 | MCF7, OVCA-R, PC3 |
| 301326 | AA883831 | Hs.252924 | ESTs | 2.41 | PRSC_con, PRSC_log, RPWE-2 |
| 308695 | AI763350 | | EST singleton (not in UniGene) with exon | 2.41 | RPWE-2, NCI-H69, NCI-H345 |
| 330166 | | CH.02_p2 g 6648220 | | 2.41 | CALU6, DU145, A549 |
| 317552 | AW451400 | Hs.127019 | ESTs | 2.41 | NCI-358, NCI-358, NCI-H23 |
| 320572 | AI929508 | Hs.159590 | lymphocyte antigen 6 complex; locus H | 2.41 | CALU6, HT29, A549 |
| 315618 | AI287341 | Hs.154029 | ESTs; Weakly similar to TRANSCRIPTION FA | 2.41 | OVCA-R, Caco2, MB-MDA-231 |
| 331610 | N91109 | Hs.54681 | ESTs | 2.41 | NCI-H23, NCI-H520, NCI-358 |
| 311731 | AW393528 | Hs.246875 | ESTs | 2.41 | NCI-H69, NCI-H345, PRSC_con |
| 318571 | Z43383 | Hs.8053 | ESTs | 2.4 | NCI-358, NCI-H23, NCI-H520 |
| 334958 | | CH22_FGENES.465_27 | | 2.4 | DU145, PRSC_con, RPWE-2 |
| 323570 | AI038623 | Hs.208752 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.4 | OVCA-R, EB, BT474 |
| 301685 | W67730 | | EST cluster (not in UniGene) with exon h | 2.4 | MB-MDA-231, NCI-H345, EB |
| 303849 | AW163324 | | EST cluster (not in UniGene) with exon h | 2.4 | RPWE-2, PRSC_log, NCI-H345 |
| 325702 | | CH.14_hs g 5867028 | | 2.4 | NCI-H23, NCI-H460, NCI-H520 |
| 313074 | N48261 | Hs.127171 | ESTs | 2.4 | MB-MDA-231, RPWE-2, PRSC_log |
| 308994 | AI880051 | | EST singleton (not in UniGene) with exon | 2.4 | RPWE-2, EB, PRSC_con |
| 330338 | | CH.08_p2 g 5457162 | | 2.4 | DU145, EB, LnCap |
| 327274 | | CH.01_hs g 5867470 | | 2.4 | OVCA-R, DU145, MB-MDA-231 |
| 325953 | | CH.16_hs g 5867140 | | 2.4 | MB-MDA-453, MB-MDA-435s, MCF7 |
| 333281 | | CH22_FGENES.128_7 | | 2.4 | NCI-H23, HT28, DU145 |
| 314778 | AW079559 | Hs.152258 | ESTs | 2.39 | EB, CALU6, Caco2 |
| 317005 | AI800251 | Hs.197773 | ESTs | 2.38 | MB-MDA-231, BT474, HT29 |
| 334257 | | CH22_FGENES.367_5 | | 2.38 | HT29, NCI-358, MB-MDA-231 |
| 324783 | AA640770 | | EST cluster (not in UniGene) | 2.38 | EB, OVCA-R, MB-MDA-453 |
| 300949 | AA534325 | Hs.162183 | ESTs | 2.38 | NCI-H69, NCI-H345, PRSC_log |
| 314957 | AW029274 | Hs.208368 | ESTs; Moderately similar to !!! ALU SUB | 2.38 | LnCap, DU145, DU145 |
| 324350 | AW292501 | Hs.157174 | ESTs; Weakly similar to similar to SH3-b | 2.38 | HT29, NCI-H23, NCI-H23 |
| 338235 | | CH22_EM:AC005500.GENSCAN.260-16 | | 2.38 | NCI-H69, NCI-H460, NCI-H23 |
| 300937 | AW297302 | Hs.255631 | ESTs | 2.38 | PRSC_log, PRSC_ox, PRSC_con |
| 317439 | AW451327 | Hs.170623 | ESTs | 2.38 | A549, DU145, EB |
| 324745 | AI742120 | Hs.116506 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.38 | NCI-358, NCI-H460, BT474 |
| 338306 | | CH22_EM:AC005500.GENSCAN.302-2 | | 2.38 | NCI-H69, PRSC_con, PRSC_log |
| 318765 | Z42071 | Hs.23961 | ESTs | 2.38 | LnCap, NCI-H23, NCI-H520 |
| 310254 | AI239811 | Hs.157491 | ESTs | 2.37 | OVCA-R, DU145, EB |
| 305116 | AA649244 | | EST singleton (not in UniGene) with exon | 2.37 | CALU6, MB-MDA-453s, MB-MDA-453 |
| 324016 | AI045285 | Hs.246849 | ESTs; Moderately similar to !!! ALU SUB | 2.37 | EB, DU145, OVCA-R |
| 322774 | AA131111 | | EST cluster (not in UniGene) | 2.37 | OVCA-R, EB, A549 |
| 335745 | | CH22_FGENES.601_16 | | 2.37 | PRSC_log, PRSC_con, NCI-H69 |
| 300972 | AI979100 | Hs.211518 | ESTs | 2.37 | NCI-H69, NCI-H345, PRSC_log |
| 338809 | | CH22_EM:AC005500.GENSCAN.531-10 | | 2.37 | NCI-H23, NCI-H69, NCI-H520 |
| 316983 | AI480204 | Hs.177131 | ESTs | 2.37 | NCI-H345, PRSC_con, PRSC_log |

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| 321308 | AI247480 | Hs.117029 | ESTs | 2.37 | BT474, NCI-H69, HT29 |
| 323578 | AA299492 | Hs.168166 | ESTs | 2.37 | LnCap, EB, MB-MDA-453 |
| 335747 | | CH22_FGENES.601_20 | | 2.36 | NCI-H69, LnCap, PRSC_con |
| 322362 | AF039697 | | EST cluster (not in UniGene) | 2.36 | DU145, PRSC_con, NCI-H345 |
| 314430 | N76302 | Hs.78110 | ESTs; Weakly similar to F17A9.2 [C.elega | 2.36 | DU145, MB-MDA-453, CALU6 |
| 304831 | AA586422 | | EST singleton (not in UniGene) with exon | 2.36 | NCI-H23, NCI-H60, CALU6 |
| 337432 | | CH22_FGENES.765-1 | | 2.36 | MB-MDA-231, BT474, HT29 |
| 305984 | AA887654 | | EST singleton (not in UniGene) with exon | 2.36 | DU145, HT29, CALU6 |
| 313486 | AW134523 | Hs.247186 | ESTs | 2.36 | DU145, A549, CALU6 |
| 309028 | AI889109 | Hs.212032 | EST | 2.36 | NCI-358, NCI-H520, NCI-H23 |
| 318282 | AI679966 | Hs.150603 | ESTs | 2.35 | NCI-H460, Caco2, NCI-H23 |
| 334198 | | CH22_FGENES.354_4 | | 2.35 | NCI-H69, PRSC_log, PRSC_con |
| 314458 | AI217440 | Hs.143873 | ESTs | 2.35 | Caco2, A549, PC3 |
| 333346 | | CH22_FGENES.139_15 | | 2.35 | CALU6, DU145, LnCap |
| 325408 | | CH12_hs gl 5866921 | | 2.35 | NCI-H460, NCI-H520, NCI-H23 |
| 313758 | AA076743 | Hs.129770 | ESTs | 2.35 | NCI-H23, MB-MDA-435s, NCI-H345 |
| 309825 | AW293701 | | EST singleton (not in UniGene) with exon | 2.35 | NCI-H460, NCI-H23, NCI-H520 |
| 303536 | R55497 | Hs.183941 | ESTs; Moderately similar to H beta 58 ho | 2.35 | DU145, CALU6, NCI-H520 |
| 331534 | NS1583 | Hs.133756 | EST | 2.35 | NCI-H23, NCI-H520, NCI-358 |
| 325164 | T16981 | Hs.21963 | ESTs | 2.34 | NCI-H345, PRSC_log, NCI-H460 |
| 327710 | | CH.04_hs gl 5867880 | | 2.34 | BT474, MB-MDA-231, NCI-H345 |
| 306351 | AA961356 | | EST singleton (not in UniGene) with exon | 2.34 | BT474, MB-MDA-231, MB-MDA-435s |
| 304968 | AA614308 | | EST singleton (not in UniGene) with exon | 2.34 | CALU6, HT29, MB-MDA-453 |
| 334015 | | CH22_FGENES.313_7 | | 2.34 | HT29, MB-MDA-231, BT474 |
| 318315 | AI091370 | Hs.134852 | ESTs | 2.33 | CALU6, NCI-H520, DU145 |
| 306809 | AI057134 | | EST singleton (not in UniGene) with exon | 2.33 | PC3, DU145, EB |
| 337697 | | CH22_EM:AC000097.GENSCAN.66-1 | | 2.33 | RPWE-2, PRSC_log, NCI-H345 |
| 329630 | | CH.11_p2 gl 6729050 | | 2.33 | NCI-H520, NCI-H23, NCI-H460 |
| 326577 | | CH.19_hs gl 5867317 | | 2.33 | NCI-H460, NCI-358, NCI-H23 |
| 333428 | | CH22_FGENES.149_1 | | 2.33 | NCI-H345, PRSC_con, RPWE-2 |
| 301080 | AI479391 | Hs.155405 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.33 | OVCA-R, MCF7, MCF7 |
| 324829 | AA714311 | | EST cluster (not in UniGene) | 2.33 | NCI-H460, NCI-358, NCI-H23 |
| 302776 | AJ133798 | | EST cluster (not in UniGene) with exon h | 2.32 | NCI-H23, NCI-H460, NCI-H520 |
| 325801 | | CH.14_hs gl 6552451 | | 2.32 | PRSC_log, MCF7, NCI-H23 |
| 332122 | AA609698 | Hs.112389 | ESTs | 2.32 | DU145, HT29, PC3 |
| 314167 | AA243633 | Hs.208983 | ESTs | 2.32 | DU145, MCF7, PC3 |
| 324023 | AA669615 | Hs.214226 | ESTs | 2.31 | DU145, NCI-H345, EB |
| 320503 | NM_00589 | | EST cluster (not in UniGene) | 2.31 | A549, OVCA-R, PC3 |
| 312217 | T98289 | | EST cluster (not in UniGene) | 2.31 | NCI-H23, Caco2, NCI-H69 |
| 321304 | AA078293 | | EST cluster (not in UniGene) | 2.31 | DU145, OVCA-R, EB |
| 323517 | AA527359 | Hs.154366 | ESTs | 2.31 | NCI-H345, DU145, EB |
| 336455 | | CH22_FGENES.829_13 | | 2.31 | NCI-H345, PRSC_con, RPWE-2 |
| 313352 | AW292127 | Hs.144758 | ESTs | 2.31 | MCF7, DU145, OVCA-R |
| 331457 | H93135 | Hs.41840 | ESTs | 2.31 | Caco2, NCI-H460, NCI-H23 |
| 333054 | | CH22_FGENES.73_8 | | 2.31 | NCI-H69, NCI-358, NCI-H23 |
| 308598 | AI719237 | | EST singleton (not in UniGene) with exon | 2.31 | OVCA-R, CALU6, Caco2 |
| 327059 | | CH.21_hs gl 5531965 | | 2.3 | NCI-H460, LnCap, LnCap |
| 334120 | | CH22_FGENES.333_1 | | 2.3 | NCI-H69, RPWE-2, MB-MDA-435s |
| 324154 | AI457449 | Hs.192817 | ESTs | 2.3 | NCI-H460, MB-MDA-453, NCI-358 |
| 326509 | | CH.19_hs gl 6682496 | | 2.3 | NCI-H345, CALU6, OVCA-R |
| 316855 | AW291384 | Hs.254974 | ESTs | 2.3 | NCI-H345, NCI-H460, BT474 |
| 337918 | | CH22_EM:AC005500.GENSCAN.66-4 | | 2.3 | RPWE-2, NCI-H345, PRSC_log |
| 317471 | AI825351 | Hs.144084 | ESTs | 2.29 | HT29, OVCA-R, DU145 |
| 331023 | N32599 | Hs.5856 | ESTs | 2.29 | OVCA-R, LnCap, A549 |
| 332231 | N48008 | Hs.102629 | EST | 2.29 | CALU6, DU145, EB |
| 309912 | AW339671 | | EST singleton (not in UniGene) with exon | 2.29 | MB-MDA-435s, PRSC_con, NCI-358 |
| 316427 | AI241019 | Hs.145644 | ESTs | 2.29 | Caco2, HT29, EB |
| 313329 | AW293704 | Hs.122658 | ESTs | 2.29 | OVCA-R, DU145, Caco2 |
| 335019 | | CH22_FGENES.474_7 | | 2.29 | HT29, CALU6, MB-MDA-231 |
| 324394 | F20654 | Hs.152128 | ESTs; Moderately similar to !!! ALU SUB | 2.29 | NCI-H345, MB-MDA-231, RPWE-2 |
| 339357 | | CH22_BA35412.GENSCAN.31-2 | | 2.29 | NCI-H69, OVCA-R, BT474 |
| 322128 | AI346033 | | EST cluster (not in UniGene) | 2.28 | NCI-H23, NCI-H520, NCI-H460 |
| 301310 | AI239457 | Hs.130794 | ESTs | 2.28 | OVCA-R, DU145, MB-MDA-231 |
| 300623 | AI929130 | Hs.118261 | ESTs; Moderately similar to finger prote | 2.28 | BT474, RPWE-2, PRSC_con |
| 323409 | AL135534 | | EST cluster (not in UniGene) | 2.27 | NCI-H345, NCI-358, Caco2 |
| 308406 | AI634885 | | EST singleton (not in UniGene) with exon | 2.27 | OVCA-R, EB, HT29 |
| 322518 | AI133446 | | EST cluster (not in UniGene) | 2.27 | DU145, MB-MDA-435s, OVCA-R |
| 338381 | | CH22_EM:AC005500.GENSCAN.330-10 | | 2.27 | NCI-H69, PRSC_con, PRSC_log |
| 316003 | AA704584 | Hs.119993 | ESTs | 2.27 | NCI-358, NCI-H520, NCI-H23 |
| 307090 | AI161024 | | EST singleton (not in UniGene) with exon | 2.27 | NCI-H345, DU145, RPWE-2 |
| 300356 | AA758411 | Hs.121335 | ESTs | 2.27 | LnCap, NCI-H460, Caco2 |
| 331887 | AA431328 | Hs.98660 | ESTs | 2.27 | NCI-358, NCI-H520, CALU6 |
| 330951 | H02566 | Hs.191268 | H saptens mRNA; cDNA DKFZp434N174 (from | 2.27 | 2.27 OVCA-R, BT474, BT474 |
| 305547 | AA773111 | | EST singleton (not in UniGene) with exon | 2.27 | LnCap, DU145, BT474 |
| 312457 | AA776743 | Hs.191589 | ESTs | 2.26 | NCI-H345, RPWE-2, PRSC_con |
| 333929 | | CH22_FGENES.300_2 | | 2.26 | HT29, CALU6, EB |

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| 319845 | AA649011 | Hs.187902 | ESTs | 2.26 | LnCap, DU145, MCF7 |
| 306739 | AI028393 | | EST singleton (not in UniGene) with exon | 2.26 | MB-MDA-435s, NCI-358, CALU6 |
| 306919 | AI096832 | | EST singleton (not in UniGene) with exon | 2.26 | HT29, BT474, PC3 |
| 333312 | | CH22_FGENES.138_4 | | 2.26 | OVCA-R, DU145, PC3 |
| 334955 | | CH22_FGENES.465_24 | | 2.25 | RPWE-2, PRSC_con, NCI-H345 |
| 312295 | AA578233 | Hs.173863 | ESTs | 2.25 | OVCA-R, DU145, NCI-H345 |
| 307643 | AI302124 | | EST singleton (not in UniGene) with exon | 2.25 | CALU8, CALU6, OVCA-R |
| 324252 | AA421989 | | EST cluster (not in UniGene) | 2.25 | OVCA-R, EB, A549 |
| 309767 | AW271805 | | EST singleton (not in UniGene) with exon | 2.25 | DU145, NCI-H460, CALU6 |
| 311492 | AW410240 | Hs.4437 | ribosomal protein L28 | 2.25 | NCI-H69, NCI-H460, NCI-H520 |
| 312260 | H05392 | Hs.230597 | EST | 2.25 | Caco2, EB, DU145 |
| 327125 | | CH.21_hs g 6531971 | | 2.25 | HT29, NCI-358, BT474 |
| 316919 | AA845382 | Hs.204520 | ESTs | 2.24 | NCI-H23, NCI-H345, NCI-H520 |
| 316361 | AI433833 | Hs.164159 | ESTs; Weakly similar to III ALU SUBFAMI | 2.24 | DU145, EB, PC3 |
| 315772 | AW515373 | Hs.158893 | ESTs | 2.24 | OVCA-R, EB, LnCap |
| 320236 | H03688 | | EST cluster (not in UniGene) | 2.24 | NCI-358, DU145, NCI-H23 |
| 315444 | AW138821 | Hs.221737 | ESTs | 2.24 | NCI-358, CALU6, PRSC_con |
| 333903 | | CH22_FGENES.294_1 | | 2.24 | MB-MDA-231, BT474, A549 |
| 335234 | | CH22_FGENES.515_3 | | 2.24 | NCI-H69, PRSC_con, PRSC_log |
| 333727 | | CH22_FGENES.256_1 | | 2.23 | MB-MDA-231, NCI-H69, BT474 |
| 332002 | AA482009 | Hs.105104 | ESTs | 2.23 | EB, NCI-H520, HT29 |
| 329611 | | CH.10_p2_g 3962478 | | 2.23 | BT474, HT29, MB-MDA-231 |
| 310559 | AI783594 | Hs.155718 | ESTs | 2.22 | BT474, MCF7, MB-MDA-231 |
| 327315 | | CH.01_hs g 5867508 | | 2.22 | NCI-H69, EB, EB |
| 323170 | U83527 | | EST cluster (not in UniGene) | 2.22 | EB, DU145, LnCap |
| 331522 | N49309 | Hs.117012 | ESTs | 2.22 | A549, LnCap, DU145 |
| 313261 | AA730472 | Hs.142805 | ESTs | 2.22 | OVCA-R, PC3, LnCap |
| 312740 | R97191 | Hs.134106 | ESTs | 2.22 | BT474, MCF7, OVCA-R |
| 325055 | Z44631 | Hs.21658 | ESTs | 2.22 | MB-MDA-453, DU145, CALU6 |
| 337895 | | CH22_EM:AC005500.GENSCAN.56-2 | | 2.22 | NCI-H345, PRSC_log, PRSC_con |
| 307140 | AI185762 | | EST singleton (not in UniGene) with exon | 2.22 | NCI-H520, NCI-H460, EB |
| 321643 | W76005 | Hs.32094 | ESTs | 2.21 | EB, NCI-H345, PRSC_con |
| 302683 | X85153 | | EST cluster (not in UniGene) with exon h | 2.21 | BT474, MB-MDA-231, MCF7 |
| 322644 | AA340904 | | EST cluster (not in UniGene) | 2.21 | NCI-H460, NCI-H23, NCI-H520 |
| 330415 | D83777 | Hs.75137 | KIAA0193 gene product | 2.21 | CALU6, A549, Caco2 |
| 302334 | AF120491 | | EST cluster (not in UniGene) with exon h | 2.21 | NCI-H69, NCI-H345, PC3 |
| 326710 | | CH.20_hs g 5867593 | | 2.21 | NCI-H520, NCI-358, NCI-H23 |
| 323561 | AA825426 | Hs.238832 | ESTs; Weakly similar to III ALU SUBFAMI | 2.21 | NCI-H345, DU145, NCI-H69 |
| 337706 | | CH22_EM:AC000097.GENSCAN.87-11 | | 2.21 | MB-MDA-435s, NCI-358, NCI-H520 |
| 339309 | | CH22_BA354112.GENSCAN.22-7 | | 2.21 | BT474, HT29, PC3 |
| 330436 | HG2724-H | | Oncogene Tls/Chop, Fusion Activated | 2.21 | PRSC_con, NCI-H69, Caco2 |
| 312360 | AI922972 | Hs.196073 | ESTs | 2.21 | OVCA-R, MB-MDA-435s, DU145 |
| 301855 | AF053356 | | multiple UniGene matches | 2.21 | NCI-H69, HT29, NCI-H23 |
| 331192 | T55182 | Hs.152571 | ESTs; Highly similar to IGF-II mRNA-bind | 2.2 | OVCA-R, PC3, CALU6 |
| 315872 | AW051819 | Hs.204516 | ESTs | 2.2 | LnCap, OVCA-R, EB |
| 337904 | | CH22_EM:AC005500.GENSCAN.56-17 | | 2.2 | OVCA-R, LnCap, EB |
| 308258 | AI565612 | | EST singleton (not in UniGene) with exon | 2.2 | DU145, MB-MDA-231, CALU6 |
| 320965 | H18166 | | EST cluster (not in UniGene) | 2.2 | DU145, EB, LnCap |
| 333910 | | CH22_FGENES.295_3 | | 2.2 | DU145, MB-MDA-231, EB |
| 300707 | AA080921 | | EST cluster (not in UniGene) with exon h | 2.2 | BT474, MCF7, HT29 |
| 336011 | | CH22_FGENES.668_9 | | 2.19 | NCI-H460, BT474, NCI-H345 |
| 325712 | | CH.14_hs g 6682473 | | 2.19 | NCI-H460, NCI-H23, NCI-358 |
| 322738 | AF201832 | | EST cluster (not in UniGene) | 2.19 | PC3, RPWE-2, PRSC_con |
| 335339 | | CH22_FGENES.535_16 | | 2.19 | HT29, PRSC_log, MCF7 |
| 320733 | AA738436 | Hs.134407 | ESTs | 2.19 | DU145, EB, Caco2 |
| 319412 | AA679426 | Hs.187505 | ESTs | 2.19 | NCI-H345, PRSC_log, PRSC_con |
| 337132 | | CH22_FGENES.526-3 | | 2.19 | NCI-H69, NCI-H345, PRSC_con |
| 301544 | AI951651 | Hs.224290 | ESTs | 2.19 | PRSC_con, MB-MDA-231, NCI-H23 |
| 325285 | | CH.11_hs g 5866903 | | 2.18 | PRSC_con, PRSC_log, MB-MDA-231 |
| 338280 | | CH22_EM:AC005500.GENSCAN.290-11 | | 2.18 | PC3, NCI-358, HT29 |
| 311421 | AI701635 | Hs.207077 | ESTs | 2.18 | RPWE-2, NCI-H345, NCI-358 |
| 330638 | X89576 | Hs.159581 | matrix metalloproteinase 17 (membrane-In | 2.18 | HT29, MB-MDA-435s, MB-MDA-453 |
| 326603 | | CH.20_hs g 6056312 | | 2.18 | CALU6, DU145, HT29 |
| 319055 | AA412305 | | EST cluster (not in UniGene) | 2.18 | A549, OVCA-R, MB-MDA-435s |
| 335451 | | CH22_FGENES.562_9 | | 2.18 | DU145, LnCap, CALU6 |
| 317989 | AI203009 | Hs.130664 | ESTs | 2.18 | NCI-H345, NCI-H69, NCI-H520 |
| 322024 | AA334384 | | EST cluster (not in UniGene) | 2.18 | Caco2, PC3, NCI-H520 |
| 300734 | AW205197 | Hs.240951 | ESTs | 2.18 | NCI-358, A549, EB |
| 304022 | T02990 | | EST singleton (not in UniGene) with exon | 2.18 | NCI-H23, NCI-358, NCI-H460 |
| 330082 | | CH.19_p2_g 6015314 | | 2.18 | NCI-H23, Caco2, Caco2 |
| 312516 | AA363245 | Hs.189831 | ESTs | 2.18 | BT474, HT29, MB-MDA-231 |
| 333832 | | CH22_FGENES.300_5 | | 2.17 | PC3, Caco2, EB |
| 308115 | AI479071 | | EST singleton (not in UniGene) with exon | 2.17 | BT474, OVCA-R, OVCA-R |
| 320184 | U91510 | Hs.123036 | CD39-like 1 | 2.17 | NCI-H520, NCI-358, NCI-H23 |
| 324432 | AA464510 | | EST cluster (not in UniGene) | 2.17 | CALU6, RPWE-2, HT29 |
| 320882 | AI832098 | | EST cluster (not in UniGene) | 2.17 | OVCA-R, PC3, BT474 |

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| 312251 | H03952 | EST cluster (not in UniGene) | 2.17 | NCI-H460, NCI-H23, NCI-358 |
| 315049 | AW340486 | Hs.121210 ESTs | 2.17 | NCI-H520, NCI-358, NCI-H23 |
| 305018 | AA627127 | EST singleton (not in UniGene) with exon | 2.17 | MB-MDA-231, MB-MDA-453, EB |
| 303807 | A1792765 | Hs.130434 ESTs | 2.16 | NCI-H345, PRSC_con, PRSC_log |
| 317792 | AI653389 | Hs.196121 ESTs | 2.16 | NCI-H345, PRSC_con, LnCap |
| 321668 | AA872730 | Hs.125229 ESTs | 2.16 | OVCA-R, PC3, MCF7 |
| 328863 | | CH.07_hs g 6381929 | 2.16 | PRSC_con, NCI-H345, NCI-H460 |
| 319373 | R00371 | EST cluster (not in UniGene) | 2.16 | PRSC_con, RPWE-2, NCI-H345 |
| 320069 | T86541 | Hs.189732 ESTs | 2.16 | NCI-H23, NCI-358, NCI-H345 |
| 320235 | AF064090 | Hs.129708 tumor necrosis factor (ligand) superfamily | 2.16 | NCI-H23, NCI-H460, NCI-H520 |
| 338880 | | CH22_DJ3210.GENSCAN.6-2 | 2.16 | BT474, MCF7, OVCA-R |
| 318314 | AI091349 | Hs.161133 ESTs | 2.16 | NCI-H23, NCI-H520, NCI-H460 |
| 332696 | D86973 | Hs.75354 GCN1 (general control of amino-acid synt | 2.16 | A549, PC3, DU145 |
| 331352 | AA406133 | Hs.7482 KIAA0682 gene product | 2.16 | PC3, EB, MB-MDA-231 |
| 339019 | | CH22_DA59H18.GENSCAN.21-15 | 2.15 | LnCap, EB, OVCA-R |
| 306975 | AI127042 | EST singleton (not in UniGene) with exon | 2.15 | MB-MDA-435s, NCI-H520, NCI-358 |
| 318069 | AI024557 | Hs.131540 ESTs | 2.15 | Caco2, Caco2, BT474 |
| 312997 | AW205686 | Hs.135130 ESTs | 2.15 | NCI-H460, NCI-H23, NCI-358 |
| 331372 | AA433935 | Hs.55044 DKFZP58H2123 protein | 2.15 | PRSC_con, HT29, CALU6 |
| 335049 | | CH22_FGENES.481_5 | 2.15 | NCI-H69, NCI-H345, PRSC_log |
| 324280 | AA429772 | Hs.191610 ESTs | 2.15 | MB-MDA-453, MB-MDA-435s, MCF7 |
| 330363 | | CH.X_p2 g 3126882 | 2.15 | NCI-H23, NCI-H460, NCI-358 |
| 322896 | AW470288 | Hs.144830 ESTs | 2.15 | HT29, CALU6, EB |
| 321981 | AA948204 | Hs.127361 ESTs | 2.15 | MB-MDA-231, DU145, HT29 |
| 333294 | | CH22_FGENES.130_6 | 2.14 | EB, DU145, MB-MDA-453 |
| 330170 | | CH.02_p2 g 5648220 | 2.14 | HT29, MB-MDA-453, PC3 |
| 312973 | AI123346 | Hs.135241 ESTs | 2.14 | LnCap, DU145, EB |
| 311104 | AI627352 | Hs.201449 ESTs | 2.14 | NCI-H520, NCI-H23, LnCap |
| 325086 | T10019 | Hs.4194 ESTs | 2.14 | NCI-H460, NCI-H23, NCI-358 |
| 317182 | AW183524 | Hs.192298 ESTs | 2.14 | HT29, BT474, MB-MDA-435s |
| 323644 | AA310711 | Hs.124340 ESTs | 2.14 | RPWE-2, PRSC_con, PRSC_log |
| 308092 | AI474896 | EST singleton (not in UniGene) with exon | 2.14 | BT474, MCF7, MB-MDA-231 |
| 322265 | AF086244 | EST cluster (not in UniGene) | 2.14 | NCI-H345, RPWE-2, PRSC_con |
| 303521 | AA746272 | EST cluster (not in UniGene) with exon h | 2.14 | DU145, MB-MDA-453, EB |
| 312102 | AW439340 | Hs.189720 ESTs | 2.14 | NCI-H23, NCI-H460, MB-MDA-435s |
| 316559 | AI249468 | Hs.228251 EST | 2.14 | NCI-H460, NCI-358, NCI-H23 |
| 338486 | | CH22_EM:AC005500.GENSCAN.382-8 | 2.14 | NCI-H520, NCI-H23, NCI-H69 |
| 301302 | AI825444 | Hs.210956 ESTs | 2.14 | BT474, HT29, MB-MDA-231 |
| 310591 | AI650372 | Hs.195979 ESTs | 2.14 | CALU6, CALU6, Caco2 |
| 316231 | AA732301 | EST cluster (not in UniGene) | 2.14 | NCI-H23, NCI-H520, NCI-358 |
| 326559 | | CH.19_hs g 5867310 | 2.14 | DU145, NCI-H460, NCI-H23 |
| 324062 | AA525291 | Hs.204099 ESTs; Weakly similar to !!! ALU SUBFAMI | 2.13 | OVCA-R, DU145, EB |
| 323844 | AI811303 | Hs.143490 ESTs | 2.13 | MB-MDA-453, MCF7, MB-MDA-435s |
| 333895 | | CH22_FGENES.293_2 | 2.13 | CALU6, LnCap, DU145 |
| 308264 | AI567114 | Hs.171454 EST | 2.13 | DU145, CALU6, MB-MDA-453 |
| 306081 | AA908472 | EST singleton (not in UniGene) with exon | 2.13 | HT29, BT474, MB-MDA-231 |
| 333101 | | CH22_FGENES.79_6 | 2.13 | NCI-H345, NCI-H69, PRSC_log |
| 328544 | | CH.07_hs g 5868486 | 2.13 | NCI-H23, NCI-H69, PRSC_log |
| 333355 | | CH22_FGENES.141_6 | 2.13 | DU145, EB, CALU6 |
| 323397 | AI524519 | Hs.239699 ESTs | 2.13 | EB, NCI-H460, NCI-H345 |
| 305697 | AA814956 | EST singleton (not in UniGene) with exon | 2.13 | NCI-H520, NCI-H460, NCI-358 |
| 327809 | | CH.05_hs g 5867968 | 2.13 | HT29, PC3, OVCA-R |
| 325092 | T10115 | Hs.92423 ESTs | 2.13 | HT29, NCI-358, MB-MDA-231 |
| 322299 | AI971935 | Hs.252784 ESTs | 2.13 | PRSC_con, DU145, DU145 |
| 312145 | AA028526 | Hs.126706 ESTs | 2.12 | OVCA-R, A549, MB-MDA-435s |
| 323704 | AA319421 | Hs.193577 ESTs | 2.12 | Caco2, LnCap, OVCA-R |
| 328971 | | CH.08_hs g 5478806 | 2.12 | NCI-358, NCI-H23, NCI-H520 |
| 325338 | | CH.11_hs g 5866883 | 2.12 | LnCap, NCI-H69, NCI-H345 |
| 331332 | AA282554 | Hs.89034 ESTs | 2.12 | NCI-H520, NCI-H23, Caco2 |
| 327159 | | CH.01_hs g 5867550 | 2.12 | EB, DU145, PC3 |
| 335180 | | CH22_FGENES.505_2 | 2.12 | LnCap, NCI-H69, A549 |
| 338052 | | CH22_EM:AC005500.GENSCAN.162-3 | 2.12 | PRSC_con, PRSC_log, NCI-H69 |
| 318350 | AI636018 | Hs.135538 ESTs | 2.12 | EB, HT29, DU145 |
| 312070 | AW293140 | Hs.108790 ESTs | 2.11 | Caco2, NCI-H23, A549 |
| 328314 | | CH.07_hs g 5868371 | 2.11 | HT29, NCI-H23, NCI-H460 |
| 315869 | AI033547 | Hs.132826 ESTs | 2.11 | BT474, CALU6, MCF7 |
| 339246 | | CH22_BA354112.GENSCAN.5-9 | 2.11 | CALU6, CALU6, BT474 |
| 329921 | | CH.16_p2 g 5165205 | 2.11 | BT474, MB-MDA-231, HT29 |
| 324981 | Z25333 | Hs.4947 ESTs | 2.11 | A549, NCI-H460, NCI-H520 |
| 331291 | AA159323 | Hs.109929 ESTs | 2.11 | NCI-H345, A549, PRSC_con |
| 332729 | AA058907 | Hs.83190 fatty acid synthase | 2.11 | NCI-358, LnCap, MB-MDA-453 |
| 325448 | | CH.12_hs g 5866941 | 2.11 | DU145, MCF7, CALU6 |
| 314929 | AW188286 | Hs.143612 ESTs | 2.1 | EB, BT474, MB-MDA-231 |
| 301063 | AI057634 | Hs.124596 ESTs | 2.1 | NCI-H23, NCI-H460, BT474 |
| 301952 | AB029016 | Hs.117333 KIAA1093 protein | 2.1 | OVCA-R, A549, CALU6 |
| 326309 | | CH.17_hs g 5867277 | 2.1 | MB-MDA-435s, NCI-H69, MB-MDA-453 |

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| 315406 | AI823453 | Hs.146625 | ESTs | 2.1 | OVCA-R, DU145, EB |
| 302376 | AB007867 | Hs.200480 | KIAA0407 protein | 2.1 | OVCA-R, Caco2, HT29 |
| 312181 | AA417281 | Hs.191595 | ESTs | 2.1 | OVCA-R, A549, DU145 |
| 334254 | | CH22_FGENES.366_4 | | 2.1 | LnCap, OVCA-R, DU145 |
| 318073 | AW167087 | Hs.131562 | ESTs | 2.1 | A549, CALU6, EB |
| 304724 | AA569881 | Hs.65114 | keratin 18 | 2.1 | NCI-H23, NCI-H520, NCI-H460 |
| 332359 | W87704 | Hs.211558 | ESTs | 2.1 | MB-MDA-435s, PRSC_con, NCI-H460 |
| 331884 | AA431302 | Hs.98721 | EST; Weakly similar to N-copine [H.saple | 2.1 | NCI-H345, MB-MDA-231, PRSC_con |
| 308226 | AI559106 | Hs.181165 | eukaryotic translation elongation factor | 2.1 | EB, CALU6, OVCA-R |
| 324279 | AA501412 | Hs.191688 | ESTs; Weakly similar to Pro-Pol-dUTPase | 2.09 | OVCA-R, LnCap, PC3 |
| 337203 | | CH22_FGENES.591-3 | | 2.09 | NCI-H69, NCI-H345, MB-MDA-231 |
| 322346 | AA227618 | Hs.10882 | HMG-box containing protein 1 | 2.09 | HT29, BT474, MB-MDA-231 |
| 304470 | AA426654 | Hs.195188 | glyceraldehyde-3-phosphate dehydrogenase | 2.09 | NCI-H23, CALU6, NCI-H520 |
| 325977 | | CH.16_hs g 6249602 | | 2.09 | NCI-H23, NCI-H520, HT29 |
| 304696 | AA554758 | | EST singleton (not in UniGene) with exon | 2.09 | MB-MDA-435s, NCI-H23, BT474 |
| 317412 | AI301528 | Hs.132604 | ESTs | 2.09 | Caco2, EB, NCI-358 |
| 315570 | AI860360 | Hs.160316 | ESTs | 2.08 | PRSC_con, PRSC_log, NCI-H345 |
| 327341 | | CH.01_hs g 6017016 | | 2.08 | MB-MDA-231, PRSC_con, NCI-H69 |
| 327431 | | CH.02_hs g 5867754 | | 2.08 | NCI-H23, NCI-358, NCI-H520 |
| 314685 | AI870811 | Hs.158709 | ESTs; Weakly similar to KIAA0938 protein | 2.08 | MB-MDA-433, MCF7, OVCA-R |
| 328624 | | CH.07_hs g 5868246 | | 2.08 | MCF7, NCI-358, RPWE-2 |
| 303596 | AW303377 | | EST cluster (not in UniGene) with exon h | 2.08 | RPWE-2, PRSC_con, PRSC_log |
| 335717 | | CH22_FGENES.81-1 | | 2.08 | BT474, HT29, MCF7 |
| 317370 | AW204139 | Hs.174424 | ESTs; Weakly similar to p140mDia [M.musc | 2.08 | NCI-H23, NCI-H460, NCI-H69 |
| 331287 | AA149051 | Hs.172971 | ESTs | 2.08 | OVCA-R, EB, NCI-H345 |
| 304211 | N62228 | | EST singleton (not in UniGene) with exon | 2.08 | BT474, MCF7, MB-MDA-231 |
| 315613 | AW137420 | Hs.192311 | ESTs | 2.08 | PRSC_con, PRSC_log, PRSC_log |
| 325636 | | CH.14_hs g 5867002 | | 2.08 | NCI-358, NCI-H460, MB-MDA-433 |
| 336406 | | CH22_FGENES.823_21 | | 2.08 | HT29, EB, DU145 |
| 301714 | F06529 | | EST cluster (not in UniGene) with exon h | 2.08 | LnCap, PRSC_log, PRSC_con |
| 300496 | R45159 | Hs.221804 | ESTs | 2.08 | PRSC_con, LnCap, RPWE-2 |
| 318970 | R21114 | Hs.21383 | ESTs | 2.08 | NCI-H23, NCI-H520, NCI-H460 |
| 334115 | | CH22_FGENES.330_15 | | 2.08 | BT474, NCI-H69, HT29 |
| 308082 | AI473682 | | EST singleton (not in UniGene) with exon | 2.08 | MB-MDA-435s, NCI-H345, MB-MDA-231 |
| 308282 | AI569456 | | EST singleton (not in UniGene) with exon | 2.08 | LnCap, EB, PRSC_con |
| 313038 | AW451618 | Hs.124195 | ESTs | 2.07 | NCI-H345, PRSC_con, LnCap |
| 317974 | AW444468 | Hs.144900 | ESTs | 2.07 | NCI-358, NCI-H23, NCI-H520 |
| 324063 | AW292740 | Hs.254815 | ESTs | 2.07 | Caco2, NCI-358, NCI-H520 |
| 334759 | | CH22_FGENES.428_8 | | 2.07 | CALU6, HT29, NCI-H520 |
| 307664 | AI367417 | | EST singleton (not in UniGene) with exon | 2.07 | NCI-H460, NCI-358, NCI-H23 |
| 304356 | AA196027 | Hs.195188 | glyceraldehyde-3-phosphate dehydrogenase | 2.07 | HT29, MCF7, MB-MDA-435s |
| 303929 | AW470753 | | EST singleton (not in UniGene) with exon | 2.07 | NCI-H345, PRSC_con, RPWE-2 |
| 331857 | AA421160 | Hs.9456 | SWI/SNF related; matrix assoccd; actin de | 2.07 | EB, A549, PC3 |
| 322814 | AI824495 | Hs.211038 | ESTs | 2.06 | PRSC_con, RPWE-2, Caco2 |
| 303650 | AA430709 | | EST cluster (not in UniGene) with exon h | 2.06 | RPWE-2, NCI-H345, PRSC_con |
| 333403 | | CH22_FGENES.144_21 | | 2.06 | OVCA-R, CALU6, PC3 |
| 313663 | AI953261 | Hs.169813 | ESTs | 2.06 | NCI-H345, OVCA-R, NCI-H23 |
| 338594 | | CH22_EM:AC005500.GENSCAN.435-4 | | 2.06 | DU145, LnCap, EB |
| 334676 | | CH22_FGENES.418_29 | | 2.06 | NCI-H69, PRSC_log, PRSC_con |
| 310046 | AI198032 | Hs.210356 | ESTs | 2.06 | MB-MDA-435s, NCI-H23, Caco2 |
| 309169 | AI949216 | | EST singleton (not in UniGene) with exon | 2.06 | CALU6, EB, NCI-358 |
| 329752 | | CH.14_p2 g 6065777 | | 2.06 | CALU6, HT29, DU145 |
| 325085 | T10001 | Hs.4168 | ESTs | 2.06 | EB, OVCA-R, MB-MDA-435s |
| 332052 | AA521016 | Hs.185375 | ESTs | 2.06 | OVCA-R, MB-MDA-453, MCF7 |
| 302074 | AA382871 | Hs.132794 | phosphate cytidylyltransferase 1; cholin | 2.06 | LnCap, EB, NCI-H69 |
| 326344 | | CH.17_hs g 6525295 | | 2.06 | HT29, BT474, MB-MDA-453 |
| 330855 | AA079318 | | zm98c2.31 Stratagene colon HT29 (#937221 | | |
| | | IMAGE:545954 3, mRNA seq | | 2.06 | RPWE-2, LnCap, PRSC_con |
| 302525 | AF024690 | Hs.248056 | G protein-coupled receptor 43 | 2.05 | NCI-358, NCI-H23, DU145 |
| 331803 | AA436673 | Hs.29417 | H sapiens mRNA; cDNA DKFZp586B0323 (from | 2.05 | Caco2, DU145, A549 |
| 316322 | AW296618 | Hs.120637 | ESTs | 2.05 | BT474, MB-MDA-453, OVCA-R |
| 321525 | H78875 | | EST cluster (not in UniGene) | 2.05 | NCI-H23, PRSC_con, NCI-H520 |
| 305071 | AA640579 | | EST singleton (not in UniGene) with exon | 2.05 | MB-MDA-231, BT474, HT29 |
| 326033 | | CH.17_hs g 5867178 | | 2.05 | HT29, DU145, BT474 |
| 334730 | | CH22_FGENES.424_5 | | 2.05 | BT474, EB, OVCA-R |
| 305335 | AA704235 | | EST singleton (not in UniGene) with exon | 2.05 | MCF7, OVCA-R, MB-MDA-453 |
| 320521 | N31464 | Hs.24743 | ESTs | 2.05 | MB-MDA-453, MB-MDA-231, PC3 |
| 333515 | | CH22_FGENES.172_5 | | 2.04 | NCI-H345, RPWE-2, PRSC_con |
| 311020 | AI918672 | Hs.213783 | ESTs | 2.04 | NCI-H460, NCI-H23, NCI-H520 |
| 324323 | AA393739 | | EST cluster (not in UniGene) | 2.04 | OVCA-R, PC3, LnCap |
| 305486 | AA748889 | | EST singleton (not in UniGene) with exon | 2.04 | NCI-H345, PRSC_log, CALU6 |
| 312162 | T91823 | | EST cluster (not in UniGene) | 2.04 | NCLH520, NCI-H23, NCI-358 |
| 330980 | H28794 | Hs.6659 | ESTs | 2.04 | MCF7, MB-MDA-453, MB-MDA-435s |
| 317463 | AA927290 | Hs.130462 | ESTs | 2.04 | NCI-H23, Caco2, NCI-H69 |
| 303460 | AA700155 | Hs.117900 | ESTs | 2.04 | DU145, EB, CALU6 |
| 337435 | | CH22_FGENES.766-2 | | 2.03 | NCI-H345, OVCA-R, LnCap |

| | | | | |
|--------|----------|--|------|--------------------------------|
| 305464 | AA742425 | EST singleton (not in UniGene) with exon | 2.03 | CALU6, NCI-H520, NCI-358 |
| 307918 | AI383496 | EST singleton (not in UniGene) with exon | 2.03 | NCI-H23, BT474, MB-MDA-231 |
| 322209 | H89360 | EST cluster (not in UniGene) | 2.03 | DU145, OVCA-R, MB-MDA-453 |
| 310295 | AW205198 | Hs.149146 ESTs | 2.03 | NCI-H23, NCI-H460, NCI-358 |
| 325886 | | CH.16_hs g 5867087 | 2.03 | NCI-H345, NCI-H345, RPWE-2 |
| 329719 | | CH.14_p2 g 6065785 | 2.03 | NCI-H69, RPWE-2, PRSC_con |
| 309247 | AI972768 | EST singleton (not in UniGene) with exon | 2.03 | LnCap, PRSC_con, RPWE-2 |
| 328277 | | CH.07_hs g 5004471 | 2.03 | LnCap, RPWE-2, A549 |
| 307296 | AI205705 | Hs.147222 EST | 2.03 | NCI-H460, NCI-358, NCI-H23 |
| 327203 | | CH.01_hs g 5867447 | 2.03 | HT29, BT474, MB-MDA-231 |
| 306866 | AI086683 | EST singleton (not in UniGene) with exon | 2.03 | BT474, NCI-H345, HT29 |
| 333339 | | CH22_FGENES.139_8 | 2.03 | HT29, DU145, CALU6 |
| 323115 | AI921875 | EST cluster (not in UniGene) | 2.03 | BT474, BT474, MB-MDA-231 |
| 304811 | AA584361 | EST singleton (not in UniGene) with exon | 2.03 | NCI-H23, NCI-358, NCI-H460 |
| 323372 | AL135125 | Hs.13913 ESTs | 2.02 | DU145, EB, A549 |
| 312854 | AA828713 | EST cluster (not in UniGene) | 2.02 | NCI-H345, PRSC_con, PRSC_log |
| 307904 | AI381019 | EST singleton (not in UniGene) with exon | 2.02 | HT29, MCF7, MB-MDA-453 |
| 332099 | AA608983 | af5d4_s1 Soares_tests_NHT H sapiens cDN | 2.02 | PRSC_con, NCI-H345, RPWE-2 |
| 324634 | AI684571 | Hs.175831 ESTs | 2.02 | NCI-H460, Caco2, NCI-358 |
| 335721 | | CH22_FGENES.599_24 | 2.02 | NCI-H69, PRSC_log, NCI-H345 |
| 312452 | AI692643 | Hs.172749 ESTs | 2.02 | HT29, Caco2, MB-MDA-231 |
| 325396 | | CH.12_hs g 5866921 | 2.01 | HT29, NCI-H520, NCI-H460 |
| 328770 | | CH.07_hs g 6017031 | 2.01 | NCI-H23, NCI-H460, NCI-358 |
| 335585 | | CH22_FGENES.581_24 | 2.01 | MB-MDA-453, DU145, MCF7 |
| 335634 | | CH22_FGENES.584_14 | 2.01 | NCI-H23, NCI-H460, NCI-H69 |
| 338271 | | CH22_EMAC005500.GENSCAN.287-1 | 2.01 | MCF7, DU145, PC3 |
| 328607 | | CH.07_hs g 5868233 | 2.01 | NCI-H460, NCI-H23, NCI-358 |
| 307050 | AI147341 | Hs.146734 EST | 2.01 | NCI-H520, NCI-H23, NCI-358 |
| 334946 | | CH22_FGENES.465_13 | 2.01 | CALU6, BT474, DU145 |
| 319793 | R56360 | EST cluster (not in UniGene) | 2.01 | NCI-H460, HT29, NCI-358 |
| 307223 | AI193698 | Hs.184776 ribosomal protein L23a | 2.01 | NCI-358, NCI-H520, NCI-H23 |
| 312627 | AA344698 | Hs.133169 ESTs | 2.01 | PC3, LnCap, MB-MDA-231 |
| 329221 | | CH.X_hs g 5868727 | 2.01 | NCI-H345, NCI-H69, NCI-358 |
| 305145 | AA653589 | EST singleton (not in UniGene) with exon | 2.01 | LnCap, EB, OVCA-R |
| 328428 | | CH.07_hs g 5868417 | 2.01 | NCI-H69, MB-MDA-453, BT474 |
| 305990 | AA888866 | Hs.125919 EST | 2.01 | NCI-H520, NCI-358, NCI-H23 |
| 319368 | R00003 | Hs.133171 ESTs | 2 | OVCA-R, LnCap, PC3 |
| 324805 | AA927002 | Hs.131350 ESTs | 2 | NCI-H460, NCI-H23, NCI-358 |
| 301138 | AA719179 | Hs.189419 ESTs | 2 | NCI-H69, NCI-H23, PRSC_con |
| 304675 | AA541740 | EST singleton (not in UniGene) with exon | 2 | NCI-H460, NCI-H520, MB-MDA-231 |
| 326194 | | CH.17_hs g 5867213 | 2 | HT29, NCI-358, BT474 |

Table 5: H chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UniG_ID | Complete_Title | Ratio Met/B surv. |
|--------|----------|-----------|---|-------------------|
| 102193 | U20758 | Hs.313 | secreted phosphoprotein 1 (osteopontin) | 5.56 |
| 128530 | AA504343 | Hs.183475 | Homo sapiens clone 25061 mRNA sequence | 4.62 |
| 129093 | AA262710 | Hs.108614 | KIAA0627 protein | 4.23 |
| 124690 | R05818 | Hs.173830 | ESTs | 3.96 |
| 115558 | AA393806 | Hs.1010 | regulator of mitotic spindle assembly 1 | 3.39 |
| 134281 | AA227678 | Hs.8084 | Human DNA sequence from clone 465N24 on c3.22 | |
| 104792 | AA029288 | Hs.29147 | ESTs; Highly similar to ZINC FINGER PROT | 3.17 |
| 133770 | M69197 | Hs.242279 | haptoglobin-related protein | 3.07 |

Table 6: H chip – B survivor vs Met query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UniG_ID | Complete_Title | Ratio Met/B surv. |
|--------|---------|-----------|---|-------------------|
| 100116 | D00654 | Hs.77443 | actin; gamma 2; smooth muscle; enteric | 0.07 |
| 101923 | S75256 | | HNL=neutrophil lipocalin [human, ovarian] | 0.2 |
| 129982 | M87789 | Hs.140 | immunoglobulin gamma 3 (Gm marker) | 0.2 |
| 130064 | T67053 | Hs.181125 | immunoglobulin lambda gene cluster | 0.2 |

Table 7: I chip – B survivor vs Met query – up in Mets

Pkey: Unique Bos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex_Accn | UniG_ID | Title | Ratio Met/B surv |
|--------|----------|-----------|--|------------------|
| 319379 | T91443 | Hs.193963 | ESTs | 19.65 |
| 321920 | N63915 | | | 11.9 |
| 324302 | AA543008 | Hs.136806 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 9.31 |
| 314522 | A1732331 | Hs.187750 | ESTs; Moderately similar to !!!! ALU CLA | 5.79 |
| 331433 | H68097 | Hs.161023 | EST | 4.79 |
| 324643 | A1436356 | Hs.130729 | ESTs | 4.59 |
| 332471 | AA416967 | Hs.120980 | nuclear receptor co-repressor 2 | 4.58 |
| 314915 | AA573072 | Hs.187748 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 4.3 |
| 321354 | AA078493 | | EST cluster (not in UniGene) | 4.26 |
| 322309 | AF086372 | | EST cluster (not in UniGene) | 3.89 |
| 325100 | T10265 | Hs.116122 | ESTs; Weakly similar to coded for by C. | 3.81 |
| 314071 | AA192455 | Hs.188690 | ESTs | 3.74 |
| 315178 | AW362945 | Hs.162459 | ESTs | 3.66 |
| 330987 | H40988 | Hs.131965 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 3.51 |
| 337898 | | | CH22_EMAC005500.GENSCAN.56-5 | 3.21 |
| 319403 | T98413 | | EST cluster (not in UniGene) | 3.2 |
| 331469 | N22273 | Hs.39140 | ESTs | 3.15 |
| 331549 | N56866 | Hs.237507 | EST | 3.14 |
| 331644 | T99544 | Hs.173734 | ESTs; Weakly similar to !!!! ALU CLASS B | 3.14 |
| 313220 | A1971981 | Hs.118241 | ESTs | 3.04 |

Table 8: I chip – B survivor vs Met query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UniGeneID: UniGene number
 UniGene Title: UniGene gene title

| Pkey | Ex_Accn | UniG_ID | Title | Ratio Met/B surv |
|--------|----------|-----------|--|------------------|
| 333658 | | | CH22_FGENES.241_4 | 0.06 |
| 333657 | | | CH22_FGENES.241_2 | 0.07 |
| 333654 | | | CH22_FGENES.240_2 | 0.07 |
| 332859 | | | CH22_FGENES.27_2 | 0.07 |
| 333656 | | | CH22_FGENES.240_4 | 0.07 |
| 304480 | AA430373 | | EST singleton (not in UniGene) with exon | 0.08 |
| 333737 | | | CH22_FGENES.261_1 | 0.09 |
| 308601 | AI719930 | | EST singleton (not in UniGene) with exon | 0.1 |
| 334030 | | | CH22_FGENES.320_2 | 0.1 |
| 333637 | | | CH22_FGENES.229_2 | 0.13 |
| 302347 | AF039400 | Hs.194659 | chloride channel; calcium activated; fam | 0.16 |
| 333653 | | | CH22_FGENES.239_2 | 0.16 |
| 333635 | | | CH22_FGENES.228_2 | 0.19 |
| 333647 | | | CH22_FGENES.235_2 | 0.19 |
| 307588 | AI285535 | | EST singleton (not in UniGene) with exon | 0.2 |
| 337954 | | | CH22_EM:AC005500.GENSCAN.96-3 | 0.2 |
| 333588 | | | CH22_FGENES.206_2 | 0.21 |
| 320244 | AA296922 | Hs.129778 | gastrointestinal peptide | 0.22 |
| 333642 | | | CH22_FGENES.231_2 | 0.23 |
| 337951 | | | CH22_EM:AC005500.GENSCAN.94-1 | 0.23 |
| 333730 | | | CH22_FGENES.258_1 | 0.23 |
| 333646 | | | CH22_FGENES.234_2 | 0.24 |

Table 9: H chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UnigID | Complete_Title | Median Mets AI vs Median B-Sur AI |
|--------|---------------|-----------|--|-----------------------------------|
| 100655 | HG2841-HT2970 | | Albumin, Alt. Splice 5 | 11.98 |
| 124875 | R70506 | Hs.207693 | ESTs; Weakly similar to !!! ALU SUBFAMI | 9.21 |
| 102193 | U20758 | Hs.313 | secreted phosphoprotein 1 (osteopontin; | 6.73 |
| 100654 | HG2841-HT2969 | | Albumin, Alt. Splice 3, Missplicing In Albaalbumin Venezia | 6.18 |
| 118828 | N79496 | Hs.50824 | EST | 5.93 |
| 128046 | AA873285 | Hs.137947 | ESTs | 5.9 |
| 128896 | D14446 | Hs.107 | fibrinogen-like 1 | 5.17 |
| 127917 | AA211895 | Hs.118831 | EST; Highly similar to dJ1163J1.2.1 [H.s | 5.11 |
| 125090 | T91518 | | ye2085.s1 Stratagene lung (#937210) Hom | 4.47 |
| 118579 | N68905 | | small inducible cytokine A5 (RANTES) | 4.23 |
| 123526 | AA608657 | | ESTs; Moderately similar to !!! ALU SUB | 4.21 |
| 128062 | AA379500 | Hs.193155 | ESTs | 4.14 |
| 119174 | R71234 | | y54c08.s1 Soares placenta Nb2HP Homo sa | 4.11 |
| 128530 | AA504343 | Hs.183475 | Homo sapiens clone 25061 mRNA sequence | 4.09 |
| 119404 | T92950 | | ye27c10.s1 Stratagene lung (#937210) Hom | 3.98 |
| 118475 | N66845 | Hs.165411 | ESTs; Weakly similar to !!! ALU CLASS B | 3.96 |
| 129974 | K00629 | Hs.199300 | Human kpni repeat mma (cdna clone pcd-k | 3.87 |
| 108888 | AA135606 | Hs.189384 | ESTs; Weakly similar to !!! ALU SUBFAMI | 3.85 |
| 123963 | C13961 | Hs.210115 | EST | 3.8 |
| 123523 | AA608588 | Hs.193634 | ESTs | 3.76 |
| 128230 | AA984074 | Hs.176757 | ESTs | 3.75 |
| 124090 | H09570 | Hs.143032 | ESTs; Weakly similar to neuronal thread | 3.67 |
| 124690 | R05818 | Hs.173830 | ESTs | 3.58 |
| 134261 | AA227678 | Hs.8084 | Human DNA sequence from clone 465N24 on | 3.57 |
| 126917 | AA176225 | Hs.193929 | ESTs | 3.52 |
| 126050 | H27267 | Hs.75860 | hydroxacyl-Coenzyme A dehydrogenase/3-k | 3.45 |
| 126649 | AA856990 | Hs.125059 | ESTs | 3.42 |
| 115096 | AA255991 | Hs.175319 | ESTs | 3.4 |
| 129906 | H39216 | Hs.239970 | ESTs; Weakly similar to ZNF91L [H.sapien | 3.38 |
| 123022 | AA480909 | | aa28f10.s1 NCL_CGAP_GCB1 Homo sapiens cD | 3.38 |
| 106145 | AA424791 | Hs.5734 | KIAA0679 protein | 3.38 |
| 125191 | W67257 | Hs.138871 | ESTs; Weakly similar to !!! ALU CLASS B | 3.35 |
| 108836 | AA132061 | Hs.222727 | ESTs; Weakly similar to ubiquitous TPR m | 3.3 |
| 128710 | J04813 | Hs.104117 | cytochrome P450; subfamily IIIA (niphedi | 3.27 |
| 123460 | AA598981 | Hs.251122 | EST | 3.25 |
| 133735 | AC002045 | Hs.251928 | nuclear pore complex Interacting protein | 3.24 |
| 124636 | R06273 | Hs.186467 | ESTs; Moderately similar to !!! ALU SUB | 3.24 |
| 120748 | AA303153 | Hs.237994 | EST; Weakly similar to !!! ALU SUBFAMIL | 3.21 |
| 133770 | M69197 | Hs.242279 | haptoglobin-related protein | 3.17 |
| 128336 | AI242720 | Hs.146043 | ESTs; Weakly similar to alternatively sp | 3.14 |
| 135357 | AA235803 | Hs.79572 | cathepsin D (lysosomal aspartyl protease | 3.12 |
| 128088 | R02443 | Hs.186467 | ESTs; Moderately similar to !!! ALU SUB | 3.08 |
| 124055 | F10904 | Hs.100516 | Homo sapiens clone 23605 mRNA sequence | 3.06 |
| 124896 | R82053 | Hs.101594 | EST | 3.06 |
| 127598 | AA610677 | Hs.168851 | ESTs | 3.04 |
| 116802 | H44061 | Hs.194026 | ESTs | 3.01 |

Table 10: H chip – B survivor vs Met query – Down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UniG_ID | Complete_Title | Ratio Met/B surv. |
|--------|---------|-----------|--|-------------------|
| 100116 | D00654 | Hs.77443 | actin; gamma 2; smooth muscle; enteric | 0.09 |
| 130064 | T57053 | Hs.181125 | immunoglobulin lambda gene cluster | 0.11 |
| 129982 | M87789 | Hs.140 | immunoglobulin gamma 3 (Gm marker) | 0.12 |
| 131219 | C00476 | Hs.24395 | small inducible cytokine subfamily B (Cy | 0.13 |
| 133806 | M12759 | Hs.76325 | Human Ig J chain gene | 0.17 |
| 132982 | L02326 | Hs.198118 | immunoglobulin lambda-like polypeptide 2 | 0.18 |
| 131713 | X57809 | Hs.181125 | immunoglobulin lambda gene cluster | 0.18 |
| 131791 | S71043 | Hs.32225 | immunoglobulin alpha 1 | 0.2 |
| 133725 | V00563 | Hs.179543 | immunoglobulin mu | 0.22 |
| 101923 | S75256 | | HNL=neutrophil lipocalin [human, ovarian | 0.23 |
| 101461 | M22430 | Hs.76422 | phospholipase A2; group II A (platelets; | 0.24 |
| 103448 | X99133 | Hs.204238 | lipocalin 2 (oncogene 24p3) | 0.24 |

Table 11: H chip – Met vs Normal query – up in Mets

| Pkey | Ex Accn | UniG_ID | Complete_Title | Median Mets AI vs Median Normal AI |
|--------|---------------|-----------|--|------------------------------------|
| 100655 | HG2841-HT2970 | | Albumin, Alt. Splice 5 | 15.91 |
| 102193 | U20758 | Hs.313 | secreted phosphoprotein 1 (osteopontin; | 6.83 |
| 124675 | R70506 | Hs.207693 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 6.68 |
| 100654 | HG2841-HT2969 | | Albumin, Alt. Splice 3, Missplicing In Alloalbumin Venezia | 5.28 |
| 124059 | F13673 | Hs.99769 | ESTs | 5.11 |
| 128896 | D14446 | Hs.107 | fibrinogen-like 1 | 5.05 |
| 134453 | X70683 | Hs.83484 | SRY (sex determining region Y)-box 4 | 4.82 |
| 131564 | AA491465 | Hs.28792 | ESTs | 4.78 |
| 127917 | AA211895 | Hs.118831 | EST; Highly similar to dJ1163J1.2.1 [H.s | 4.76 |
| 115096 | AA255991 | Hs.175319 | ESTs | 4.67 |
| 104558 | R56678 | Hs.88959 | Human DNA sequence from clone 967N21 on | 4.63 |
| 123526 | AA608657 | | ESTs; Moderately similar to !!!! ALU SUB | 4.61 |
| 125090 | T91518 | | ye20105.e1 Stratagene lung (#937210) Hom | 4.59 |
| 129666 | M77349 | Hs.118787 | transforming growth factor, beta-induced | 4.58 |
| 118828 | N79496 | Hs.50824 | EST | 4.56 |
| 128046 | AA873285 | Hs.137947 | ESTs | 4.45 |
| 133421 | AA436560 | Hs.7327 | claudin 1 | 4.09 |
| 129158 | J05257 | Hs.109 | dipeptidase 1 (renal) | 4.04 |
| 128062 | AA379500 | Hs.193155 | ESTs | 4.03 |
| 124696 | R06273 | Hs.186467 | ESTs; Moderately similar to !!!! ALU SUB | 4.01 |
| 118475 | N66845 | Hs.165411 | ESTs; Weakly similar to !!!! ALU CLASS B | 3.96 |
| 104755 | AA024482 | Hs.9029 | DKFZP434G032 protein | 3.83 |
| 104978 | AA088458 | Hs.19322 | ESTs | 3.74 |
| 118579 | N68905 | | small inducible cytokine A5 (RANTES) | 3.7 |
| 123796 | AA620390 | Hs.247444 | ESTs | 3.62 |
| 127240 | AA888387 | Hs.243845 | ESTs; Moderately similar to !!!! ALU SUB | 3.61 |
| 104105 | AA422123 | Hs.42457 | ESTs | 3.55 |
| 129349 | D86974 | Hs.110613 | KIAA0220 protein | 3.54 |
| 119329 | T51832 | | ESTs; Moderately similar to !!!! ALU SUB | 3.53 |
| 114617 | AA084148 | Hs.110659 | ESTs | 3.52 |
| 123143 | AA487595 | | aa95e2.s1 Stratagene fetal retina 93722 | 3.48 |
| 103119 | X63629 | Hs.2877 | cadherin 3; P-cadherin (placental) | 3.48 |
| 119404 | T92950 | | ye27c10.e1 Stratagene lung (#937210) Hom | 3.47 |
| 123963 | C13951 | Hs.210115 | EST | 3.47 |
| 116480 | C14088 | Hs.195188 | glyceraldehyde-3-phosphate dehydrogenase | 3.4 |
| 108836 | AA1132061 | Hs.222727 | ESTs; Weakly similar to ubiquitous TPR m | 3.39 |
| 120748 | AA303153 | Hs.237994 | EST; Weakly similar to !!!! ALU SUBFAMIL | 3.38 |
| 133770 | M69197 | Hs.242279 | haptoglobin-related protein | 3.38 |
| 132358 | X60486 | Hs.46423 | H4 histone family, member G | 3.37 |
| 127759 | AI369384 | | arylsulfatase D | 3.37 |
| 129095 | L12350 | Hs.108623 | thrombospondin 2 | 3.37 |
| 128261 | AI081213 | Hs.13179 | ESTs; Moderately similar to !!!! ALU SUB | 3.36 |
| 126908 | AA169866 | | ESTs; Weakly similar to !!!! ALU SUBFAMI | 3.36 |
| 128954 | N32118 | Hs.209100 | DKFZP434C171 protein | 3.34 |
| 119174 | R71234 | | y154c08.s1 Soares placenta Nb2HP Homo sa | 3.33 |
| 106687 | AA463234 | Hs.119387 | KIAA0792 gene product | 3.32 |
| 128230 | AA984074 | Hs.176757 | ESTs | 3.3 |
| 126649 | AA856990 | Hs.125058 | ESTs | 3.25 |
| 124620 | N74051 | Hs.194092 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 3.24 |
| 135427 | | | AFFX control: human alu repeats | 3.23 |
| 129967 | H99653 | Hs.138618 | ESTs | 3.22 |
| 125191 | W67257 | Hs.138871 | ESTs; Weakly similar to !!!! ALU CLASS B | 3.2 |
| 124684 | R02401 | Hs.221078 | ESTs | 3.2 |
| 128010 | AA856953 | Hs.23348 | S-phase kinase-associated protein 2 (p45 | 3.17 |
| 119423 | T99544 | Hs.173734 | ESTs; Weakly similar to !!!! ALU CLASS B | 3.16 |
| 123022 | AA4480909 | | aa28f10.s1 NCL_CGAP_GCB1 Homo sapiens cD | 3.15 |
| 103654 | Z70759 | | H.sapiens mitochondrial 16S rRNA gene (p | 3.13 |
| 128336 | AI242720 | Hs.146043 | ESTs; Weakly similar to alternatively sp | 3.12 |
| 124690 | R05818 | Hs.173830 | ESTs | 3.1 |
| 129791 | F02778 | Hs.173887 | KIAA0876 protein | 3.07 |
| 114472 | AA028924 | Hs.177407 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 3.07 |
| 115429 | AA284139 | Hs.89295 | EST | 3.06 |
| 130020 | AA433930 | Hs.240443 | ESTs; Weakly similar to HNK-1 sulfotrans | 3.06 |
| 126050 | H27267 | Hs.75860 | hydroxyacyl-Coenzyme A dehydrogenase/3-k | 3.05 |

| | | | | |
|--------|----------|------------|--|------|
| 129906 | H39216 | Hs.239970 | ESTs; Weakly similar to ZNF91L [H.sapien | 3.04 |
| 123422 | AA598484 | Hs.238476 | EST | 3.03 |
| 103059 | X57351 | Hs.174195 | Interferon induced transmembrane protein | 3.02 |
| 124253 | H69742 | Hs.102201 | ESTs | 3.02 |
| 123523 | AA608588 | Hs.193634 | ESTs | 3.02 |
| 132659 | AA188378 | Hs.54602 | ESTs; Weakly similar to 60S RIBOSOMAL PR3.02 | |
| 123196 | AA489250 | Hs.59403 | serine palmitoyltransferase; subunit II | 3.01 |
| 122948 | AA477483 | zu44h2.s1 | Soares ovary tumor NbHOT Homo | 3.01 |
| 119053 | R11501 | yf28f1.s1 | Soares fetal liver spleen 1NFL | 3.01 |
| 125953 | H40829 | yo05d11.r1 | Soares adult brain N2b5HB55Y | 3 |
| 119155 | R61715 | Hs.138237 | ESTs | 3 |

Table 12: H chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number; Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UniG_ID | Complete_Title | Median Mets AI vs Median Normal AI |
|--------|----------|-----------|--|------------------------------------|
| 103466 | Y00339 | Hs.155097 | carbonic anhydrase II | 0.01 |
| 104258 | AF007216 | Hs.5462 | solute carrier family 4; sodium bicarbon | 0.02 |
| 108999 | AA156064 | Hs.72115 | ESTs | 0.04 |
| 101046 | K01160 | | Accession not listed in Genbank | 0.04 |
| 133565 | H57056 | Hs.204831 | ESTs | 0.05 |
| 101346 | L76465 | Hs.77348 | hydroxyprostaglandin dehydrogenase 15-(N | 0.05 |
| 123137 | AA487468 | Hs.100686 | ESTs; Weakly similar to secreted cement | 0.05 |
| 134534 | X73501 | Hs.84905 | H. Sapiens mRNA for cytokeratin 20 | 0.05 |
| 118823 | N79237 | Hs.50813 | ESTs; Weakly similar to long chain fatty | 0.06 |
| 102095 | U11313 | Hs.75760 | sterol carrier protein 2 | 0.06 |
| 111855 | R37362 | Hs.21351 | ESTs | 0.06 |
| 129105 | AA224351 | Hs.108681 | ESTs | 0.07 |
| 130320 | U19495 | Hs.237356 | stromal cell-derived factor 1 | 0.07 |
| 113778 | W15263 | Hs.5422 | ESTs | 0.07 |
| 115786 | H25836 | Hs.83429 | tumor necrosis factor (ligand) superfamily | 0.07 |
| 100116 | D00654 | Hs.77443 | actin; gamma 2; smooth muscle; enteric | 0.07 |
| 104636 | AA004415 | Hs.106106 | ESTs | 0.07 |
| 107032 | AA599472 | Hs.247309 | succinate-CoA ligase; GDP-forming; beta | 0.08 |
| 106605 | AA457718 | Hs.21103 | Homo sapiens mRNA; cDNA DKFZp564B076 (fr | 0.08 |
| 128906 | AA487557 | Hs.10706 | ESTs | 0.08 |
| 130016 | AA055811 | Hs.143131 | transmembrane glycoprotein | 0.08 |
| 113523 | T90037 | Hs.16866 | ESTs | 0.08 |
| 102638 | U67319 | Hs.9216 | caspase 7; apoptosis-related cysteine pr | 0.09 |
| 124308 | H93575 | Hs.227146 | Homo sapiens mRNA; cDNA DKFZp564J142 (fr | 0.09 |
| 129519 | AA298786 | Hs.112242 | ESTs | 0.09 |
| 134749 | L10955 | Hs.89485 | carbonic anhydrase IV | 0.09 |
| 130366 | L11708 | Hs.155109 | hydroxysteroid (17-beta) dehydrogenase 2 | 0.09 |
| 109272 | AA195718 | Hs.86030 | ESTs | 0.09 |
| 102124 | U14528 | Hs.29981 | solute carrier family 26 (sulfate transp | 0.1 |
| 132711 | N73702 | Hs.238927 | ESTs | 0.1 |
| 131861 | D11925 | Hs.184245 | KIAA0929 protein Msx2 interacting nuclea | 0.1 |
| 133806 | M12759 | Hs.76325 | Human Ig J chain gene | 0.1 |
| 102571 | U80115 | | Homo sapiens skeletal muscle LIM-protein | 0.1 |
| 114846 | AA234929 | Hs.44343 | ESTs | 0.11 |
| 131328 | V01512 | Hs.25647 | v-fos FBX murine osteosarcoma viral onco | 0.11 |
| 106569 | AA455983 | Hs.117816 | sorcin | 0.11 |
| 103542 | Z11793 | Hs.3314 | seleoprotein P; plasma; 1 | 0.11 |
| 128915 | C02386 | Hs.107139 | ESTs | 0.11 |
| 120914 | AA377254 | Hs.97107 | EST | 0.11 |
| 130867 | J04093 | Hs.2056 | UDP glycosyltransferase 1 | 0.11 |
| 110837 | N30796 | Hs.17424 | ESTs; Weakly similar to semaphorin F [H. | 0.12 |
| 101877 | M97496 | Hs.778 | guanylate cyclase activator 1B (retina) | 0.12 |
| 132617 | AA171913 | Hs.5338 | carbonic anhydrase XI | 0.12 |
| 129113 | AA147646 | Hs.108740 | DKFZP586A0522 protein | 0.12 |
| 133435 | T23983 | Hs.7365 | ESTs | 0.13 |
| 132836 | F09557 | Hs.57929 | slit (Drosophila) homolog 3 | 0.13 |
| 125832 | AA626600 | Hs.117587 | ESTs | 0.13 |
| 104613 | AA001049 | Hs.24713 | Homo sapiens mRNA; cDNA DKFZp586G0123 (f | 0.13 |
| 132903 | AA235404 | Hs.5985 | Homo sapiens clone 25186 mRNA sequence | 0.13 |
| 119479 | W32094 | Hs.55501 | ESTs | 0.14 |
| 131273 | AA421139 | Hs.173542 | ESTs | 0.14 |
| 106674 | AA461303 | Hs.7946 | DKFZP586D1519 protein | 0.14 |
| 108980 | AA151576 | Hs.33455 | peptidyl arginine deiminase; type II | 0.14 |
| 103211 | X73079 | Hs.205126 | polymeric immunoglobulin receptor | 0.14 |
| 131219 | C00476 | Hs.24395 | small inducible cytokine subfamily B (Cy | 0.15 |
| 116459 | AA621399 | Hs.64193 | ESTs | 0.15 |
| 130219 | R77539 | Hs.15285 | ESTs | 0.15 |
| 113863 | W68388 | Hs.21288 | ESTs; Weakly similar to KIAA0704 protein | 0.15 |
| 101564 | M32886 | Hs.117816 | sorcin | 0.15 |
| 109502 | AA233837 | Hs.44755 | ESTs; Weakly similar to membrane glycopr | 0.15 |
| 107222 | D51235 | Hs.82689 | tumor rejection antigen (gp96) 1 | 0.15 |
| 135237 | AA454930 | Hs.9691 | ESTs | 0.15 |

| | | | | |
|--------|---------------|-----------|---|------|
| 112483 | R66534 | Hs.28403 | ESTs | 0.15 |
| 132387 | R70914 | Hs.8997 | heat shock 70kD protein 1 | 0.15 |
| 130343 | AA490262 | Hs.15485 | ESTs; Weakly similar to APICAL-LIKE PROT | 0.16 |
| 105496 | AA256323 | Hs.25264 | DKFZP434N126 protein | 0.16 |
| 104037 | AA372630 | Hs.100347 | differentially expressed in hematopoieti | 0.16 |
| 101461 | M22430 | Hs.76422 | phospholipase A2; group IIA (platelets; | 0.16 |
| 116551 | D20458 | Hs.229071 | EST | 0.16 |
| 133889 | AA099391 | Hs.211582 | myosin; light polypeptide kinase | 0.16 |
| 103653 | Z70295 | Hs.32966 | guanylate cyclase activator 2B (uruguayan | 0.16 |
| 101070 | L02785 | Hs.1650 | down-regulated in adenoma | 0.17 |
| 131501 | AA121127 | Hs.181307 | H3 histone; family 3A | 0.17 |
| 133515 | X98311 | Hs.74466 | carinoembryonic antigen-related cell ad | 0.17 |
| 108604 | AA099820 | Hs.49696 | ESTs | 0.17 |
| 132982 | L02326 | Hs.198118 | immunoglobulin lambda-like polypeptide 2 | 0.17 |
| 131676 | C20785 | Hs.30514 | ESTs | 0.17 |
| 134575 | AA250745 | Hs.87773 | protein kinase; cAMP-dependent; catalyt | 0.17 |
| 133441 | M82962 | Hs.179704 | mephrin A; alpha (PABA peptide hydrolase) | 0.18 |
| 130455 | X17059 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acetyl | 0.18 |
| 131734 | D62965 | Hs.31297 | ESTs | 0.18 |
| 100749 | HG3521-HT3715 | | Ras-Related Protein Rap1b | 0.18 |
| 116724 | F13665 | Hs.65641 | ESTs | 0.18 |
| 129265 | X68277 | Hs.171695 | dual specificity phosphatase 1 | 0.18 |
| 102347 | U37518 | Hs.83429 | tumor necrosis factor (ligand) superfam | 0.18 |
| 114542 | AA055768 | Hs.122576 | ESTs | 0.18 |
| 123900 | AA621223 | Hs.112853 | EST | 0.19 |
| 121780 | AA422086 | Hs.124660 | ESTs | 0.19 |
| 115662 | AA405715 | Hs.64179 | hypothetical protein | 0.19 |
| 113803 | W42789 | Hs.31446 | ESTs | 0.19 |
| 105493 | AA256268 | Hs.10283 | ESTs | 0.19 |
| 113195 | T57112 | | yc20g11.s1 Stratagene lung (#937210) Hnm | 0.19 |
| 129462 | D84239 | Hs.111732 | IgG Fc binding protein | 0.19 |
| 133664 | X86693 | Hs.75445 | hevin | 0.2 |
| 126180 | R18070 | Hs.3712 | ubiquinol-cytochrome c reductase; Rieske | 0.2 |
| 100687 | HG3115-HT3291 | | Golf-Mbp (Gb:L18862) | 0.2 |
| 130064 | T67053 | Hs.181125 | immunoglobulin lambda gene cluster | 0.2 |
| 101367 | M12963 | Hs.73843 | alcohol dehydrogenase 1 (class I); alpha | 0.2 |
| 132254 | L20826 | Hs.430 | plastin 1 (I isoform) | 0.2 |
| 105646 | AA282147 | Hs.5888 | ESTs | 0.2 |
| 132883 | AA047151 | Hs.5897 | Homo sapiens mRNA; cDNA DKFZp586P1622 (f | 0.21 |
| 132618 | AA253330 | Hs.5344 | adaptor-related protein complex 1; gamma | 0.21 |
| 108931 | AA147186 | Hs.250746 | ESTs | 0.22 |
| 131421 | X64177 | Hs.2657 | metallothionein 1H | 0.22 |
| 107295 | T34527 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 0.22 |
| 103576 | Z26317 | Hs.2631 | desmoglein 2 | 0.22 |
| 105173 | AA182030 | Hs.8364 | ESTs | 0.22 |
| 134843 | H60595 | Hs.90061 | progesterone binding protein | 0.22 |
| 102009 | U02680 | Hs.82643 | protein tyrosine kinase 9 | 0.23 |
| 123997 | D51171 | Hs.78902 | voltage-dependent anion channel 2 | 0.23 |
| 106609 | AA458652 | Hs.32181 | ESTs | 0.23 |
| 101300 | L40391 | Hs.6445 | Homo sapiens (clone s153) mRNA fragment | 0.23 |
| 129717 | AA481670 | Hs.12150 | ESTs; Weakly similar to retinal short-ch | 0.23 |
| 108565 | AA085342 | Hs.1526 | ATPase; Ca++ transporting; cardiac muscl | 0.23 |
| 121314 | AA402799 | Hs.182538 | ESTs | 0.23 |
| 124803 | R45480 | Hs.164866 | cyclin K | 0.23 |
| 130208 | AA620556 | Hs.15250 | peroxisomal D3:D2-enoyl-CoA isomerase | 0.23 |
| 132888 | AA4490775 | Hs.5920 | UDP-N-acetylglucosamine-2-epimerase/N-ac | 0.23 |
| 132720 | Z69881 | Hs.5541 | ATPase; Ca++ transporing; ubiquitous | 0.23 |
| 102239 | U28726 | Hs.1376 | hydroxysteroid (11-beta) dehydrogenase 2 | 0.23 |
| 115764 | AA421562 | Hs.91011 | anterior gradient 2 (<i>Xenopus laevis</i>) hom | 0.24 |
| 130558 | H96654 | Hs.15984 | ESTs; Weakly similar to gene pp21 protei | 0.24 |
| 122666 | AA455052 | Hs.99387 | ESTs | 0.24 |
| 134495 | D63477 | Hs.84087 | KIAA0143 protein | 0.24 |
| 124017 | F02202 | Hs.100960 | ESTs | 0.24 |
| 106925 | AA491261 | Hs.37558 | Homo sapiens clone 23923 mRNA sequence | 0.24 |
| 115187 | AA261805 | Hs.44021 | ESTs | 0.24 |
| 105309 | AA233790 | Hs.4104 | ESTs; Weakly similar to cDNA EST yk386g7 | 0.24 |
| 124457 | N50114 | Hs.128704 | ESTs | 0.24 |
| 130616 | AA233763 | Hs.16726 | Homo sapiens mRNA; cDNA DKFZp564A132 (fr | 0.25 |
| 105795 | AA369245 | Hs.17448 | ESTs; Weakly similar to III ALU SUBFAMI | 0.25 |
| 134579 | N23222 | Hs.85963 | CD36 antigen (collagen type I receptor; | 0.25 |

Table 13: H chip – Met vs Normal query – up in Mets

Pkey: Unique Hos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UniG_ID | Complete_Title | Ratio Met/Normal |
|--------|----------|-----------|--|------------------|
| 102193 | U20758 | Hs.313 | secreted phosphoprotein 1 (osteopontin; | 8.457 |
| 111307 | N73988 | Hs.37477 | ESTs; Weakly similar to CGI-141 protein | 6.05 |
| 103119 | X63629 | Hs.2877 | cadherin 3; P-cadherin (placental) | 5.207 |
| 131564 | AA491465 | Hs.28792 | ESTs | 5.136 |
| 119729 | W69747 | Hs.94806 | KIAA1062 protein | 4.667 |
| 124059 | F13673 | Hs.99769 | ESTs | 4.398 |
| 123987 | C21171 | Hs.95497 | ESTs; Weakly similar to GLUCOSE TRANSPOR | 4.292 |
| 128817 | N47524 | Hs.28491 | spermidine/spermine N1-acetyltransferase | 3.964 |
| 133770 | M69197 | Hs.242279 | haptoglobin-related protein | 3.823 |
| 130412 | AA406554 | Hs.241572 | golgi autoantigen; golgin subfamily a; 5 | 3.719 |
| 104755 | AA024482 | Hs.8029 | DKFZP434G032 protein | 3.702 |
| 132676 | AA283035 | Hs.54813 | ESTs | 3.645 |
| 134453 | X70583 | Hs.83484 | SRY (sex determining region Y)-box 4 | 3.581 |
| 124690 | R05818 | Hs.173830 | ESTs | 3.446 |
| 106949 | AA496805 | Hs.177425 | KIAA0964 protein | 3.42 |
| 130724 | AA370091 | Hs.179680 | ESTs | 3.402 |
| 128992 | R49693 | Hs.107708 | ESTs | 3.32 |
| 133421 | AA436560 | Hs.7327 | claudin 1 | 3.255 |
| 103047 | X55990 | Hs.73839 | ribonuclease; RNase A family; 3 (eosinop | 3.229 |
| 102990 | X51441 | Hs.181062 | serum amyloid A1 | 3.149 |
| 115429 | AA284139 | Hs.89295 | EST | 3.114 |
| 129158 | J05257 | Hs.109 | dipeptidase 1 (renal) | 3.019 |
| 123533 | AA608751 | Hs.244904 | ESTs; Weakly similar to !!! ALU SUBFAMI | 3.011 |

Table 14: H chip - Met vs Normal query - down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| PkeyY | Ex Accn | UniG_ID | Complete_Title | Ratio Met/Normal |
|--------|----------|-----------|--|------------------|
| 103466 | Y00339 | Hs.155097 | carbonic anhydrase II | 0.012 |
| 104258 | AF007216 | Hs.5462 | solute carrier family 4; sodium bicarbon | 0.025 |
| 108999 | AA156064 | Hs.72115 | ESTs | 0.034 |
| 101046 | K01160 | | Accession not listed in Genbank | 0.041 |
| 133565 | H57056 | Hs.204831 | ESTs | 0.042 |
| 101346 | L76465 | Hs.77348 | hydroxyprostaglandin dehydrogenase 15-(N | 0.043 |
| 102095 | U11313 | Hs.75760 | sterol carrier protein 2 | 0.054 |
| 111855 | R37362 | Hs.21351 | ESTs | 0.055 |
| 130320 | U19495 | Hs.237356 | stromal cell-derived factor 1 | 0.058 |
| 123137 | AA487468 | Hs.100686 | ESTs; Weakly similar to secreted cement | 0.06 |
| 107222 | D51235 | Hs.82689 | tumor rejection antigen (gp96) 1 | 0.06 |
| 102638 | U67319 | Hs.9216 | caspase 7; apoptosis-related cysteine pr | 0.063 |
| 128906 | AA487557 | Hs.10706 | ESTs | 0.065 |
| 129105 | AA224351 | Hs.108681 | ESTs | 0.069 |
| 110837 | N30796 | Hs.17424 | ESTs; Weakly similar to semaphorin F [H. | 0.069 |
| 100116 | D00654 | Hs.77443 | actin; gamma 2; smooth muscle; enteric | 0.071 |
| 116786 | H25836 | Hs.83429 | tumor necrosis factor (ligand) superfam | 0.074 |
| 130867 | J04093 | Hs.2055 | UDP glycosyltransferase 1 | 0.075 |
| 132836 | F09557 | Hs.57929 | slit (Drosophila) homolog 3 | 0.076 |
| 131861 | D11925 | Hs.184245 | KIAA0929 protein Msx2 interacting nuclea | 0.081 |
| 106674 | AA461303 | Hs.7946 | DKFZP586D1519 protein | 0.084 |
| 109272 | AA195718 | Hs.86030 | ESTs | 0.088 |
| 132711 | N73702 | Hs.238927 | ESTs | 0.091 |
| 106569 | AA455983 | Hs.117816 | sorcin | 0.092 |
| 104636 | AA004415 | Hs.106106 | ESTs | 0.093 |
| 118823 | N79237 | Hs.50813 | ESTs; Weakly similar to long chain fatty | 0.094 |
| 134534 | X73501 | Hs.84905 | H. Sapiens mRNA for cytokeratin 20 | 0.095 |
| 119479 | W32094 | Hs.55501 | ESTs | 0.096 |
| 113778 | W15263 | Hs.5422 | ESTs | 0.098 |
| 128482 | U83908 | Hs.100407 | programmed cell death 4 | 0.102 |
| 124653 | N92884 | Hs.109641 | ESTs | 0.106 |
| 133407 | AA093348 | Hs.7306 | secreted frizzled-related protein 1 | 0.108 |
| 135237 | AA454930 | Hs.8691 | ESTs | 0.109 |
| 116250 | AA480975 | Hs.44829 | ESTs | 0.111 |
| 132617 | AA171913 | Hs.5338 | carbonic anhydrase XII | 0.112 |
| 131273 | AA421139 | Hs.173542 | ESTs | 0.113 |
| 116710 | F10577 | Hs.70312 | ESTs | 0.114 |
| 131791 | S71043 | Hs.32225 | immunoglobulin alpha 1 | 0.114 |
| 112483 | R66534 | Hs.28403 | ESTs | 0.115 |
| 132017 | W67251 | Hs.37331 | Homo sapiens vav 3 oncogene (VAV3) mRNA | 0.116 |
| 124308 | H93575 | Hs.227146 | Homo sapiens mRNA; cDNA DKFZp564J142 (fr | 0.117 |
| 114846 | AA234929 | Hs.44343 | ESTs | 0.119 |
| 116551 | D20458 | Hs.229071 | EST | 0.12 |
| 105299 | AA233511 | Hs.194720 | ATP-binding cassette; sub-family G (WHIT | 0.122 |
| 130366 | L11708 | Hs.155109 | hydroxysteroid (17-beta) dehydrogenase 2 | 0.122 |
| 133806 | M12759 | Hs.76325 | Human Ig J chain gene | 0.122 |
| 104776 | AA026349 | Hs.31412 | ESTs | 0.125 |
| 129565 | X77777 | Hs.198726 | vasoactive intestinal peptide receptor 1 | 0.125 |
| 131272 | AA423884 | Hs.139033 | paternally expressed gene 3 | 0.127 |
| 105774 | AA348014 | Hs.23412 | ESTs | 0.128 |
| 134604 | M22995 | Hs.865 | RAP1A; member of RAS oncogene family | 0.128 |
| 134711 | X04011 | Hs.88974 | cytochrome b-245; beta polypeptide (chro | 0.128 |
| 129113 | AA147646 | Hs.108740 | DKFZP586A0522 protein | 0.133 |
| 123995 | D51119 | Hs.100090 | tetraspan 3 | 0.133 |
| 129168 | T90621 | Hs.109052 | chromosome 14 open reading frame 2 | 0.133 |
| 123891 | AA621103 | Hs.99216 | ESTs; Moderately similar to III ALU SUB | 0.135 |
| 132694 | M60830 | Hs.5509 | ectotropic viral integration site 2B | 0.135 |
| 135342 | W60097 | Hs.99120 | DEAD/H (Asp-Glu-Ala-Asp/His) box polype | 0.135 |
| 131510 | AA207114 | Hs.27842 | ESTs; Weakly similar to similar to 1-acy | 0.137 |
| 133652 | AA287383 | Hs.7540 | ESTs | 0.137 |
| 134749 | L10955 | Hs.89485 | carbonic anhydrase IV | 0.139 |
| 106586 | AA455598 | Hs.256269 | ESTs | 0.139 |

| | | | | |
|--------|---------------|--|--|-------|
| 106893 | AA489636 | Hs.25253 | ESTs | 0.139 |
| 101070 | L02785 | Hs.1650 | down-regulated in adenoma | 0.14 |
| 114293 | Z40718 | Hs.20196 | adenylate cyclase 9 | 0.14 |
| 113966 | W86600 | Hs.9842 | ESTs | 0.141 |
| 101185 | L19872 | Hs.170087 | aryl hydrocarbon receptor | 0.145 |
| 131492 | AA393876 | Hs.1255 | nuclear receptor subfamily 2; group F; m | 0.145 |
| 133889 | AA099391 | Hs.211582 | myosin; light polypeptide kinase | 0.145 |
| 120914 | AA377254 | Hs.97107 | EST | 0.147 |
| 118771 | N74690 | Hs.50547 | ESTs | 0.149 |
| 105496 | AA256323 | Hs.25264 | DKFZP434N126 protein | 0.151 |
| 131011 | R41771 | Hs.22146 | ESTs | 0.153 |
| 106210 | AA428239 | Hs.10338 | ESTs | 0.154 |
| 114069 | Z38161 | Hs.197335 | plasma glutamate carboxypeptidase | 0.154 |
| 133011 | AA042990 | Hs.171921 | sema domain; immunoglobulin domain (Ig); | 0.154 |
| 115967 | AA446887 | Hs.42911 | ESTs | 0.154 |
| 102571 | U60115 | Homo sapiens skeletal muscle LIM-protein | 0.155 | |
| 100687 | HG3115-HT3291 | Golf-Mbp (Gb:18862) | 0.155 | |
| 132903 | AA235404 | Hs.5985 | Homo sapiens clone 25186 mRNA sequence | 0.155 |
| 125832 | AA628600 | Hs.117587 | ESTs | 0.155 |
| 130084 | T67053 | Hs.181125 | immunoglobulin lambda gene cluster | 0.157 |
| 123264 | AA491003 | Hs.99824 | BCE-1 protein | 0.159 |
| 130919 | AA291710 | Hs.21276 | collagen; type IV; alpha 3 (Goodpasture | 0.159 |
| 103542 | Z11793 | Hs.3314 | selenoprotein P; plasma; 1 | 0.161 |
| 101478 | M23379 | Hs.758 | RAS p21 protein activator (GTPase activa | 0.162 |
| 108921 | AA142913 | Hs.71721 | ESTs | 0.164 |
| 100642 | HG2743-HT3926 | Caldesmon 1, Alt. Splice 6, Non-Muscle | 0.167 | |
| 132109 | AA599801 | Hs.40098 | ESTs | 0.167 |
| 115719 | AA416397 | Hs.59622 | ESTs | 0.169 |
| 128915 | C02386 | Hs.107139 | ESTs | 0.171 |
| 117634 | N36421 | Hs.107854 | ESTs; Weakly similar to SODIUM- AND CHLO | 0.172 |
| 129462 | D84239 | Hs.111732 | IgG Fc binding protein | 0.174 |
| 131328 | V01512 | Hs.25647 | v-fos FBJ murine osteosarcoma viral onco | 0.176 |
| 130343 | AA490262 | Hs.15485 | ESTs; Weakly similar to APICAL-LIKE PROT | 0.177 |
| 115764 | AA421562 | Hs.91011 | anterior gradient 2 (Xenopus laevis) hom | 0.177 |
| 122261 | AA436830 | Hs.98902 | ESTs | 0.179 |
| 106605 | AA457718 | Hs.21103 | Homo sapiens mRNA; cDNA DKFZp564B076 (fr | 0.179 |
| 109991 | H09813 | Hs.12896 | KIAA1034 protein | 0.181 |
| 101300 | L40391 | Hs.6445 | Homo sapiens (clone s153) mRNA fragment | 0.181 |
| 123080 | AA485303 | Hs.205126 | polymeric immunoglobulin receptor | 0.182 |
| 130016 | AA055811 | Hs.143131 | transmembrane glycoprotein | 0.186 |
| 122666 | AA455052 | Hs.99387 | ESTs | 0.188 |
| 105453 | AA252893 | Hs.9001 | ESTs | 0.189 |
| 108980 | AA151676 | Hs.33455 | peptidyl arginine deiminase; type II | 0.19 |
| 100248 | D31888 | Hs.78398 | KIAA0071 protein | 0.192 |
| 130036 | AA195260 | Hs.208738 | ESTs; Moderately similar to !!! ALU SUB | 0.192 |
| 110882 | N36001 | Hs.17348 | ESTs; Weakly similar to !!! ALU SUBFAMI | 0.193 |
| 131676 | C20785 | Hs.30514 | ESTs | 0.195 |
| 111029 | N54792 | Hs.24697 | cytidine monophosphate-N-acetylneuramini | 0.196 |
| 131257 | AA256042 | Hs.24908 | ESTs | 0.196 |
| 133348 | T23517 | Hs.7149 | ESTs | 0.196 |
| 133784 | AA214305 | Hs.76173 | ESTs | 0.196 |
| 113863 | W68388 | Hs.21288 | ESTs; Weakly similar to KIAA0704 protein | 0.197 |
| 103158 | X67235 | Hs.118651 | hematopoietically expressed homeobox | 0.198 |
| 102347 | U37518 | Hs.83429 | tumor necrosis factor (ligand) superfamily | 0.2 |
| 111351 | N90223 | Hs.23392 | ESTs | 0.2 |
| 123495 | AA599850 | Hs.106747 | ESTs; Weakly similar to similar to BPTI/ | 0.2 |
| 123802 | AA620448 | Hs.61408 | Homo sapiens clone 24760 mRNA sequence | 0.2 |
| 129243 | H88033 | Hs.109727 | KIAA0733 protein | 0.2 |
| 130219 | R77539 | Hs.15285 | ESTs | 0.2 |
| 131171 | H04644 | Hs.167619 | ESTs; Weakly similar to !!! ALU SUBFAMI | 0.2 |
| 133746 | U44378 | Hs.75862 | MAD (mothers against decapentaplegic; Dr | 0.2 |
| 116459 | AA621399 | Hs.64183 | ESTs | 0.201 |
| 109613 | F03031 | Hs.27519 | ESTs | 0.202 |
| 133435 | T23983 | Hs.7365 | ESTs | 0.202 |
| 103002 | X52001 | Hs.1408 | endothelin 3 | 0.204 |
| 125153 | W38294 | Accession not listed in Genbank | | 0.204 |
| 131919 | AA121266 | Hs.34641 | ESTs | 0.204 |
| 100749 | HG3521-HT3715 | Ras-Related Protein Rap1b | | 0.205 |
| 105085 | AA147537 | Hs.4811 | ESTs | 0.208 |
| 124571 | N67470 | Hs.173074 | DKFZP564O1853 protein | 0.21 |
| 129519 | AA298786 | Hs.112242 | ESTs | 0.21 |
| 116724 | F13665 | Hs.65641 | ESTs | 0.21 |
| 132932 | T15482 | Hs.6093 | ESTs | 0.21 |
| 113803 | W42789 | Hs.31446 | ESTs | 0.211 |
| 110792 | N24899 | Hs.6630 | ESTs | 0.212 |
| 105178 | AA187490 | Hs.21941 | ESTs | 0.212 |

| | | | | |
|--------|----------|--|--|-------|
| 107295 | T34527 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:poly | 0.212 |
| 115262 | AA279112 | Hs.88594 | ESTs | 0.213 |
| 115839 | AA429038 | Hs.40541 | ESTs | 0.213 |
| 103211 | X73079 | Hs.205126 | polymeric immunoglobulin receptor | 0.214 |
| 108604 | AA099820 | Hs.49696 | ESTs | 0.215 |
| 105173 | AA182030 | Hs.8364 | ESTs | 0.217 |
| 108539 | AA084677 | Hs.54558 | ESTs; Weakly similar to protein B [H.sap | 0.217 |
| 109984 | H09594 | Hs.10299 | ESTs | 0.217 |
| 133536 | Y00264 | Hs.177486 | amyloid beta (A4) precursor protein (pro | 0.217 |
| 129965 | T71333 | Hs.13854 | ESTs | 0.219 |
| 114542 | AA055768 | Hs.122576 | ESTs | 0.219 |
| 132982 | L02325 | Hs.198118 | immunoglobulin lambda-like polypeptide 2 | 0.22 |
| 101809 | MB6849 | Homo sapiens connexin 26 (GJB2) mRNA, co | | |
| 105795 | AA369245 | Hs.17448 | ESTs; Weakly similar to !!! ALU SUBFAMI | 0.222 |
| 132119 | H99211 | Hs.40334 | ESTs | 0.222 |
| 132733 | R25385 | Hs.123654 | KIAA0824 protein | 0.222 |
| 109415 | AA227219 | Hs.110826 | trinucleotide repeat containing 9 | 0.222 |
| 113083 | T40530 | Hs.8241 | ESTs; Weakly similar to heat shock prote | 0.223 |
| 107053 | AA600147 | Hs.5741 | ESTs; Weakly similar to NADH-cytochrome | 0.224 |
| 103653 | Z70285 | Hs.32966 | guanylate cyclase activator 2B (uroguany | 0.225 |
| 104613 | AA001049 | Hs.24713 | Homo sapiens mRNA; cDNA DKFZp588G0123 (f | 0.225 |
| 126180 | R18070 | Hs.3712 | ubiquinol-cytochrome c reductase; Rieske | 0.227 |
| 132015 | D11900 | Hs.3731 | ESTs | 0.227 |
| 130616 | AA233763 | Hs.16726 | Homo sapiens mRNA; cDNA DKFZp564A132 (fr | 0.227 |
| 132883 | AA047151 | Hs.5897 | Homo sapiens mRNA; cDNA DKFZp588P1622 (f | 0.23 |
| 123169 | AA488892 | Hs.104472 | ESTs; Weakly similar to Gag-Pol polyprot | 0.233 |
| 115187 | AA261805 | Hs.44021 | ESTs | 0.234 |
| 116787 | H28581 | Hs.15641 | ESTs | 0.234 |
| 113195 | T57112 | yc20g11.s1 Stratagene lung (#937210) Hom | | |
| 130707 | W45457 | Hs.203559 | ESTs | 0.235 |
| 124803 | R45480 | Hs.164866 | cyclin K | 0.235 |
| 116844 | H64938 | Hs.38331 | ESTs | 0.235 |
| 102759 | U81607 | Hs.788 | A kinase (PRKA) anchor protein (gravin) | 0.238 |
| 130584 | AA009839 | Hs.180841 | tumor necrosis factor receptor superfamily | 0.238 |
| 133240 | D31161 | Hs.88613 | ESTs | 0.238 |
| 132952 | AA425154 | Hs.61426 | ESTs | 0.239 |
| 132720 | Z69881 | Hs.5541 | ATPase; Ca++ transporting; ubiquitous | 0.24 |
| 131734 | D62965 | Hs.31297 | ESTs | 0.24 |
| 111890 | R38678 | Hs.12365 | ESTs | 0.241 |
| 102325 | U35139 | Hs.50130 | necdin (mouse) homolog | 0.244 |
| 104988 | AA084602 | Hs.29569 | ESTs | 0.244 |
| 105674 | AA284755 | Hs.214742 | CDW52 antigen (CAMPATH-1 antigen) | 0.244 |
| 120519 | AA258585 | Hs.129887 | cadherin 19 (NOTE: redefinition of symbo | 0.244 |
| 134675 | AA250745 | Hs.87773 | protein kinase; cAMP-dependent; catalyt | 0.244 |
| 130642 | M63438 | Hs.158110 | Immunoglobulin kappa variable 1D-8 | 0.245 |
| 134418 | R78190 | Hs.82933 | ESTs; Weakly similar to cDNA EST EMBL:T0 | 0.245 |
| 115137 | AA257976 | Hs.56156 | ESTs | 0.245 |
| 131713 | X57809 | Hs.181125 | immunoglobulin lambda gene cluster | 0.246 |
| 108931 | AA147186 | Hs.250746 | ESTs | 0.246 |
| 106609 | AA458652 | Hs.32181 | ESTs | 0.248 |
| 115559 | AA393810 | Hs.41067 | ESTs | 0.25 |
| 133985 | L34657 | Hs.78146 | platelet/endothelial cell adhesion molec | 0.25 |
| 134088 | D43636 | Hs.79025 | KIAA0096 protein | 0.25 |
| 134487 | R38185 | Hs.83954 | Homo sapiens unknown mRNA | 0.25 |

Table 15: I chip – Met vs Normal query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex_Accn | UniG_ID | Title | Ratio Met/Normal |
|--------|----------|-----------|--|------------------|
| 319379 | T91443 | Hs.193963 | ESTs | 18.71 |
| 321920 | N63915 | | EST cluster (not in UniGene) | 11.9 |
| 314522 | AI732331 | Hs.187750 | ESTs; Moderately similar to !!! ALU CLA | 7.23 |
| 315720 | AW291875 | Hs.163900 | ESTs | 6.06 |
| 308010 | AI439190 | Hs.181165 | eukaryotic translation elongation factor | 5.76 |
| 313774 | AW136836 | Hs.144583 | ESTs | 5.01 |
| 300734 | AW205197 | Hs.240951 | ESTs | 3.98 |
| 337895 | | | CH22_EM:AC005500.GENSCAN.56-2 | 3.98 |
| 312339 | AA524394 | | EST cluster (not in UniGene) | 3.66 |
| 331644 | T99544 | Hs.173734 | ESTs; Weakly similar to !!! ALU CLASS B | 3.53 |
| 324643 | AI436356 | Hs.130729 | ESTs | 3.52 |
| 324302 | AA543008 | Hs.136806 | ESTs; Weakly similar to !!! ALU SUBFAMI | 3.41 |
| 314912 | AI431345 | Hs.161784 | ESTs | 3.33 |
| 319403 | T98413 | | EST cluster (not in UniGene) | 3.32 |
| 308676 | AI761036 | | EST singleton (not in UniGene) with exon | 3.27 |
| 331858 | AA421163 | Hs.163848 | ESTs | 3.22 |
| 315178 | AW362945 | Hs.162459 | ESTs | 3.21 |
| 321354 | AA078493 | | EST cluster (not in UniGene) | 3.18 |
| 337898 | | | CH22_EM:AC005500.GENSCAN.56-5 | 3.16 |
| 322682 | AI110579 | | EST cluster (not in UniGene) | 3.15 |
| 313197 | AI738851 | Hs.222487 | ESTs | 3.1 |
| 308991 | AI879831 | | EST singleton (not in UniGene) with exon | 3.08 |
| 310016 | AW449612 | Hs.152475 | ESTs | 3.05 |

Table 16: I chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex_Accn | UniG_ID | Title | Ratio Met/Normal |
|--------|-----------|-----------|--|------------------|
| 303041 | AF127035 | | EST cluster (not in UniGene) with exon h | 0.02 |
| 302360 | AJ010901 | Hs.198257 | mucin 4; tracheobronchial | 0.03 |
| 301948 | AA344647 | Hs.116724 | aldo-keto reductase family 1; member B11 | 0.03 |
| 336091 | | | CH22_FGENES.689_3 | 0.04 |
| 333657 | | | CH22_FGENES.241_2 | 0.04 |
| 333658 | | | CH22_FGENES.241_4 | 0.04 |
| 333737 | | | CH22_FGENES.261_1 | 0.05 |
| 333656 | | | CH22_FGENES.240_4 | 0.05 |
| 302347 | AF039400 | Hs.194659 | chloride channel; calcium activated; fam | 0.06 |
| 336084 | | | CH22_FGENES.688_13 | 0.06 |
| 330385 | AA449749 | Hs.31386 | ESTs; Highly similar to secreted apoptos | 0.06 |
| 304487 | AA434241 | | EST singleton (not in UniGene) with exon | 0.07 |
| 302292 | AF067797 | | EST cluster (not in UniGene) with exon h | 0.07 |
| 334030 | | | CH22_FGENES.320_2 | 0.07 |
| 332859 | | | CH22_FGENES.27_2 | 0.07 |
| 333654 | | | CH22_FGENES.240_2 | 0.07 |
| 303270 | AL120518 | Hs.105352 | ESTs | 0.08 |
| 320352 | Y13323 | Hs.145296 | disintegrin protease | 0.08 |
| 333637 | | | CH22_FGENES.229_2 | 0.08 |
| 324094 | AA382603 | | EST cluster (not in UniGene) | 0.08 |
| 320590 | U67058 | Hs.168102 | Human proteinase activated receptor-2 mR | 0.08 |
| 330622 | X63597 | Hs.2996 | sucrase-isomaltase | 0.08 |
| 331441 | H75860 | Hs.39720 | ESTs | 0.08 |
| 308601 | AJ719930 | | EST singleton (not in UniGene) with exon | 0.09 |
| 323770 | AA722425 | | EST cluster (not in UniGene) | 0.09 |
| 335188 | | | CH22_FGENES.507_3 | 0.09 |
| 333730 | | | CH22_FGENES.258_1 | 0.09 |
| 304480 | AA430373 | | EST singleton (not in UniGene) with exon | 0.09 |
| 336081 | | | CH22_FGENES.688_10 | 0.1 |
| 332071 | AA598594 | Hs.112475 | ESTs | 0.1 |
| 318538 | N28625 | Hs.74034 | caveolin 1; caveolae protein; 22kD | 0.1 |
| 311331 | AI679522 | Hs.32225 | immunoglobulin alpha 1 | 0.1 |
| 319668 | NM_002731 | | EST cluster (not in UniGene) | 0.11 |
| 332567 | N23730 | Hs.25647 | v-fos FBJ murine osteosarcoma viral onco | 0.11 |
| 319395 | AW062570 | Hs.13809 | ESTs | 0.11 |
| 315594 | AI983437 | Hs.155145 | ESTs | 0.11 |
| 321539 | N98619 | Hs.62461 | ARP2 (actin-related protein 2; yeast) ho | 0.12 |
| 333647 | | | CH22_FGENES.235_2 | 0.12 |
| 333588 | | | CH22_FGENES.206_2 | 0.12 |
| 321286 | AI380940 | | EST cluster (not in UniGene) | 0.12 |
| 320727 | U96044 | | EST cluster (not in UniGene) | 0.13 |
| 335687 | | | CH22_FGENES.596_2 | 0.13 |
| 324611 | AA743462 | Hs.165337 | ESTs | 0.14 |
| 335115 | | | CH22_FGENES.496_2 | 0.14 |
| 324660 | AA541644 | Hs.186044 | ESTs | 0.14 |
| 337951 | | | CH22_EM:AC005500.GENSCAN.94-1 | 0.14 |
| 302332 | AI833168 | Hs.184507 | Homo sapiens Chromosome 16 BAC clone CIT | 0.14 |
| 300921 | AW293224 | Hs.232165 | ESTs | 0.14 |
| 333646 | | | CH22_FGENES.234_2 | 0.14 |
| 335116 | | | CH22_FGENES.496_3 | 0.14 |
| 320241 | AL039402 | Hs.125783 | DEME-6 protein | 0.15 |
| 336092 | | | CH22_FGENES.689_6 | 0.15 |
| 330673 | D57823 | Hs.92962 | Sec23 (S. cerevisiae) homolog A | 0.16 |
| 303042 | AF129532 | | EST cluster (not in UniGene) with exon h | 0.16 |
| 337954 | | | CH22_EM:AC005500.GENSCAN.96-3 | 0.16 |
| 336645 | | | CH22_FGENES.26_1 | 0.16 |
| 335651 | | | CH22_FGENES.590_2 | 0.16 |
| 314499 | AL044570 | Hs.147975 | ESTs | 0.17 |
| 336124 | | | CH22_FGENES.701_9 | 0.17 |
| 315199 | AA877996 | Hs.125376 | ESTs | 0.17 |
| 324525 | AW044647 | Hs.196284 | ESTs | 0.17 |
| 320825 | NM_004751 | | EST cluster (not in UniGene) | 0.18 |

| | | | | |
|--------|----------|------------------------------|--|------|
| 302049 | AA377072 | Hs.129792 | Homo sapiens Chromosome 16 BAC clone C1T | 0.18 |
| 336083 | | CH22_FGENES.688_12 | | 0.18 |
| 333653 | | CH22_FGENES.239_2 | | 0.18 |
| 323243 | W44372 | EST cluster (not in UniGene) | | 0.19 |
| 316610 | AW087973 | Hs.126731 | ESTs | 0.19 |
| 315033 | AI493046 | Hs.146133 | ESTs | 0.19 |
| 330651 | U39840 | Hs.105440 | hepatocyte nuclear factor 3; alpha | 0.19 |
| 333642 | | CH22_FGENES.231_2 | | 0.19 |
| 301281 | AA843986 | Hs.190586 | ESTs | 0.2 |
| 333626 | | CH22_FGENES.224_2 | | 0.21 |
| 303792 | C75094 | Hs.199839 | ESTs; Highly similar to NG22 [H.sapiens] | 0.21 |
| 332325 | T79428 | Hs.191264 | ESTs | 0.21 |
| 321223 | AA431366 | | EST cluster (not in UniGene) | 0.21 |
| 333635 | | CH22_FGENES.228_2 | | 0.22 |
| 314645 | AI808999 | Hs.207570 | ESTs | 0.22 |
| 322929 | AI365585 | Hs.146246 | ESTs | 0.22 |
| 324718 | AI557019 | Hs.116467 | ESTs | 0.22 |
| 335652 | | CH22_FGENES.590_3 | | 0.22 |
| 307783 | AI347274 | | EST singleton (not in UniGene) with exon | 0.22 |
| 331344 | AA357927 | Hs.70208 | ESTs | 0.22 |
| 336088 | | CH22_FGENES.688_17 | | 0.23 |
| 320802 | D83824 | Hs.185055 | BENE protein | 0.23 |
| 335692 | | CH22_FGENES.596_7 | | 0.23 |
| 333593 | | CH22_FGENES.210_2 | | 0.23 |
| 335667 | | CH22_FGENES.590_18 | | 0.24 |
| 314853 | AA729232 | Hs.153279 | ESTs | 0.24 |
| 320244 | AA286922 | Hs.129778 | gastrointestinal peptide | 0.24 |
| 300601 | AI762130 | Hs.165619 | ESTs | 0.24 |
| 305080 | AA641485 | | EST singleton (not in UniGene) with exon | 0.25 |
| 335189 | | CH22_FGENES.507_4 | | 0.25 |

Table 17: B survivor vs Mets – Up in B survivor

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UniG_ID | Complete Title | Ratio BS/Met |
|--------|---------------|-----------|--|--------------|
| 101006 | J04132 | Hs.97087 | CD3Z antigen; zeta polypeptide (ITIM com | 7.28 |
| 114173 | Z39050 | Hs.21963 | ESTs | 6.13 |
| 130284 | X82206 | Hs.153961 | ARP1 (actin-related protein 1; yeast) ho | 5.77 |
| 100787 | HG3872-HT4142 | | immunoglobulin Gamma Heavy Chain, V(5)D(j) Regions (Gb:U13200) | 5.63 |
| 132461 | AA405775 | Hs.49005 | hypothetical protein | 5.62 |
| 133808 | M12759 | Hs.76325 | Human Ig J chain gene | 5.46 |
| 133747 | D86972 | Hs.75863 | KIAA0218 gene product | 5.45 |
| 123328 | AA495968 | Hs.105403 | EST | 5.28 |
| 132671 | X76302 | Hs.54649 | putative nucleic acid binding protein RY | 5.25 |
| 132018 | AA293194 | Hs.3737 | ESTs | 5.22 |
| 100188 | D17516 | Hs.4748 | adenylate cyclase activating polypeptide | 5.14 |
| 107155 | AA621202 | Hs.7946 | DKFZP586D1519 protein | 5.1 |
| 103568 | Z22555 | Hs.180616 | CD36 antigen (collagen type I receptor; | 5.06 |
| 113355 | T79203 | Hs.14480 | ESTs | 4.99 |
| 129040 | U38864 | Hs.108139 | zinc finger protein 212 | 4.96 |
| 130214 | H78003 | Hs.15266 | ESTs | 4.93 |
| 129550 | AA480991 | Hs.113025 | ESTs | 4.92 |
| 129704 | W81301 | Hs.12064 | ubiquitin specific protease 22 | 4.91 |
| 116425 | AA609574 | Hs.51483 | ESTs | 4.77 |
| 105166 | AA179787 | Hs.30570 | polyglutamine binding protein 1 | 4.65 |
| 118765 | N74442 | Hs.183696 | ESTs | 4.6 |
| 108999 | AA156084 | Hs.72115 | ESTs | 4.57 |
| 112756 | R33908 | Hs.35258 | ESTs | 4.54 |
| 111655 | R16884 | Hs.187462 | ESTs | 4.48 |
| 118392 | T90672 | Hs.238859 | ESTs | 4.42 |
| 131957 | AA609008 | Hs.183232 | ESTs | 4.41 |
| 129275 | D82061 | Hs.109993 | Ke6 gene; mouse; human homolog of | 4.4 |
| 113634 | T95085 | Hs.125182 | ESTs | 4.4 |
| 127187 | AA297138 | Hs.207422 | ESTs | 4.32 |
| 101147 | L13266 | Hs.105 | glutamate receptor; ionotropic; N-methyl | 4.3 |
| 134901 | S78873 | Hs.90875 | RAB interacting factor | 4.26 |
| 100896 | HG4593-HT4998 | | Sodium Channel 1 | 4.24 |
| 100687 | HG3115-HT3291 | | Golli-Mbp (Gb:L18862) | 4.21 |
| 129758 | AA599552 | Hs.183770 | Homo sapiens mRNA; cDNA DKFZp566P2346(f | 4.19 |
| 105440 | AA252243 | Hs.22851 | ESTs | 4.16 |
| 131551 | AA127867 | Hs.28608 | ESTs | 4.15 |
| 113761 | T93973 | Hs.189786 | ESTs | 4.09 |
| 105897 | AA401091 | | ESTs | 4.07 |
| 129495 | AA382529 | Hs.239676 | ESTs | 4.06 |
| 103436 | X98206 | | H.sapiens mRNA for UV-B repressed sequen | 4.03 |
| 104673 | AA007633 | Hs.20010 | ESTs | 4.03 |
| 128886 | L36720 | Hs.106880 | bystin-like | 4.02 |
| 100702 | HG3236-HT3413 | | Neurofibromatosis 2 Tumor Suppressor (Gb:L27065) | 3.99 |
| 123547 | AA608820 | Hs.124085 | KIAA0921 protein | 3.98 |
| 134877 | AA445241 | Hs.90527 | ESTs | 3.97 |
| 123650 | AA609332 | Hs.180696 | ESTs | 3.94 |
| 106482 | AA451672 | Hs.108824 | ESTs; Weakly similar to cDNA EST yk415c1 | 3.94 |
| 101909 | S69265 | | Homo sapiens mRNA for PLE21 protein; com | 3.93 |
| 108390 | AA075070 | | zm86bb.s1 Stratagene ovarian cancer #93 | 3.93 |
| 135403 | U06643 | Hs.99923 | LYMPHOCYTE ANTIGEN LY-6A.2/LY-6E.1 PREC | 3.93 |
| 121038 | AA398536 | Hs.97365 | lectin; galactoside-binding; soluble; 7 | 3.89 |
| 128496 | T83496 | Hs.100610 | ESTs | 3.88 |
| 108785 | AA128946 | | ESTs | 3.86 |
| 119838 | W79499 | Hs.58580 | ESTs | 3.85 |
| 130109 | L12060 | Hs.1497 | retinoic acid receptor; gamma | 3.84 |
| 134538 | U79288 | Hs.85053 | KIAA0513 gene product | 3.83 |
| 110310 | H38209 | Hs.32728 | EST | 3.81 |
| 110433 | H49425 | Hs.32992 | ESTs | 3.78 |
| 111834 | R36138 | Hs.152458 | ESTs | 3.76 |
| 130903 | N27086 | Hs.21068 | ESTs | 3.74 |
| 105142 | AA164851 | Hs.15380 | ESTs; Weakly similar to HERV-E envelope | 3.73 |

| | | | | |
|--------|---------------|-----------|---|------|
| 130248 | U84569 | Hs.153452 | chromosome 21 open reading frame 2 | 3.73 |
| 130645 | AA020942 | Hs.17200 | STAM-like protein containing SH3 and ITA | 3.73 |
| 123378 | AA521043 | Hs.185832 | ESTs | 3.73 |
| 103985 | AA313880 | | EST185737 Colon carcinoma (HCC) cell lin | 3.73 |
| 112397 | R60822 | Hs.26805 | EST | 3.72 |
| 100980 | J03069 | Hs.72931 | v-myc avian myelocytomatisis viral oncogene | 3.72 |
| 102609 | U64863 | Hs.158297 | programmed cell death 1 | 3.7 |
| 108974 | AA151402 | Hs.46531 | ESTs | 3.7 |
| 130192 | Y12661 | Hs.171014 | VGF nerve growth factor inducible | 3.69 |
| 131318 | X51699 | Hs.2558 | bone gamma-carboxyglutamate (gla) protein | 3.68 |
| 113759 | T99364 | Hs.16074 | Homo sapiens mRNA; cDNA DKFZp564I153 (fr | 3.66 |
| 133712 | L19267 | Hs.198836 | dystrophia myotonica-containing WD repeat | 3.65 |
| 134229 | R15108 | Hs.8037 | ESTs | 3.65 |
| 134241 | AA300265 | Hs.80540 | KIAA0195 gene product | 3.65 |
| 124699 | R06413 | Hs.112278 | arrestin; beta 1 | 3.62 |
| 107343 | U03115 | Hs.103945 | Human V beta T-cell receptor (TCRBV) gene | 3.62 |
| 128511 | AA425536 | Hs.10082 | potassium intermediate/small conductance | 3.62 |
| 105466 | AA253412 | Hs.21489 | ESTs | 3.61 |
| 131377 | R41389 | Hs.26159 | ESTs | 3.6 |
| 119135 | R49548 | Hs.169681 | death effector domain-containing | 3.6 |
| 132982 | L02326 | Hs.198118 | immunoglobulin lambda-like polypeptide 2 | 3.59 |
| 128514 | H84261 | Hs.100843 | ESTs; Weakly similar to similar to GTP-b | 3.56 |
| 102396 | U41804 | Hs.54411 | putative T1/ST2 receptor binding protein | 3.55 |
| 134945 | R50247 | Hs.91600 | ESTs | 3.55 |
| 134913 | X60483 | Hs.91031 | H4 histone family; member D | 3.54 |
| 102053 | U07664 | Hs.37035 | homeo box HB9 | 3.52 |
| 121569 | AA412686 | Hs.97955 | ESTs | 3.52 |
| 132560 | AA005315 | Hs.204524 | ESTs; Weakly similar to KIAA0747 protein | 3.51 |
| 118456 | N66580 | Hs.161496 | EST; Weakly similar to HC1 ORF [M.muscul | 3.51 |
| 111518 | R08160 | Hs.222529 | ESTs; Weakly similar to III ALU SUBFAMI | 3.51 |
| 116795 | H38858 | Hs.251783 | EST | 3.5 |
| 130377 | AA378316 | Hs.155182 | KIAA1036 protein | 3.5 |
| 121774 | AA421758 | Hs.98361 | ESTs | 3.49 |
| 123413 | AA521448 | Hs.103845 | ESTs | 3.49 |
| 133798 | AA444115 | Hs.76277 | ESTs; Weakly similar to salivary proline | 3.49 |
| 135183 | X93996 | Hs.239663 | myeloid/lymphoid or mixed-lineage leukemia | 3.48 |
| 132479 | AA477715 | Hs.4953 | golgi autoantigen; golgin subfamily a; 3 | 3.47 |
| 117191 | H99394 | Hs.40339 | EST | 3.47 |
| 130942 | X87852 | Hs.21432 | H.splans mRNA for SEX gene | 3.46 |
| 130700 | D55696 | Hs.18069 | protease; cysteine; 1 (legumain) | 3.43 |
| 131301 | T17386 | Hs.164501 | ESTs | 3.43 |
| 100818 | HG4018-HT4288 | | Opioid-Binding Cell Adhesion Molecule | 3.43 |
| 103393 | X94612 | Hs.41749 | protein kinase; cGMP-dependent; type II | 3.43 |
| 131337 | AA228116 | Hs.170204 | KIAA0551 protein | 3.42 |
| 133403 | X68688 | Hs.72991 | zinc finger protein 33b (KOX 31) | 3.42 |
| 124728 | R16231 | Hs.106620 | Homo sapiens clone 23950 mRNA sequence | 3.41 |
| 123168 | AA488881 | Hs.105218 | EST | 3.39 |
| 123324 | AA496932 | Hs.105398 | KIAA0809 protein | 3.38 |
| 106947 | AA496885 | Hs.37936 | suppressor of variegation 3-9 (Drosophil | 3.38 |
| 116717 | F11065 | Hs.79363 | ESTs | 3.36 |
| 102794 | U88629 | Hs.173334 | ELL-RELATED RNA POLYMERASE II; ELONGATIO | 3.34 |
| 117503 | N31963 | Hs.44286 | ESTs | 3.33 |
| 112220 | R50295 | Hs.25703 | ESTs | 3.33 |
| 106340 | AA441792 | Hs.22857 | chord domain-containing protein 1 | 3.33 |
| 106308 | AA436186 | Hs.30662 | ESTs | 3.32 |
| 130894 | D16105 | Hs.210 | leukocyte tyrosine kinase | 3.31 |
| 120039 | W92548 | Hs.94985 | ESTs | 3.31 |
| 131428 | U17838 | Hs.26719 | PR domain containing 2; with ZNF domain | 3.3 |
| 113285 | T66830 | Hs.182712 | ESTs | 3.3 |
| 109458 | AA232648 | Hs.87068 | ESTs | 3.29 |
| 132134 | AA242804 | Hs.40637 | proline-rich Gla (G-carboxyglutamic acid | 3.29 |
| 118964 | N93330 | Hs.54937 | Homo sapiens clone 24722 unknown mRNA; p | 3.29 |
| 127621 | AI218205 | Hs.116204 | ESTs | 3.29 |
| 135149 | U40002 | Hs.95351 | lipase; hormone-sensitive | 3.28 |
| 114371 | Z41835 | Hs.27810 | ESTs | 3.28 |
| 130043 | AA055404 | Hs.193953 | ESTs; Weakly similar to III ALU SUBFAMI | 3.27 |
| 121347 | AA405181 | Hs.97972 | ESTs | 3.25 |
| 105754 | AA302657 | Hs.192028 | ESTs | 3.25 |
| 121327 | AA404286 | Hs.173125 | peptidylprolyl isomerase F (cyclophilin | 3.25 |
| 111204 | N68295 | Hs.37982 | ESTs | 3.25 |
| 120949 | AA397830 | Hs.98347 | ESTs; Weakly similar to GLIOMA PATHOGENE | 3.25 |
| 130024 | U15197 | Hs.241560 | Human histo-blood group ABO protein mRNA | 3.24 |
| 125005 | T61449 | Hs.193727 | ESTs | 3.24 |
| 121067 | AA398662 | Hs.97302 | ESTs | 3.24 |
| 120996 | AA398281 | Hs.143684 | ESTs | 3.23 |
| 117101 | H94043 | Hs.24341 | DKFZP586I1419 protein | 3.23 |

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|--------|---------------|-----------|--|------|
| 130708 | U40490 | Hs.18136 | nicotinamide nucleotide transhydrogenase | 3.23 |
| 130270 | L40399 | Hs.153820 | hypothetical protein | 3.22 |
| 131605 | AA256220 | Hs.29383 | ESTs | 3.22 |
| 100854 | HG4194-HT4464 | | Sodium/Hydrogen Exchanger 5 | 3.22 |
| 123026 | AA481072 | Hs.99743 | ESTs | 3.21 |
| 108328 | AA070204 | | zm68b3.s1 Stratagene neuroepithelium (#9 | 3.2 |
| 104259 | AF007833 | Hs.159265 | Homo sapiens kruppel-related zinc finger | 3.2 |
| 133711 | J04130 | Hs.75703 | small inducible cytokine A4 (homologous | 3.2 |
| 112261 | R52145 | Hs.25894 | ESTs; Highly similar to hypothetical pro | 3.19 |
| 119529 | W38053 | | Accession not listed in Genbank | 3.19 |
| 122386 | AA46221 | Hs.6092 | F-box protein containing leucine-rich re | 3.19 |
| 109157 | AA179161 | Hs.73562 | ESTs | 3.19 |
| 119903 | W85707 | Hs.75936 | erythrocyte membrane protein band 4.9 (d | 3.18 |
| 127452 | AA491317 | | aa65c01.r1 NCI_CGAP_GCB1 Homo sapiens cD | 3.18 |
| 124229 | H62793 | Hs.221892 | ESTs | 3.18 |
| 128221 | AA417126 | Hs.109571 | translocase of inner mitochondrial membr | 3.17 |
| 133185 | AA481404 | Hs.6586 | ESTs | 3.16 |
| 121479 | AA411911 | Hs.98110 | ESTs | 3.16 |
| 133872 | T79868 | Hs.180903 | hypothetical protein | 3.16 |
| 132504 | U12897 | Hs.5022 | imprinted in Prader-Willi syndrome | 3.16 |
| 103089 | X60382 | Hs.179729 | collagen; type X; alpha 1 (Schmid metaph | 3.15 |
| 129654 | AA019943 | Hs.118463 | H.sapiens mRNA for unknown liver orphan | 3.15 |
| 117295 | N22360 | Hs.43153 | ESTs | 3.15 |
| 107349 | U48224 | Hs.158321 | beaded filament structural protein 2; ph | 3.14 |
| 103451 | X99459 | Hs.154782 | adaptor-related protein complex 3; sigma | 3.14 |
| 114854 | AA235056 | Hs.120244 | ESTs | 3.14 |
| 121044 | AA398551 | Hs.97374 | ESTs | 3.13 |
| 128582 | U22963 | Hs.101840 | major histocompatibility complex; class | 3.13 |
| 112598 | R78565 | Hs.138395 | EST | 3.13 |
| 113170 | T54342 | Hs.222506 | ESTs | 3.13 |
| 111714 | R23146 | Hs.23466 | ESTs | 3.13 |
| 111809 | R33616 | Hs.24688 | EST | 3.12 |
| 115249 | AA278981 | Hs.711124 | ESTs | 3.11 |
| 103228 | X75546 | Hs.230 | fibromodulin | 3.11 |
| 129944 | L00389 | Hs.1381 | cytochrome P450; subfamily 1 (aromatic c | 3.11 |
| 107927 | AA028915 | Hs.237709 | EST | 3.11 |
| 130297 | H94949 | Hs.171955 | trophinin-assisting protein (tasin) | 3.1 |
| 125742 | H81181 | Hs.183654 | ESTs; Weakly similar to unknown [S.cerev | 3.1 |
| 134802 | L35546 | Hs.89709 | glutamate-cysteine ligase (gamma-glutamy | 3.1 |
| 112560 | R72293 | Hs.6179 | Homo sapiens mRNA; cDNA DKFZp586K2322 (f | 3.1 |
| 129266 | AA343881 | Hs.209051 | sudD (suppressor of bimD6; Aspergillus n | 3.09 |
| 126982 | AA211419 | | small inducible cytokine A5 (RANTES) | 3.09 |
| 131594 | H29723 | Hs.29261 | ESTs; Weakly similar to serine protease | 3.08 |
| 134910 | AA431320 | Hs.9100 | ESTs | 3.08 |
| 103505 | Y09912 | Hs.33102 | transcription factor AP-2 beta (activati | 3.08 |
| 110525 | H57330 | Hs.37430 | EST | 3.07 |
| 123276 | AA491270 | Hs.187946 | ESTs | 3.06 |
| 130519 | H91819 | Hs.10669 | ESTs; Moderately similar to KIAA0400 [H. | 3.06 |
| 126621 | AA192638 | | zq01h08.R1 Stratagene muscle 937209 Homo | 3.05 |
| 134327 | AF006041 | Hs.178743 | death-associated protein 6 | 3.04 |
| 103513 | Y10209 | | H.sapiens mRNA for CD3L protein | 3.04 |
| 131243 | R16667 | Hs.24752 | spectrin SH3 domain binding protein 1 | 3.04 |
| 115187 | AA261805 | Hs.44021 | ESTs | 3.04 |
| 107543 | Z43703 | Hs.4552 | Homo sapiens HRIHFB2157 mRNA; partial cd | 3.04 |
| 134051 | S67070 | Hs.78846 | heat shock 27kD protein 2 | 3.04 |
| 113461 | T86737 | Hs.193536 | ESTs | 3.03 |
| 130490 | X57522 | Hs.158164 | ATP-binding cassette; sub-family B (MDR/ | 3.03 |
| 128843 | AA234141 | Hs.203004 | katanin p80 (WD40-containing) subunit B | 3.03 |
| 100941 | HG862-HT862 | | Transition Protein 2 | 3.03 |
| 122268 | AA435855 | Hs.178202 | ESTs | 3.02 |
| 107425 | W26719 | Hs.30204 | ESTs | 3.02 |
| 130930 | U19261 | | TNF receptor-associated factor 1 | 3.02 |
| 132958 | W90398 | Hs.6147 | KIAA1075 protein | 3.02 |
| 100973 | J02888 | Hs.73956 | NAD(P)H menadione oxidoreductase 2; diox | 3.01 |
| 104924 | AA058532 | Hs.28774 | ESTs | 3.01 |
| 129998 | Y10055 | Hs.162808 | phosphoinositide-3-kinase; catalytic; de | 3.01 |
| 130023 | X13461 | Hs.239600 | calmodulin-like 3 | 3.01 |
| 129536 | M33493 | Hs.184504 | tryptase; alpha | 3 |
| 112015 | R42836 | Hs.23198 | ESTs | 3 |
| 103036 | X54925 | Hs.83169 | matrix metalloproteinase 1 (intersitial | 2.99 |
| 100756 | HG3555-HT3768 | | Zinc Finger Protein (Gb;M88357) | 2.99 |
| 103425 | X97301 | | H.sapiens mRNA for Plg-11 protein | 2.99 |
| 118291 | N53076 | Hs.138746 | EST | 2.98 |
| 125877 | H15229 | | ym30g04.R1 Soares Infant brain 1NIB Homo | 2.98 |
| | | | repetitive element;, mRNA sequence. | 2.98 |
| 101371 | M13232 | Hs.36989 | coagulation factor VII (serum prothrombi | 2.98 |

| | | | | |
|--------|---------------|---|--|------|
| 102958 | X15675 | Hs.93174 | Human endogenous retrovirus pHE.1 (ERV9) | 2.97 |
| 121183 | AA400138 | Hs.97703 | ESTs | 2.97 |
| 119241 | T12559 | Hs.221382 | ESTs | 2.96 |
| 115067 | AA253458 | Hs.91299 | postmeiotic segregation increased 2-like | 2.96 |
| 128196 | AA084394 | zr05g10.1 Stratagene hNT neuron (#93723 | 2.96 | |
| 111642 | R18153 | Hs.128740 | ESTs; Highly similar to DNb-5 [H.sapiens | 2.95 |
| 100898 | HG4638-HT5050 | | Spliceosomal Protein Sap 49 | 2.95 |
| 129370 | AA287879 | Hs.110796 | ESTs; Moderately similar to GTP-binding | 2.94 |
| 128915 | C02386 | Hs.107139 | ESTs | 2.94 |
| 101868 | M96233 | Hs.82891 | glutathione S-transferase M4 | 2.94 |
| 124394 | N29724 | | gamma2-adaptin | 2.93 |
| 103559 | Z19585 | Hs.75774 | thrombospondin 4 | 2.93 |
| 107882 | AA025630 | Hs.17801 | ESTs; Moderately similar to serine/proline | 2.93 |
| 134919 | T99839 | Hs.91142 | KH-type splicing regulatory protein (FUS | 2.92 |
| 110293 | H30258 | Hs.37165 | collagen; type IX; alpha 2 | 2.92 |
| 132433 | AA082546 | Hs.48516 | ESTs | 2.92 |
| 127347 | AA428350 | | ESTs | 2.92 |
| 121976 | AA429807 | Hs.98632 | ESTs | 2.91 |
| 133025 | AA135492 | Hs.6318 | ESTs; Highly similar to peroxisomal short | 2.91 |
| 133413 | S72043 | Hs.73133 | metallothionein 3 (growth inhibitory fac | 2.91 |
| 111694 | R22035 | Hs.23331 | ESTs | 2.91 |
| 128369 | F12681 | Hs.205300 | ESTs | 2.9 |
| 102464 | U49260 | Hs.3828 | mevalonate (diphospho) decarboxylase | 2.9 |
| 135358 | C21431 | Hs.99486 | ESTs; Weakly similar to aralar1 [H.sapiens | 2.9 |
| 108661 | AA113287 | Hs.65905 | ESTs; Weakly similar to PTB-ASSOCIATED S2.9 | |
| 102185 | U20230 | | Human guanylyl cyclase C gene, partial cds | 2.89 |
| 122071 | AA431787 | Hs.98762 | EST | 2.89 |
| 102040 | U06088 | Hs.159479 | galactosamine (N-acetyl)-6-sulfate sulfat | 2.89 |
| 115689 | AA410645 | Hs.199014 | ESTs | 2.88 |
| 135110 | T15817 | Hs.193788 | nitrile oxide synthase 2A (inducible; hep | 2.88 |
| 118729 | N73717 | Hs.161526 | EST | 2.88 |
| 129518 | AA369807 | Hs.112238 | ESTs | 2.88 |
| 125788 | R74309 | Hs.44499 | small EDRK-rich factor 2 | 2.87 |
| 128650 | U57971 | Hs.103124 | ATPase; Ca++ transporting; plasma membra | 2.87 |
| 125936 | H30751 | Hs.182859 | lifeguard | 2.87 |
| 100779 | HG3731-HT4001 | | Immunoglobulin Heavy Chain, VdjC Regions (Gb:L23566) | 2.87 |
| 104451 | M13299 | Hs.102119 | blue cone pigment | 2.86 |
| 133539 | M21574 | Hs.74615 | platelet-derived growth factor receptor; | 2.86 |
| 119506 | W37833 | Hs.55563 | ESTs | 2.86 |
| 126568 | AA190515 | | zp85d12.r1 Stratagene HeLa cell s3 93721 | 2.86 |
| 134184 | X53742 | Hs.79732 | fibulin 1 | 2.86 |
| 127633 | AI339609 | Hs.152733 | potassium voltage-gated channel; Isk-rel | 2.86 |
| 128716 | AA045978 | Hs.173611 | NADH dehydrogenase (ubiquinone) Fe-S pro | 2.86 |
| 107135 | AA620782 | Hs.23247 | ESTs | 2.85 |
| 117748 | N47317 | Hs.141858 | ESTs | 2.85 |
| 124030 | F04143 | Hs.151032 | Homo sapiens clone 23856 unknown mRNA; p | 2.85 |
| 135120 | AA449841 | Hs.108300 | NOT3 (negative regulator of transcription | 2.84 |
| 102156 | U17977 | | HSU17977 Human fibroblast cDNA H.sapiens | 2.84 |
| 129418 | AA401401 | Hs.11127 | PET112 (yeast homolog)-like | 2.84 |
| 103222 | X74795 | Hs.77171 | minichromosome maintenance deficient (S. | 2.84 |
| 125145 | W38001 | | Accession not listed in Genbank | 2.83 |
| 100560 | HG2228-HT2305 | | Crystallin, Beta B | 2.83 |
| 105370 | AA236476 | Hs.22791 | ESTs; Weakly similar to transmembrane pr | 2.83 |
| 127036 | A1468598 | | ESTs | 2.83 |
| 128788 | AA029073 | Hs.105685 | ESTs | 2.83 |
| 119523 | W38041 | | Accession not listed in Genbank | 2.82 |
| 126436 | N31224 | Hs.211579 | melanoma adhesion molecule | 2.82 |
| 126559 | R15866 | Hs.170263 | tumor protein 53-binding protein; 1 | 2.82 |
| 118183 | N59287 | Hs.48361 | EST | 2.82 |
| 101298 | L40387 | Hs.118633 | 2'-Oligoadenylate synthetase-like | 2.81 |
| 131830 | U33054 | Hs.32959 | G protein-coupled receptor kinase 2 (Dro | 2.81 |
| 124173 | H41281 | Hs.107619 | ESTs | 2.81 |
| 102295 | U32581 | | Homo sapiens KIAA0421 mRNA; partial cds | 2.81 |
| 129719 | N66396 | Hs.167766 | ESTs; Moderately similar to Pro-a2(XI) | 2.81 |
| 126573 | AA482023 | Hs.155218 | E1B-55kDa-associated protein 5 | 2.81 |
| 125477 | AI270093 | Hs.234642 | aquaporin 3 | 2.81 |
| 106492 | AA451896 | Hs.7922 | ESTs; Weakly similar to contains similar | |
| | | | p19; an RNA polymerase II elongation fa | 2.8 |
| 132881 | T86118 | Hs.58875 | ESTs | 2.8 |
| 114733 | AA133778 | Hs.95734 | ESTs | 2.79 |
| 104618 | AA001611 | Hs.186494 | ESTs | 2.79 |
| 134137 | F10045 | Hs.79347 | KIAA0211 gene product | 2.79 |
| 133212 | U82979 | Hs.67846 | leukocyte Ig-like receptor; subfamily B | 2.78 |
| 100882 | HG4460-HT4729 | | Immunoglobulin Heavy Chain, VdjC Regions (Gb:L23564) | 2.78 |
| 104756 | AA024622 | Hs.15813 | solute carrier family 22 (organic cation | 2.78 |
| 129861 | N69507 | Hs.129849 | DKFZP564M182 protein | 2.78 |

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|--------|---------------|-----------|--|------|
| 120824 | AA347548 | Hs.96876 | ESTs | 2.78 |
| 100684 | HG3107-HT3283 | | Plasma Membrane Calcium Pump Hpmca2a | 2.78 |
| 121789 | AA423970 | Hs.178111 | ESTs | 2.78 |
| 101647 | M59941 | Hs.118200 | colony stimulating factor 2 receptor; be | 2.78 |
| 113722 | T97957 | Hs.202948 | ESTs; Weakly similar to alternatively sp | 2.77 |
| 115107 | AA256371 | Hs.186645 | ESTs | 2.77 |
| 111464 | R05518 | Hs.19521 | ESTs | 2.77 |
| 108446 | AA079120 | | zm95e1.s1 Stratagene colon HT29 (#937221 | 2.77 |
| 123921 | AA621329 | Hs.250671 | Hu DNA seq frm clone 1163J1 on chr 22q13 | |
| | | | prot (similar to mouse Celsr1; rat MEGF | 2.77 |
| 134445 | M59488 | Hs.83384 | S100 calcium-binding protein; beta (neur | 2.76 |
| 114132 | Z38688 | Hs.24192 | ESTs | 2.76 |
| 120500 | AA256430 | Hs.132525 | ESTs | 2.76 |
| 101860 | M95610 | Hs.37165 | collagen; type IX; alpha 2 | 2.76 |
| 134430 | H52105 | Hs.8309 | KIAA0747 protein | 2.76 |
| 124152 | H27216 | Hs.107635 | ESTs | 2.76 |
| 132268 | AA058833 | Hs.23445 | ESTs; Weakly smlr to similar to M. muscu | 2.76 |
| 116257 | AA481493 | Hs.88537 | ESTs | 2.76 |
| 102438 | U46570 | Hs.7733 | tetratricopeptide repeat domain 1 | 2.75 |
| 122393 | AA446334 | Hs.99064 | ESTs | 2.75 |
| 107653 | AA010210 | Hs.47041 | ESTs | 2.75 |
| 123574 | AA609473 | Hs.105187 | ESTs; Moderately similar to kinesin like | 2.75 |
| 129858 | T66906 | Hs.12970 | ESTs | 2.75 |
| 130117 | U05641 | Hs.150207 | UDP glycosyltransferase 2 family; polype | 2.75 |
| 133464 | M13982 | Hs.73917 | interleukin 4 | 2.75 |
| 127039 | AA233366 | Hs.256491 | ESTs | 2.74 |
| 128318 | AA418202 | Hs.13810 | ESTs | 2.74 |
| 123363 | AA504818 | Hs.171279 | ESTs | 2.74 |
| 127654 | AA649249 | Hs.75640 | natriuretic peptide precursor A | 2.74 |
| 132087 | L20860 | Hs.178382 | glycoprotein lb (platelet); beta polypep | 2.74 |
| 125664 | AA948418 | Hs.25744 | ESTs; Weakly similar to Ydr412wp [S.cere | 2.73 |
| 132354 | L05187 | Hs.211913 | small proline-rich protein 1A | 2.73 |
| 101568 | M33764 | Hs.75212 | ornithine decarboxylase 1 | 2.73 |
| 101438 | M20777 | Hs.159263 | Homo sapiens; alpha-2 (VI) collagen | 2.73 |
| 116233 | AA479082 | Hs.61142 | ESTs | 2.73 |
| 122194 | AA435882 | Hs.97531 | ESTs | 2.72 |
| 113995 | W88466 | Hs.22010 | ESTs | 2.72 |
| 124251 | H68286 | Hs.107924 | ESTs | 2.71 |
| 120583 | AA281304 | Hs.78614 | complement component 1; q subcomponent b | 2.71 |
| 134958 | U72507 | Hs.234216 | Human 40871 mRNA partial sequence | 2.71 |
| 124280 | H85835 | Hs.100058 | dihydropyrimidinase-like 4 | 2.71 |
| 130113 | M64673 | Hs.1499 | heat shock transcription factor 1 | 2.71 |
| 106588 | AA456612 | Hs.25682 | ESTs; Weakly smlr to PHOSPHATIDYLETHANOL | 2.71 |
| 132023 | F01927 | Hs.3743 | ESTs; Weakly similar to proline-rich pro | 2.7 |
| 112284 | R53558 | Hs.26052 | ESTs | 2.7 |
| 107897 | AA026240 | Hs.61387 | ESTs | 2.7 |
| 122610 | AA453598 | Hs.99336 | ESTs | 2.7 |
| 119070 | R27788 | Hs.52302 | ESTs | 2.7 |
| 103491 | Y08836 | | Homo sapiens mRNA for HRX-like protein | 2.7 |
| 108225 | AA058843 | Hs.161620 | EST | 2.7 |
| 105829 | AA398290 | Hs.21985 | ESTs | 2.69 |
| 127749 | AI251757 | Hs.145234 | ESTs | 2.69 |
| 128428 | AI185718 | Hs.143900 | ESTs | 2.69 |
| 108409 | AA075578 | | zm88h3.s1 Stratagene ovarian cancer (#93 | 2.69 |
| 114739 | AA134923 | Hs.103833 | ESTs; Weakly similar to predicted using | 2.68 |
| 128821 | D87002 | Hs.135 | multiple UniGene matches | 2.68 |
| 107412 | W26105 | Hs.8961 | ESTs | 2.68 |
| 117012 | H85893 | Hs.194387 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.68 |
| 135262 | AA416551 | Hs.9732 | ESTs | 2.68 |
| 105357 | AA236397 | Hs.20304 | ESTs | 2.68 |
| 134771 | L13939 | Hs.89576 | adaptor-related protein complex 1; beta | 2.68 |
| 105036 | AA128617 | Hs.25549 | ESTs | 2.68 |
| 125093 | T92930 | Hs.186750 | ESTs | 2.68 |
| 119340 | T61899 | Hs.90677 | ESTs; Highly similar to CGI-82 protein [| 2.67 |
| 132603 | H62900 | Hs.53066 | hsp70-interacting protein | 2.67 |
| 113733 | T88386 | Hs.184548 | ESTs | 2.67 |
| 123564 | AA608902 | Hs.112612 | ESTs | 2.66 |
| 116059 | AA454165 | Hs.53455 | ESTs | 2.66 |
| 125803 | R79373 | Hs.29852 | ESTs | 2.66 |
| 123012 | AA479962 | Hs.139636 | EST | 2.66 |
| 106080 | AA418046 | Hs.35124 | ESTs | 2.66 |
| 128809 | T59668 | Hs.102267 | lysyl oxidase | 2.66 |
| 104354 | H08988 | Hs.113759 | ESTs | 2.66 |
| 107068 | AA609028 | Hs.8032 | ESTs | 2.65 |
| 101418 | M17754 | Hs.1276 | BN51 (BHK21) temperature sensitivity com | 2.65 |
| 135157 | AA460138 | Hs.95582 | SRY (sex-determining region Y)-box 20 | 2.65 |

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|---------|----------|-----------|--|------|
| 123312 | AA496258 | Hs.99601 | ESTs | 2.65 |
| 130034 | C00350 | Hs.14454 | chromosome 2 open reading frame 1 | 2.65 |
| 103897 | AA248870 | Hs.55058 | ESTs | 2.65 |
| 117771 | N47961 | Hs.46794 | ESTs | 2.65 |
| 109980 | H09529 | Hs.98693 | DKFZP586J0917 protein | 2.64 |
| 121966 | AA429553 | Hs.98616 | EST | 2.64 |
| 114233 | Z39652 | Hs.27457 | ESTs | 2.64 |
| 129594 | R70379 | Hs.115396 | Human germline IgD chain gene; C-region; | 2.63 |
| 102319 | U34587 | Hs.66578 | corticotropin releasing hormone receptor | 2.63 |
| 111700 | R22212 | Hs.23381 | ESTs | 2.63 |
| 127365 | AA001628 | Hs.74335 | heat shock 90kD protein 1; beta | 2.63 |
| 104205 | AA496240 | Hs.17270 | DKFZP434C211 protein | 2.63 |
| 124559 | N66223 | Hs.135928 | ESTs; Weakly similar to III ALU SUBFAMI | 2.63 |
| 106351 | AA442772 | Hs.191987 | ESTs; Weakly similar to III ALU SUBFAMI | 2.63 |
| 121903 | AA427605 | Hs.258742 | myosin-binding protein C; cardiac | 2.62 |
| 116442 | AA620310 | Hs.184343 | ESTs; Weakly similar to KIAA0585 protein | 2.62 |
| 127041 | F08090 | | HSC0WG031 normalized infant brain cDNA H | 2.62 |
| 132860 | U93049 | Hs.58435 | FYN-binding protein (FYB-120/130) | 2.62 |
| 131591 | L22454 | Hs.180069 | nuclear respiratory factor 1 | 2.61 |
| 118118 | N56901 | Hs.47995 | ESTs | 2.61 |
| 134809- | X52611 | Hs.18387 | transcription factor AP-2 alpha (activat | 2.61 |
| 117706 | N45091 | Hs.46472 | ESTs | 2.61 |
| 127488 | AA312179 | Hs.178617 | ESTs; Weakly similar to CGI-82 protein [| 2.61 |
| 114891 | AA235984 | Hs.87469 | ESTs | 2.6 |
| 116426 | AA609668 | Hs.71657 | ESTs | 2.6 |
| 132589 | AA432197 | Hs.5260 | ESTs; Weakly similar to CGI-08 protein [| 2.6 |
| 128410 | AA452788 | | zx39g11.r1 Soares_total_fetus_Nb2HF8_9w | 2.6 |
| 106081 | AA418394 | Hs.25354 | ESTs | 2.6 |
| 129919 | R02003 | Hs.191208 | ESTs; Weakly similar to weak similarity | 2.59 |
| 124672 | R00307 | Hs.188504 | ESTs | 2.59 |
| 122758 | AA459013 | Hs.99742 | X-ray repair complementing defective rep | 2.59 |
| 125656 | AA040118 | Hs.78687 | neutral sphingomyelinase (N-SMase) activ | 2.59 |
| 130052 | J00220 | Hs.145288 | Human Ig active epsilon1 5' UT; V-D-J re | 2.59 |
| 134878 | U28055 | Hs.250826 | macrophage stimulating; pseudogene 9 | 2.59 |
| 131908 | L05624 | Hs.3446 | mitogen-activated protein kinase kinase | 2.59 |
| 126470 | AA843339 | Hs.193168 | ESTs; Weakly similar to CGI-52 protein [| 2.59 |
| 132353 | M31651 | Hs.46319 | sex hormone-binding globulin | 2.58 |
| 119588 | W44559 | Hs.142525 | ESTs | 2.58 |
| 131757 | D17532 | Hs.316 | DEAD/H (Asp-Glu-Ala-Asp/His) box polype | 2.58 |
| 118114 | N56875 | Hs.143212 | cystatin F (leukocystatin) | 2.58 |
| 128200 | A1279952 | Hs.158037 | ESTs; Weakly similar to transcription re | 2.58 |
| 131208 | C14586 | Hs.24220 | Homo sapiens mRNA; cDNA DKFZp566M051 (r | 2.58 |
| 124721 | R11131 | Hs.154966 | ESTs | 2.57 |
| 108706 | AA121820 | | Homo sapiens mRNA for KIAA0842 protein; | 2.57 |
| 118831 | N79592 | Hs.50838 | ESTs | 2.57 |
| 115708 | AA412212 | Hs.44033 | ESTs | 2.57 |
| 107233 | D59322 | Hs.22595 | ESTs | 2.57 |
| 129559 | AA234945 | Hs.11360 | ESTs | 2.57 |
| 126953 | AA743849 | Hs.127286 | ESTs | 2.56 |
| 108165 | AA055221 | Hs.63168 | ESTs | 2.56 |
| 104069 | AA401547 | Hs.172694 | ESTs | 2.56 |
| 112146 | R46512 | Hs.25374 | ESTs | 2.56 |
| 108384 | AA074891 | Hs.124917 | ESTs; Highly similar to KIAA0838 protein | 2.56 |
| 131779 | R49047 | Hs.179779 | ribosomal protein L37 | 2.56 |
| 111829 | R36070 | Hs.25079 | EST | 2.55 |
| 103424 | X97267 | Hs.155975 | protein tyrosine phosphatase; receptor t | 2.55 |
| 100133 | D13118 | Hs.80886 | ATP synthase; H+ transporting; mitochond | 2.55 |
| 130208 | AA620556 | Hs.15250 | peroxisomal D3:D2-enoyl-CoA isomerase | 2.55 |
| 124649 | N92593 | Hs.102907 | ESTs | 2.55 |
| 106511 | AA452865 | Hs.205713 | UDP-GalbetaGlcNAc beta 1:4- galactosyf | 2.55 |
| 128467 | AA176446 | Hs.180428 | ESTs; Weakly similar to hypothetical 43. | 2.55 |
| 113524 | T90072 | Hs.15060 | ESTs | 2.55 |
| 107821 | AA020991 | Hs.172856 | ESTs | 2.55 |
| 111900 | R39044 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 2.54 |
| 109908 | H05255 | Hs.203237 | EST | 2.54 |
| 132069 | D87454 | Hs.192966 | KIAA0265 protein | 2.54 |
| 130660 | T95262 | Hs.17538 | ESTs | 2.54 |
| 112983 | T23443 | Hs.7111 | ESTs | 2.54 |
| 128279 | H08885 | | yf88b08.r1 Soares infant brain 1NIB Homo | 2.54 |
| 106415 | AA447994 | Hs.29188 | ESTs | 2.53 |
| 116741 | H03268 | Hs.181746 | EST | 2.53 |
| 103148 | X66362 | Hs.2994 | PCTAIRE protein kinase 3 | 2.53 |
| 132336 | AA342422 | Hs.45073 | ESTs | 2.53 |
| 129484 | R92488 | Hs.111989 | ESTs | 2.53 |
| 110169 | H19696 | Hs.31612 | ESTs; Moderately similar to CAGH4 [H.sap | 2.53 |
| 116880 | H68380 | Hs.144174 | EST | 2.53 |

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|--------|---------------|-----------|--|------|
| 133511 | X04106 | Hs.74451 | calpain; small polypeptide | 2.53 |
| 126037 | M85772 | Hs.6068 | KIAA1112 protein | 2.53 |
| 132678 | AA599876 | Hs.5486 | ESTs | 2.53 |
| 128751 | AA442274 | Hs.183176 | ESTs | 2.52 |
| 133664 | X86693 | Hs.75445 | hevlin | 2.52 |
| 126977 | AA309665 | | EST180547 Jurkat T-cells V Homo sapiens | 2.52 |
| 120697 | AA291522 | Hs.97250 | EST | 2.52 |
| 128571 | AA416619 | Hs.101661 | ESTs | 2.52 |
| 104422 | H86858 | Hs.132909 | ESTs | 2.52 |
| 122372 | AA446008 | Hs.99044 | EST | 2.52 |
| 112154 | R46769 | Hs.25388 | ESTs | 2.52 |
| 126900 | R16034 | Hs.12701 | ESTs; Highly similar to plasmolipin [H.s | 2.51 |
| 115000 | AA251342 | Hs.144584 | ESTs | 2.51 |
| 110632 | H72344 | Hs.171635 | ESTs | 2.51 |
| 129154 | N23673 | Hs.108963 | mannosidase; alpha; class 2B; member 1 | 2.51 |
| 107440 | W28069 | Hs.251993 | ESTs; Weakly similar to similar to zinc | 2.51 |
| 105694 | AA287109 | Hs.37883 | ESTs | 2.51 |
| 106249 | AA430388 | Hs.13144 | ESTs; Weakly similar to ORF YGR038w [S.c | 2.51 |
| 134462 | U11037 | Hs.83620 | sel-1 (suppressor of lin-12; C.elegans)- | 2.51 |
| 101800 | M85276 | Hs.105808 | granulin | 2.51 |
| 119884 | W81606 | Hs.58662 | Homo sapiens mRNA; cDNA DKFZp564G212 (fr | 2.51 |
| 110289 | H29829 | Hs.31524 | ESTs | 2.51 |
| 125506 | H54273 | Hs.154073 | UDP-galactose transporter related | 2.51 |
| 102954 | X15393 | Hs.2813 | motilin | 2.51 |
| 127851 | AI469331 | Hs.130497 | ESTs; Weakly similar to CHLORIDE CONDUCT | 2.5 |
| 126179 | AI191445 | Hs.143855 | ESTs; Highly similar to IROQUOIS-CLASS H | 2.5 |
| 129443 | W69967 | Hs.111497 | ESTs; Moderately similar to neuronal pro | 2.5 |
| 104480 | N41486 | Hs.99654 | protein-O-mannosyltransferase 1 | 2.5 |
| 115580 | AA398695 | Hs.144339 | Hu DNA seq frm clone 495010 on chr 6q25- Prot(37A) pseudogene; last exon of gene for a novel prot smir to worm E04F6.2; ESTs; STSs and GSSs | 2.5 |
| 119595 | W45031 | Hs.55878 | EST | 2.5 |
| 103336 | X85785 | Hs.183 | Duffy blood group | 2.5 |
| 102792 | U87964 | Hs.227576 | GTP binding protein 1 | 2.49 |
| 129643 | L27584 | Hs.250712 | calcium channel; voltage-dependent; beta | 2.49 |
| 134503 | U34880 | Hs.84183 | diphtheria toxin resistance protein reqrd | 2.49 |
| 117245 | N20989 | Hs.42927 | ESTs | 2.49 |
| 126888 | H78745 | Hs.1063 | small nuclear ribonucleoprotein polypept | 2.49 |
| 135313 | D63484 | Hs.98508 | KIAA0150 protein | 2.49 |
| 121186 | AA400156 | Hs.183294 | ESTs | 2.49 |
| 130551 | X04445 | Hs.1734 | inhibin; alpha | 2.49 |
| 134218 | AA227480 | Hs.80205 | pim-2 oncogene | 2.49 |
| 104008 | AA334630 | | EST38874 Embryo, 9 week Homo sapiens cDN | 2.49 |
| 129705 | X78706 | Hs.12058 | camtline acetyltransferase | 2.49 |
| 127900 | AI143912 | Hs.121824 | ESTs | 2.49 |
| 104609 | R96417 | Hs.107793 | ESTs | 2.48 |
| 131628 | U47292 | Hs.2979 | trefoil factor 2 (spasmolytic protein 1) | 2.48 |
| 132184 | U51003 | Hs.419 | distal-less homeo box 2 | 2.48 |
| 130450 | U70735 | Hs.15591 | COP9 subunit 6 (MOV34 homolog; 34 kD) | 2.48 |
| 101679 | M62628 | Hs.163271 | Human alpha-1 Ig germline C-region membr | 2.48 |
| 120858 | AA350147 | Hs.95940 | EST | 2.48 |
| 101012 | J04444 | Hs.697 | cytochrome c-1 | 2.48 |
| 110453 | H52133 | Hs.33026 | ESTs; Weakly similar to similar to Enter | 2.48 |
| 133771 | M68891 | Hs.760 | GATA-binding protein 2 | 2.48 |
| 102944 | X14445 | Hs.37092 | fibroblast grwth fctr 3 (murine mammary | 2.48 |
| 113269 | T65159 | Hs.85044 | ESTs | 2.48 |
| 107069 | AA609045 | Hs.11759 | ESTs; Weakly similar to !!! ALU CLASS B | 2.48 |
| 100476 | HG1019-HT1019 | | Serine Kinase Psk-H1 | 2.47 |
| 106457 | AA449718 | Hs.27801 | zinc finger protein 278 | 2.47 |
| 105718 | AA291629 | Hs.74335 | heat shock 90kD protein 1; beta | 2.47 |
| 104925 | AA058683 | Hs.5548 | Homo sapiens clone 23765 mRNA sequence | 2.47 |
| 109913 | H05527 | Hs.31588 | ESTs | 2.47 |
| 103412 | X96698 | Hs.42957 | methyltransferase-like 1 | 2.47 |
| 102326 | U35246 | Hs.226025 | vacuolar protein sorting 45A (yeast homo | 2.47 |
| 116613 | H49911 | Hs.93102 | ESTs | 2.47 |
| 123690 | AA609566 | Hs.112723 | EST | 2.47 |
| 124714 | R09486 | Hs.193118 | ESTs | 2.47 |
| 126154 | AI004105 | Hs.14232 | ESTs; Moderately similar to KIAA0563 pro | 2.47 |
| 118880 | N90168 | Hs.54593 | EST | 2.47 |
| 122274 | AA437094 | Hs.184456 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.46 |
| 129600 | N78980 | Hs.11567 | ESTs; Moderately similar to unknown [H.s | 2.46 |
| 121356 | AA405437 | Hs.93581 | Homo sapiens mRNA; cDNA DKFZp566E171 (fr | 2.46 |
| 109560 | F01778 | Hs.8154 | ESTs | 2.46 |
| 123342 | AA504336 | Hs.31659 | thyroid hormone receptor-associated prot | 2.46 |
| 128032 | AI150084 | Hs.126678 | ESTs | 2.46 |
| 129101 | H90310 | Hs.108665 | ESTs; Weakly similar to CELL-CYCLE NUCLE | 2.46 |

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|--------|---------------|-----------|--|------|
| 131185 | M25753 | Hs.23960 | cyclin B1 | 2.46 |
| 121451 | AA411008 | Hs.38085 | EST | 2.46 |
| 104328 | D81932 | HUM424C5B | Hu fetal brain (TFujiwara) H s | 2.46 |
| 126543 | AA723810 | Hs.69517 | ESTs; Highly similar to differentially e | 2.45 |
| 123600 | AA609106 | Hs.112644 | ESTs | 2.45 |
| 131020 | AA411756 | Hs.20594 | ESTs; Weakly similar to misato [D.melano | 2.45 |
| 134191 | W28902 | Hs.7979 | KIAA0736 gene product | 2.45 |
| 130446 | X79510 | Hs.155693 | protein tyrosine phosphatase; non-recept | 2.45 |
| 131613 | R88228 | Hs.29595 | JM4 protein | 2.45 |
| 118864 | N89570 | Hs.42148 | ESTs; Weakly similar to Su(P) [D.melanog | 2.45 |
| 104232 | AB002351 | Hs.10587 | KIAA0353 protein | 2.45 |
| 122604 | AA453489 | Hs.99333 | ESTs | 2.45 |
| 120626 | AA285064 | Hs.104485 | EST | 2.45 |
| 116655 | F03866 | Hs.68090 | ESTs | 2.44 |
| 116267 | AA485080 | Hs.256539 | ESTs | 2.44 |
| 114944 | AA243172 | Hs.87619 | TED protein | 2.44 |
| 127629 | AA293279 | Hs.29173 | ESTs | 2.44 |
| 120350 | AA211303 | Hs.104166 | ESTs | 2.44 |
| 103620 | Z47087 | Hs.182643 | transcription elongation factor B (SII) | 2.44 |
| 131420 | Z11737 | Hs.2664 | flavin containing monooxygenase 4 | 2.44 |
| 131312 | AA399226 | Hs.25527 | tight junction protein 3 (zona occludens | 2.43 |
| 122812 | AA461044 | Hs.142980 | EST | 2.43 |
| 135100 | AA398926 | Hs.251108 | Homo sapiens mRNA; chromosome 1 specific | 2.43 |
| 113464 | T86931 | Hs.16295 | ESTs | 2.43 |
| 100045 | M11507. | | AFFX control: transferrin receptor | 2.43 |
| 128975 | AA092129 | Hs.107538 | ESTs; Moderately similar to /prediction | 2.43 |
| 103688 | AA011479 | Hs.154701 | ESTs | 2.43 |
| 127331 | F20186 | | HSPD05873 HM3 Homo sapiens cDNA clone 05 | 2.43 |
| 107337 | T97111 | Hs.191235 | ESTs; Weakly similar to Ydr324cp [S.cere | 2.43 |
| 122171 | AA435750 | Hs.98830 | EST | 2.43 |
| 107601 | AA004636 | Hs.50223 | ESTs | 2.43 |
| 119800 | W73523 | Hs.58314 | ESTs | 2.43 |
| 104886 | AA053348 | Hs.144626 | growth differentiation factor 11 | 2.42 |
| 122899 | AA469960 | Hs.178420 | ESTs; Highly similar to WASP interacting | 2.42 |
| 125933 | AI308037 | Hs.84120 | ESTs; Weakly similar to nucleoporin p62 | 2.42 |
| 121664 | AA417291 | Hs.97978 | ESTs | 2.42 |
| 125450 | AA377194 | Hs.238909 | ESTs; Weakly similar to POLYPOSIS LOCUS | 2.42 |
| 114611 | AA081374 | Hs.108110 | DKFZP547E2110 protein | 2.42 |
| 111595 | R11492 | Hs.191225 | ESTs | 2.42 |
| 111671 | R19368 | Hs.229084 | EST | 2.42 |
| 110687 | H93005 | Hs.177311 | ESTs | 2.42 |
| 103019 | X53414 | Hs.144567 | alanine-glyoxylate aminotransferase (oxa | 2.42 |
| 119076 | R36634 | Hs.235534 | ESTs | 2.42 |
| 130589 | AA234308 | Hs.16441 | DKFZP434H204 protein | 2.42 |
| 125975 | AA495891 | Hs.152290 | ESTs; Highly similar to PACAP type-3/VIP | 2.42 |
| 106380 | AA446188 | Hs.16614 | ESTs | 2.41 |
| 121955 | AA429552 | Hs.104901 | EST | 2.41 |
| 121604 | AA416788 | Hs.98259 | EST | 2.41 |
| 100885 | HG4490-HT4876 | | Proline-Rich Protein Prb4, Allele | 2.41 |
| 117807 | N48701 | Hs.46523 | EST | 2.41 |
| 119840 | W79525 | Hs.58586 | ESTs | 2.41 |
| 102458 | U48861 | Hs.54397 | cholinergic receptor; nicotinic; beta po | 2.41 |
| 116152 | AA460920 | Hs.215683 | ESTs; Moderately similar to !!! ALU SUB | 2.41 |
| 125741 | AA522512 | Hs.29759 | Homo sapiens mRNA; cDNA DKFZp586L2123 (f | 2.41 |
| 103381 | X92715 | Hs.3057 | zinc finger protein 7 (Cos52) | 2.41 |
| 124837 | R55630 | Hs.233602 | KIAA05956 protein | 2.41 |
| 129322 | AA437153 | Hs.110407 | ESTs; Weakly similar to coded for by C. | 2.4 |
| 129291 | AA281930 | Hs.110099 | core-binding factor; runt domain; alpha | 2.4 |
| 124789 | R43803 | Hs.78110 | ESTs; Weakly similar to F17A9.2 [C.elega | 2.4 |
| 133253 | Y00970 | Hs.183088 | acrosin | 2.4 |
| 118990 | N94447 | Hs.55047 | EST | 2.4 |
| 134897 | R71427 | Hs.9081 | phenylalanyl-tRNA synthetase beta-subunit | 2.4 |
| 116572 | D45654 | Hs.65582 | DKFZP586C1324 protein | 2.4 |
| 104294 | D14539 | Hs.234774 | myeloid/lymphoid or mixed-lineage leukem | 2.4 |
| 118764 | N74440 | Hs.205264 | ESTs | 2.4 |
| 117437 | N27645 | | yw563.s1 Weizmann Olfactory Epithelium H 3' similar to contains L1.13 L1 repeat | 2.4 |
| 111651 | R16733 | Hs.20499 | ESTs | 2.39 |
| 109583 | F02322 | Hs.26135 | ESTs | 2.39 |
| 125969 | R94247 | Hs.193879 | ESTs | 2.39 |
| 130647 | AA457216 | Hs.214190 | interleukin enhancer binding factor 1 | 2.39 |
| 113708 | T97467 | Hs.18065 | ESTs | 2.39 |
| 133469 | L03785 | Hs.170482 | myosin; light polypeptide 5; regulatory | 2.39 |
| 118266 | N62837 | Hs.48647 | immunoglobulin-like transcript 7 | 2.39 |
| 121656 | AA417248 | Hs.98212 | ESTs | 2.39 |
| 126530 | AI422841 | Hs.180086 | ESTs | 2.39 |

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|--------|---------------|------------|--|------|
| 123708 | AA609648 | Hs.207767 | EST | 2.39 |
| 107875 | AA025308 | Hs.61182 | ESTs | 2.39 |
| 111711 | R22891 | Hs.7093 | ESTs | 2.39 |
| 131405 | U79255 | Hs.26468 | amyloid beta (A4) precursor protein-bind | 2.39 |
| 127454 | AA502957 | Hs.153590 | ESTs | 2.39 |
| 132341 | AA448419 | Hs.45209 | ESTs | 2.38 |
| 133673 | D87673 | Hs.75486 | heat shock transcription factor 4 | 2.38 |
| 113213 | T58607 | ya94a02.s1 | Stratagene placenta (#937225) | 2.38 |
| 106230 | AA429356 | Hs.12047 | ESTs | 2.38 |
| 116692 | F09261 | Hs.56103 | ESTs | 2.38 |
| 126197 | AA172284 | Hs.103657 | ESTs; Weakly similar to CH-TOG PROTEIN I | 2.38 |
| 115966 | AA446866 | Hs.71371 | ESTs | 2.38 |
| 132636 | U65785 | Hs.5417 | oxygen regulated protein (150kD) | 2.38 |
| 109965 | H09077 | Hs.30895 | EST | 2.38 |
| 130203 | L14754 | Hs.1521 | immunoglobulin mu binding protein 2 | 2.38 |
| 131332 | R50487 | Hs.25717 | ESTs | 2.38 |
| 119105 | R42357 | Hs.91453 | ESTs | 2.37 |
| 129253 | W69316 | Hs.109778 | ESTs; Weakly similar to similar to beta- | 2.37 |
| 113602 | T92558 | Hs.17036 | ESTs | 2.37 |
| 118102 | N55272 | Hs.145798 | ESTs | 2.37 |
| 100734 | HG3432-HT3620 | | Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 3, K-Sam II | 2.37 |
| 111533 | R08548 | Hs.251651 | EST | 2.37 |
| 130813 | U12259 | Hs.198 | paired box gene 3 (Waardenburg syndrome | 2.37 |
| 119180 | R80413 | Hs.92520 | ESTs | 2.37 |
| 109335 | AA211443 | Hs.86492 | ESTs | 2.37 |
| 107386 | U97698 | Hs.159593 | muchn 6; gastric | 2.36 |
| 122486 | AA448328 | Hs.115527 | ESTs | 2.36 |
| 112997 | T23548 | Hs.167467 | ESTs | 2.36 |
| 109674 | F09051 | Hs.21837 | ESTs; Weakly similar to KIAA0927 protein | 2.36 |
| 128868 | AA423827 | Hs.105730 | hypothetical protein | 2.36 |
| 127027 | R17261 | yg12g07.r1 | Scires Infant brain 1NIB H sa | 2.36 |
| 123099 | AA485931 | Hs.79 | aminocyclase 1 | 2.36 |
| 115716 | AA416767 | Hs.43498 | ESTs; Weakly similar to ORF YKL201c [S.c | 2.36 |
| 130830 | D86982 | Hs.20060 | KIAA0229 protein | 2.36 |
| 109051 | AA159920 | Hs.72322 | ESTs | 2.36 |
| 130181 | R39552 | Hs.151608 | Homo sapiens clone 23622 mRNA sequence | 2.36 |
| 131114 | R46233 | Hs.23107 | ESTs | 2.36 |
| 123589 | AA609047 | Hs.188922 | ESTs | 2.36 |
| 130872 | U03891 | | phorbolin (similar to apolipoprotein B m | 2.36 |
| 131982 | H78550 | Hs.2780 | jun D proto-oncogene | 2.36 |
| 130502 | M55057 | Hs.1583 | neutrophil cytosolic factor 1 (47kD; chr | 2.36 |
| 121785 | AA423883 | Hs.142442 | ESTs | 2.35 |
| 125405 | T97171 | Hs.121570 | ESTs | 2.35 |
| 103682 | AA000993 | | ESTs | 2.35 |
| 125649 | T77395 | Hs.194816 | stomatin-like protein 1 | 2.35 |
| 115452 | AA285019 | Hs.55263 | ESTs; Highly similar to mitochondrial di | 2.35 |
| 129338 | T56800 | | Homo sapiens mRNA; cDNA DKFZp564B176 (fr | 2.35 |
| 106105 | AA421268 | Hs.149443 | putative tumor suppressor | 2.35 |
| 134770 | R72079 | Hs.89575 | CD79B antigen (immunoglobulin-associated | 2.35 |
| 119422 | T99496 | Hs.229598 | EST | 2.35 |
| 109869 | H02849 | Hs.30345 | EST | 2.35 |
| 134314 | AA263032 | Hs.81634 | ATP synthase; H+ transporting; mitochond | 2.35 |
| 114989 | AA251097 | Hs.189119 | ESTs | 2.35 |
| 122619 | AA453755 | Hs.191515 | ESTs | 2.35 |
| 133129 | AA428580 | Hs.65551 | ESTs | 2.35 |
| 128465 | AA416762 | Hs.100221 | nuclear receptor subfamily 1; group H; m | 2.35 |
| 115636 | AA402715 | Hs.58389 | ESTs | 2.35 |
| 130836 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding pr | 2.34 |
| 132385 | Y10258 | Hs.47007 | serine/threonine protein-kinase | 2.34 |
| 107776 | AA018820 | Hs.221147 | ESTs | 2.34 |
| 109791 | F10669 | Hs.13228 | DRE-antagonist modulator; calsenilin | 2.34 |
| 124409 | N33212 | Hs.107197 | ESTs | 2.34 |
| 131088 | AA397916 | Hs.22595 | ESTs | 2.34 |
| 121079 | AA398719 | Hs.14169 | ESTs; Weakly similar to CREB-binding pro | 2.34 |
| 124662 | N94340 | Hs.171835 | ESTs; Weakly smtr to PUT PRE-mRNA SPLCI | 2.34 |
| 133820 | M13686 | Hs.177582 | surfactant; pulmonary-associated protein | 2.34 |
| 129424 | M55593 | Hs.111301 | matrix metalloproteinase 2 (gelatinase A | 2.34 |
| 109066 | AA161377 | Hs.72404 | EST | 2.34 |
| 100339 | D63485 | Hs.181359 | KIAA0151 gene product | 2.34 |
| 100809 | HG3991-HT4261 | | CpG-Enriched Dna, Clone E18 | 2.34 |
| 120844 | AA349417 | Hs.96917 | ESTs | 2.33 |
| 124927 | R96146 | Hs.221459 | ESTs | 2.33 |
| 109779 | F10527 | Hs.3353 | Homo sapiens clone 24940 mRNA sequence | 2.33 |
| 101171 | L16842 | Hs.119251 | ubiquinol-cytochrome c reductase core pr | 2.33 |
| 110805 | N26904 | Hs.24048 | ESTs; Weakly similar to FK506/rapamycin- | 2.33 |
| 125440 | A1090982 | Hs.31895 | ESTs | 2.33 |

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|--------|---------------|-----------|---|------|
| 133159 | AC000061 | Hs.663 | cystic fibrosis transmemb conductance re | 2.33 |
| 101829 | M91368 | Hs.129763 | solute carrier family 8 (sodium/calcium | 2.33 |
| 126492 | AA778565 | Hs.142505 | ESTs | 2.33 |
| 102774 | U83303 | Hs.164021 | small inducible cytokine subfamily B (CX | 2.33 |
| 130480 | N50809 | Hs.15760 | ESTs; Weakly similar to similar to Yeast | 2.33 |
| 126878 | A1424759 | Hs.238928 | ESTs | 2.33 |
| 117338 | N23889 | Hs.43466 | ESTs | 2.32 |
| 118662 | N70877 | Hs.13055 | ESTs | 2.32 |
| 130354 | AA416685 | Hs.155001 | UNC13 (<i>C. elegans</i>)-like | 2.32 |
| 106760 | AA477330 | Hs.12293 | ESTs | 2.32 |
| 124294 | H90573 | Hs.102298 | EST | 2.32 |
| 119428 | W02129 | Hs.55242 | EST | 2.32 |
| 132629 | Z40942 | Hs.5383 | ESTs | 2.32 |
| 127998 | AA854181 | Hs.143585 | ESTs | 2.32 |
| 132728 | AA293334 | Hs.5566 | ESTs; Highly similar to RAS-RELATED PROT | 2.32 |
| 120292 | AA189116 | Hs.96168 | ESTs | 2.32 |
| 107598 | AA004528 | Hs.169444 | ESTs | 2.32 |
| 128164 | A1478174 | Hs.144846 | ESTs | 2.32 |
| 105753 | AA299789 | Hs.15277 | ESTs | 2.31 |
| 131256 | AA262340 | Hs.24907 | coronin; actin-binding protein; 2B | 2.31 |
| 110891 | N38863 | Hs.234392 | platelet-activating factor acetylhydrola | 2.31 |
| 116767 | H13689 | Hs.92530 | ESTs | 2.31 |
| 100545 | HG2147-HT2217 | | Mucin 3, Intestinal (Gb:M55405) | 2.31 |
| 125264 | W88995 | Hs.167641 | ESTs; Weakly similar to C15H9.5 [<i>C.eleg</i> | 2.31 |
| 118387 | N64579 | Hs.164571 | yz51d11.s1 Morton Fetal Cochlea H sapien | 2.31 |
| 104335 | D83847 | Hs.183864 | elastase 3B | 2.31 |
| 107464 | W42944 | Hs.171939 | ESTs | 2.31 |
| 112304 | R54798 | Hs.26239 | ESTs | 2.31 |
| 134313 | AA136100 | Hs.6673 | trinucleotide repeat containing 15 | 2.31 |
| 116322 | AA490900 | Hs.58643 | ESTs; Highly similar to JAK3B [H.sapiens | 2.31 |
| 111275 | N70970 | Hs.35006 | ESTs | 2.31 |
| 100109 | AJ000480 | Hs.143513 | phosphoprotein regulated by mitogenic pa | 2.31 |
| 109338 | AA211717 | Hs.86507 | ESTs | 2.31 |
| 134432 | AA053022 | Hs.8312 | ESTs | 2.31 |
| 129649 | AD000092 | Hs.182628 | Homo sapiens DNA from chr 19p13.2 cosmid EKLF; GCDH; CRTC; and RAD23A genes; gen | 2.31 |
| 122623 | AA453990 | Hs.99248 | ESTs | 2.31 |
| 112070 | R43976 | Hs.236310 | EST | 2.31 |
| 127683 | AA668123 | Hs.134170 | ESTs | 2.31 |
| 104920 | AA057620 | Hs.30807 | ESTs; Highly similar to dJ186O1.1 [H.sap | 2.31 |
| 106064 | AA417373 | Hs.15898 | ESTs | 2.31 |
| 106782 | AA478487 | | ESTs | 2.31 |
| 126709 | AA028159 | Hs.47234 | ESTs | 2.3 |
| 105129 | AA158386 | Hs.186476 | ESTs | 2.3 |
| 105719 | AA291644 | Hs.36793 | ESTs | 2.3 |
| 121698 | AA418399 | Hs.10351 | KIAA0308 protein | 2.3 |
| 119069 | R27619 | Hs.231046 | EST | 2.3 |
| 130388 | U72515 | Hs.189583 | putative protein similar to nessy (Droso | 2.3 |
| 103444 | X98801 | Hs.74617 | dynactin 1 (p150; Glued (Drosophila) hom | 2.3 |
| 114604 | AA076128 | | zm18g4.s1 Stratagene pancreas (#93728) H 3' similar to SWRS1A_HUMAN P3927 4S RI | 2.3 |
| 103878 | AA227635 | Hs.202588 | ESTs | 2.3 |
| 105828 | AA398276 | Hs.11962 | ESTs | 2.3 |
| 119778 | W72920 | Hs.58244 | ESTs | 2.3 |
| 120401 | AA234309 | Hs.193011 | ESTs | 2.3 |
| 116280 | AA488691 | Hs.57969 | phenylalanine-tRNA synthetase | 2.3 |
| 130479 | R44163 | Hs.12457 | Homo sapiens clone 23770 mRNA sequence | 2.3 |
| 104253 | AF002572 | Hs.152944 | loss of heterozygosity; 11; chromosomal | 2.29 |
| 132615 | H66367 | Hs.53358 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.29 |
| 121954 | AA429598 | Hs.98587 | ESTs | 2.29 |
| 101336 | L49169 | Hs.75678 | FBJ murine osteosarcoma viral oncogene h | 2.29 |
| 127247 | AA313802 | Hs.6289 | growth factor receptor-bound protein 2 | 2.29 |
| 117300 | N22565 | Hs.43212 | ESTs | 2.29 |
| 122229 | AA436198 | Hs.103902 | ESTs | 2.29 |
| 125105 | T95765 | Hs.189760 | ESTs | 2.29 |
| 128083 | R16100 | Hs.166476 | ESTs | 2.29 |
| 131279 | AA089853 | Hs.25197 | STIP1 homology and U-Box containing prot | 2.29 |
| 133838 | M97796 | Hs.180919 | Inhibitor of DNA binding 2; dominant neg | 2.29 |
| 111837 | R36447 | Hs.24453 | ESTs | 2.29 |
| 111435 | R01620 | Hs.19198 | ESTs | 2.29 |
| 123613 | AA609158 | Hs.112656 | EST | 2.29 |
| 133560 | AA256365 | Hs.7486 | protein expressed in thyroid | 2.29 |
| 122898 | AA469952 | Hs.97899 | ESTs; Weakly similar to dal2; len:343; C | 2.29 |
| 113378 | T80827 | Hs.14757 | ESTs | 2.29 |
| 127174 | AA293204 | Hs.139352 | ESTs | 2.29 |
| 120153 | Z39582 | Hs.65777 | EST | 2.29 |

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|--------|----------|-----------|--|------|--|
| 112741 | R93080 | Hs.35035 | ESTs | 2.28 | |
| 132152 | AA044784 | Hs.4105 | Homo sapiens mRNA; cDNA DKFZp586A0618 (f) | 2.28 | |
| 109780 | F10655 | Hs.25031 | ESTs | 2.28 | |
| 113776 | W04657 | Hs.24248 | ESTs | 2.28 | |
| 102934 | X13451 | | Hu mRNA for lymphocyte lineage-restricted | 2.28 | |
| 128168 | AA322034 | | EST24690 Cerebellum II Homo sapiens cDNA2.28 | 2.28 | |
| 125363 | N94706 | | Human Chromosome 16 BAC clone CIT987SK-A | 2.28 | |
| 101427 | M19508 | | Human myeloperoxidase gene, exons 1-4 | 2.28 | |
| 132616 | AA386264 | Hs.5337 | Isocitrate dehydrogenase 2 (NADP+); mito | 2.28 | |
| 105537 | AA258813 | Hs.27160 | ESTs | 2.28 | |
| 126527 | AA548559 | Hs.103853 | ESTs | 2.28 | |
| 115359 | AA281936 | Hs.88914 | ESTs | 2.28 | |
| 108474 | AA079667 | | zm93d1.s1 Stratagene ovarian cancer (#9372 | 2.28 | |
| 120685 | AA291066 | Hs.105099 | ESTs | 2.28 | |
| 126171 | AA704771 | Hs.191942 | ESTs | 2.28 | |
| 112858 | T02963 | Hs.4454 | ESTs | 2.28 | |
| 121817 | AA424826 | Hs.98475 | EST | 2.28 | |
| 107895 | AA026150 | Hs.61384 | ESTs | 2.28 | |
| 131161 | Z38223 | Hs.23735 | potassium voltage-gated channel; subfamily | 2.28 | |
| 135173 | M72885 | Hs.95910 | Human GOS2 protein gene; complete cds | 2.27 | |
| 103182 | X69819 | Hs.99995 | intercellular adhesion molecule 3 | 2.27 | |
| 113889 | W72720 | Hs.194347 | ESTs | 2.27 | |
| 128984 | AA319615 | Hs.238030 | secretory carrier membrane protein 2 | 2.27 | |
| 101531 | M29877 | Hs.576 | fucosidase; alpha-L- 1; tissue | 2.27 | |
| 115916 | AA436889 | Hs.91910 | ESTs | 2.27 | |
| 129892 | H96850 | Hs.89674 | dolichyl-diphosphooligosaccharide-protein | 2.27 | |
| 103035 | X54871 | Hs.77690 | RAB5B; member RAS oncogene family | 2.27 | |
| 126479 | T78141 | | ESTs | 2.27 | |
| 125778 | R71976 | Hs.161791 | ESTs; Weakly similar to III ALU SUBFAMI | 2.27 | |
| 108132 | AA053586 | Hs.63048 | ESTs | 2.27 | |
| 111017 | N53965 | Hs.256327 | ESTs | 2.27 | |
| 127165 | AA359719 | Hs.127121 | ESTs | 2.27 | |
| 126446 | AI421309 | Hs.118926 | DKFZP586K0919 protein | 2.28 | |
| 107864 | AA025061 | Hs.61246 | ESTs | 2.26 | |
| 122277 | AA437133 | Hs.98936 | ESTs | 2.26 | |
| 115604 | AA400378 | Hs.49391 | ESTs | 2.26 | |
| 105061 | AA134824 | Hs.4865 | ESTs | 2.26 | |
| 118549 | N68163 | Hs.49455 | EST | 2.26 | |
| 110509 | H56493 | Hs.61960 | ESTs; Moderately similar to HYPOTHETICAL | 2.26 | |
| 114088 | Z38280 | Hs.26971 | Human Chromosome 16 BAC clone CIT987SK-2 | 2.26 | |
| 103225 | X74837 | Hs.2750 | mannosidase; alpha; class 1A; member 1 | 2.26 | |
| 125842 | AA746654 | Hs.5181 | proliferation-associated 2G4; 38kD | 2.26 | |
| 104538 | R25059 | Hs.175681 | ESTs | 2.26 | |
| 130304 | U09368 | Hs.154205 | zinc finger protein 140 (clone pHZ-39) | 2.26 | |
| 120680 | AA290743 | Hs.97242 | ESTs | 2.26 | |
| 124062 | H00440 | Hs.144524 | ESTs; Weakly similar to signal transduce | 2.26 | |
| 103289 | X80915 | Hs.1573 | growth differentiation factor 5 (cartilag | 2.26 | |
| 109286 | AA197273 | Hs.191324 | ESTs | 2.26 | |
| 128555 | U62739 | Hs.101408 | branched chain aminotransferase 2; mitoc | 2.26 | |
| 129439 | AA171694 | Hs.111461 | ceruloplasmin (ferroxidase) | 2.26 | |
| 109221 | AA192755 | Hs.85840 | ESTs; Weakly similar to stac [H.sapiens] | 2.26 | |
| 109906 | H05084 | Hs.28077 | ESTs; Highly similar to GDP-mannose pyro | 2.26 | |
| 130540 | U35234 | Hs.159534 | protein tyrosine phosphatase; receptor t | 2.26 | |
| 122870 | AA465158 | Hs.192861 | Spi-B transcription factor (Spi-1/PU.1 r | 2.26 | |
| 120219 | Z41124 | Hs.66045 | EST | 2.26 | |
| 128021 | AI001136 | Hs.78223 | N-acylaminoacyl-peptide hydrolase | 2.26 | |
| 121732 | AA421047 | Hs.98330 | ESTs | 2.26 | |
| 107817 | AA020781 | Hs.60847 | ESTs | 2.25 | |
| 101069 | L02648 | Hs.84232 | transcobalamin II; macrocytic anemia | 2.25 | |
| 103065 | X58399 | Hs.81221 | Human L2-9 transcript of unarranged lm | 2.25 | |
| 118019 | N52585 | Hs.47517 | ESTs | 2.25 | |
| 122220 | AA436011 | Hs.98817 | ESTs | 2.25 | |
| 109161 | AA179392 | Hs.73601 | EST | 2.25 | |
| 128699 | K03207 | Hs.103972 | proline-rich protein BstNI subfamily 4 | 2.25 | |
| 101914 | S71824 | Hs.167988 | neural cell adhesion molecule 1 | 2.25 | |
| 102697 | U74657 | Hs.6364 | Tat interactive protein (60kD) | 2.25 | |
| 119939 | W86753 | Hs.82407 | ESTs | 2.25 | |
| 127793 | A1298835 | Hs.30445 | ESTs; Weakly similar to transcription re | 2.25 | |
| 104450 | L77564 | Hs.103978 | serine/threonine kinase 22B (spermion | 2.25 | |
| 133086 | AA136042 | Hs.131053 | ESTs | 2.25 | |
| 115416 | AA283893 | Hs.203866 | ESTs | 2.25 | |
| 117056 | H90322 | Hs.41387 | EST | 2.25 | |
| 115598 | AA400129 | Hs.65735 | ESTs | 2.25 | |
| 121267 | AA401397 | Hs.165296 | ESTs; Highly similar to kallikrein-like | 2.25 | |
| 104778 | AA026397 | Hs.11039 | Homo sapiens clone 24804 mRNA sequence | 2.25 | |
| 110926 | N48252 | Hs.135287 | ESTs | 2.24 | |

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|--------|---------------|-----------|--|------|
| 102795 | U88667 | Hs.198396 | ATP-binding cassette; sub-family A (ABC1 | 2.24 |
| 118643 | N70324 | Hs.49840 | ESTs | 2.24 |
| 103304 | X82240 | Hs.2484 | T-cell leukemia/lymphoma 1A | 2.24 |
| 134814 | Z48475 | Hs.89771 | glucokinase (hexokinase 4) regulatory pr | 2.24 |
| 125912 | AA171719 | Hs.5233 | eukaryotic translation initiation factor | 2.24 |
| 134365 | R32377 | Hs.82240 | syntaxin 3A | 2.24 |
| 117224 | N20300 | Hs.218707 | ESTs | 2.24 |
| 107169 | AA621601 | Hs.184446 | ESTs; Weakly similar to small GTP-bindin | 2.24 |
| 133948 | M59916 | Hs.77813 | sphingomyelin phosphodiesterase 1; acid | 2.24 |
| 101426 | M19483 | Hs.25 | ATP synthase; H ⁺ transporting; mitochond | 2.24 |
| 119922 | W86196 | Hs.177384 | ESTs | 2.24 |
| 123361 | AA504810 | Hs.139649 | EST | 2.24 |
| 123915 | AA621298 | Hs.112957 | ESTs | 2.24 |
| 123540 | AA608792 | Hs.112591 | EST | 2.24 |
| 124978 | T40560 | Hs.221759 | ESTs | 2.24 |
| 102354 | U38268 | | Human cytochrome b pseudogene, partial c | 2.24 |
| 124198 | H53099 | Hs.198271 | NADH dehydrogenase (ubiquinone) 1 alpha | 2.24 |
| 102160 | U18235 | Hs.121581 | ATP-binding cassette; sub-family A (ABC1 | 2.24 |
| 107520 | X76091 | Hs.100007 | regulatory factor X; 2 (influences HLA c | 2.24 |
| 131569 | U52100 | Hs.29191 | epithelial membrane protein 2 | 2.24 |
| 126633 | AA206993 | Hs.154145 | guanine nuc binding protein (G protein) | 2.23 |
| 130887 | AA258379 | Hs.155986 | angiotensin receptor-like 2 | 2.23 |
| 119894 | W84670 | Hs.58518 | EST | 2.23 |
| 124544 | N63837 | Hs.40500 | similar to S. cerevisiae RER1 | 2.23 |
| 103104 | X61587 | Hs.75082 | ras homolog gene family; member G (rho G | 2.23 |
| 110119 | H17306 | Hs.177229 | ESTs | 2.23 |
| 131411 | AA464043 | Hs.26506 | ESTs; Weakly similar to NY-REN-45 antigen | 2.23 |
| 102346 | U37359 | Hs.227297 | meiotic recombination (S. cerevisiae) 11 | 2.23 |
| 106003 | AA411167 | Hs.8734 | ESTs; Moderately similar to !!! ALU CLA | 2.23 |
| 122564 | AA452251 | Hs.98669 | ESTs | 2.23 |
| 133688 | U42031 | Hs.7557 | FK506-binding protein 5 | 2.23 |
| 132096 | AA131410 | Hs.3954 | Homo sapiens clone 24877 mRNA sequence | 2.23 |
| 110038 | H11746 | Hs.31097 | ESTs | 2.23 |
| 123788 | AA620293 | Hs.112853 | ESTs | 2.23 |
| 135070 | X99350 | Hs.93974 | forkhead box J1 | 2.23 |
| 104908 | AA055841 | Hs.154396 | ESTs | 2.22 |
| 128674 | AA025001 | Hs.169452 | ESTs | 2.22 |
| 100810 | HG3992-HT4262 | | CpG-Enriched Dna, Clone E35 | 2.22 |
| 120065 | W93579 | Hs.59478 | EST | 2.22 |
| 122775 | AA459592 | Hs.112143 | ESTs | 2.22 |
| 125443 | H71482 | Hs.177592 | ribosomal protein; large; P1 | 2.22 |
| 118617 | N63666 | Hs.183413 | ESTs; Moderately similar to !!! ALU SUB | 2.22 |
| 128001 | A1167814 | Hs.166664 | ESTs | 2.22 |
| 128160 | A1279080 | Hs.149971 | ESTs; Moderately similar to !!! ALU CLA | 2.22 |
| 106608 | AA458644 | Hs.27115 | ESTs | 2.22 |
| 103485 | Y08409 | Hs.248415 | thyroid hormone responsive SPOT14 (rat) | 2.22 |
| 135008 | AA173423 | Hs.92918 | ESTs; Weakly similar to R07G3.8 [C.elega | 2.22 |
| 110122 | H17333 | Hs.159837 | EST | 2.22 |
| 128397 | A1393421 | Hs.14032 | ESTs | 2.22 |
| 110231 | H24359 | Hs.28733 | ESTs | 2.22 |
| 123188 | AA489092 | Hs.177726 | ESTs | 2.22 |
| 131903 | AA481723 | Hs.3436 | deleted in oral cancer (mouse; homolog) | 2.22 |
| 122649 | AA454616 | Hs.90336 | ATPase; H ⁺ transporting; lysosomal (vacu | 2.22 |
| 133090 | AA448228 | Hs.6468 | ESTs | 2.22 |
| 108002 | AA037664 | Hs.55067 | ESTs; Weakly similar to T07F12.1 gene pr | 2.22 |
| 133120 | X64559 | Hs.65424 | tetrancin (plasminogen-binding protein | 2.21 |
| 114263 | Z40073 | Hs.6045 | ESTs | 2.21 |
| 125518 | R20148 | Hs.193851 | ESTs | 2.21 |
| 128613 | U78551 | Hs.102482 | Homo sapiens gallbladder mucin MUC5B mRNA | 2.21 |
| 102773 | U83192 | Hs.23731 | discs; large (Drosophila) homolog 4 | 2.21 |
| 119526 | W38049 | | Accession not listed in Genbank | 2.21 |
| 126844 | AA299325 | | EST11903 Uterus tumor I Homo sapiens cDN | 2.21 |
| 105860 | AA399251 | Hs.180933 | ESTs; Weakly similar to methyl-CpG bindi | 2.21 |
| 126957 | A733145 | Hs.194560 | ESTs | 2.21 |
| 108959 | AA150107 | Hs.81810 | ESTs | 2.2 |
| 131663 | AA423926 | Hs.30318 | ESTs | 2.2 |
| 127468 | H02941 | Hs.8888 | ESTs | 2.2 |
| 104483 | N42776 | Hs.146233 | ESTs | 2.2 |
| 123848 | AA620773 | Hs.221996 | ESTs | 2.2 |
| 101623 | M55905 | Hs.75342 | malic enzyme 2; NAD(+)-dependent; mitoch | 2.2 |
| 120872 | AA357993 | Hs.96996 | ESTs | 2.2 |
| 135033 | AA173241 | Hs.93454 | ESTs | 2.2 |
| 122286 | AA437259 | Hs.104944 | EST | 2.2 |
| 114862 | AA235174 | Hs.50250 | ESTs | 2.2 |
| 100255 | D38047 | Hs.78466 | proteasome (prosome; macropain) 26S subu | 2.2 |
| 103063 | X58234 | Hs.123178 | translocase of inner mitochondrial membr | 2.2 |

| | | | | |
|--------|---------------|-----------|---|------|
| 132777 | R56898 | Hs.56663 | ESTs | 2.2 |
| 133082 | AA457129 | Hs.6455 | RuvB (E coli homolog)-like 2 | 2.2 |
| 127529 | AA558980 | Hs.191750 | ESTs | 2.2 |
| 114602 | AA075642 | Hs.103594 | deleted in malignant brain tumors 1 | 2.2 |
| 120722 | AA293435 | Hs.97277 | ESTs | 2.2 |
| 102675 | U72512 | | Human B-cell receptor associated protein | 2.2 |
| 128551 | H09058 | Hs.237323 | N-acetylglucosamine-phosphate mutase; DK | 2.2 |
| 112020 | R43001 | Hs.22298 | EST | 2.2 |
| 123625 | AA609216 | Hs.112666 | EST | 2.2 |
| 120315 | AA194266 | Hs.178393 | ESTs | 2.2 |
| 122081 | AA431992 | Hs.104920 | ESTs | 2.19 |
| 101798 | M85220 | | Accession not listed in Genbank | 2.19 |
| 111501 | R07444 | Hs.163118 | ESTs | 2.19 |
| 132832 | D63482 | Hs.57734 | KIAA0148 gene product | 2.19 |
| 100544 | HG2147-HT2217 | | Much 3, Intestinal (Gb:M55405) | 2.19 |
| 106835 | AA482077 | Hs.33713 | ESTs; Weakly similar to hypothetical pr | 2.19 |
| 132834 | AA076145 | Hs.61053 | ESTs | 2.19 |
| 108762 | AA127515 | Hs.71787 | ESTs; Highly similar to 30S ribosomal pr | 2.19 |
| 120164 | Z39733 | Hs.158159 | FAT tumor suppressor (Drosophila) homolo | 2.19 |
| 135395 | L08093 | Hs.99899 | tumor necrosis factor (ligand) superfami | 2.19 |
| 101717 | M69013 | Hs.1686 | guanine nucleotide binding protein (G pr | 2.19 |
| 121172 | AA400013 | Hs.97750 | EST | 2.18 |
| 114861 | AA235123 | Hs.40719 | ESTs | 2.18 |
| 120851 | AA349662 | Hs.174248 | ESTs | 2.18 |
| 121083 | AA398736 | Hs.97653 | EST | 2.18 |
| 107171 | AA621624 | Hs.28088 | Homo sapiens clone 24515 mRNA sequence | 2.18 |
| 128754 | D31446 | Hs.10488 | Breakpoint cluster region protein; uteri | 2.18 |
| 100149 | D13897 | Hs.169249 | peptide YY | 2.18 |
| 132405 | AA323787 | Hs.4770 | KIAA1068 protein | 2.18 |
| 114666 | AA112274 | | zm27g6.s1 Stratagene pancreas (#93728) H elementcontains element LTR8 repetitive | 2.18 |
| 127008 | AA223879 | | zr10g05.r1 Stratagene NT2 neuronal precu | 2.18 |
| 110373 | H42896 | Hs.29438 | ESTs | 2.18 |
| 119354 | T66942 | Hs.100651 | golgi SNAP receptor complex member 2 | 2.18 |
| 130115 | M31627 | Hs.149923 | X-box binding protein 1 | 2.18 |
| 130514 | AA161085 | Hs.15871 | ESTs; Weakly similar to acid phosphatase | 2.18 |
| 128848 | H08077 | Hs.217179 | ESTs; Weakly similar to T27A1.5 [C.elega | 2.18 |
| 110161 | H19312 | Hs.28096 | ESTs | 2.18 |
| 132367 | X82224 | Hs.46634 | cysteine conjugate-beta lyase; cytoplasm | 2.18 |
| 125882 | H45538 | Hs.101448 | metastasis associated 1 | 2.17 |
| 113837 | W57698 | Hs.8888 | ESTs | 2.17 |
| 106376 | AA444004 | Hs.6084 | ESTs | 2.17 |
| 113755 | T99075 | Hs.18570 | ESTs | 2.17 |
| 107525 | X91817 | Hs.102866 | transketolase-like 1 | 2.17 |
| 119207 | R93186 | Hs.84298 | CD74 antigen (invar polypept of maj hist | 2.17 |
| 131862 | AA236365 | | 3-phosphoglycerale dehydrogenase | 2.17 |
| 115514 | AA297739 | Hs.55609 | ESTs; Weakly similar to ISOLEUCYL-TRNA S | 2.17 |
| 112290 | R53940 | Hs.26016 | ESTs | 2.17 |
| 126136 | H83353 | | yv82f02.r1 Soares melanocyte 2NbHM Homo | 2.17 |
| 121574 | AA412712 | Hs.119325 | Huntingtin-Interacting protein A | 2.17 |
| 118530 | N67900 | Hs.118446 | ESTs | 2.16 |
| 132327 | AA203285 | Hs.44892 | ESTs; Weakly similar to dJ733D15.1 [H.sa | 2.16 |
| 100564 | HG2239-HT2324 | | Potassium Channel Protein (Gb:Z11585) | 2.16 |
| 129376 | AA022622 | Hs.13543 | ESTs; Weakly similar to hypothetical pr | 2.16 |
| 135317 | X86012 | Hs.98602 | Human DNA sequence from intron 22 of the 9.5kb repeated region; in22h-1; involv | 2.16 |
| 114973 | AA250845 | Hs.87762 | ESTs | 2.16 |
| 107559 | AA001504 | Hs.59860 | ESTs | 2.16 |
| 111014 | N53787 | Hs.191117 | ESTs | 2.16 |
| 101250 | L34060 | Hs.79133 | cadherin 8 | 2.16 |
| 110697 | H93721 | Hs.20798 | ESTs | 2.16 |
| 126843 | AA450168 | Hs.22841 | ESTs; Moderately similar to predicted pr | 2.16 |
| 108272 | AA063616 | Hs.43773 | ESTs | 2.16 |
| 125012 | T66935 | Hs.104859 | ESTs | 2.16 |
| 111639 | R16101 | Hs.140834 | EST | 2.15 |
| 123157 | AA488443 | Hs.100426 | DKFZP564A063 protein | 2.15 |
| 102315 | U34252 | Hs.2533 | aldehyde dehydrogenase 9 (gamma-aminobut2.15 | 2.15 |
| 131897 | AA287623 | Hs.3426 | GTPase; human homolog of E. coli essenti | 2.15 |
| 121528 | AA12253 | Hs.238909 | ESTs; Weakly similar to POLYPOSIS LOCUS | 2.15 |
| 122806 | AA460707 | Hs.106397 | ESTs | 2.15 |
| 125727 | H00958 | Hs.181641 | ESTs | 2.15 |
| 133279 | AA069571 | Hs.6957 | Homo sapiens clone 24616 mRNA sequence | 2.15 |
| 103219 | X74570 | Hs.75268 | sialyltransferase 4C (beta-galactosidase | 2.15 |
| 120881 | AA362144 | Hs.104601 | EST | 2.15 |
| 134060 | D42039 | Hs.78871 | KIAA0081 protein | 2.15 |
| 106598 | AA457140 | Hs.11411 | DKFZP564O084 protein | 2.15 |

| | | | |
|--------|---------------|--|------|
| 125576 | R66208 | y30h03.r1 Soares placenta Nb2HP H sapie | |
| | | contains Alu repetitive element; contain | 2.15 |
| 126727 | AA037230 | Hs.135084 cystatin C (amyloid angiopathy and cereb | 2.15 |
| 101490 | M25629 | Hs.123107 kallikrein 1; renal/pancreas/salivary | 2.15 |
| 129708 | AA417181 | Hs.120858 ESTs | 2.14 |
| 100827 | HG2702-HT2798 | Serine/Threonine Kinase (Gb:Z25424) | 2.14 |
| 121703 | AA418671 | Hs.104807 ESTs | 2.14 |
| 106809 | AA479704 | Human DNA seq frm clone 283E3 on chr 1p36 | |
| | | Female Reproductive tract MIFR1; -2; MM | 2.14 |
| 129525 | F03873 | Hs.112306 Homo sapiens clone 24955 mRNA sequence; | 2.14 |
| 100478 | HG1057-HT1057 | Mucin (Gb:M22406) | 2.14 |
| 118593 | N69020 | Hs.207689 EST | 2.14 |
| 114047 | W94427 | Hs.3807 ESTs; Weakly similar to PHOSPHOLEMAN PR | 2.14 |
| 128823 | AA478207 | Hs.10632 ESTs; Moderately similar to sex-determin | 2.14 |
| 100534 | HG1980-HT2023 | Tubulin, Beta 2 | 2.14 |
| 105757 | AA321146 | Hs.30596 ESTs | 2.14 |
| 109617 | F03192 | Hs.26789 ESTs; Weakly similar to dJ162H14.1 [H.sa | 2.14 |
| 121547 | AA412448 | Hs.104777 ESTs | 2.14 |
| 119420 | T98291 | Hs.102484 glutathione S-transferase A3 | 2.14 |
| 120274 | AA177051 | nd02a02s1 NCL_CGAP_P3 Homo sapiens cDN | |
| | | repetitive element; contains element LTR | 2.14 |
| 132933 | AA598702 | Hs.6101 bone morphogenetic protein 6 | 2.14 |
| 133405 | X07881 | Hs.73031 proline-rich protein BstNI subfamily 3 | 2.14 |
| 119811 | W73922 | Hs.49047 ESTs | 2.14 |
| 134536 | AA457735 | Hs.850 IMP (inosine monophosphate) dehydrogenases | 2.14 |
| 105125 | AA157799 | Hs.6980 aldo-keto reductase family 7; member A2 | 2.14 |
| 101398 | M15881 | Hs.1137 uromodulin (uromucoid; Tamm-Horsfall gly | 2.14 |
| 132751 | AA397901 | Hs.55993 ESTs | 2.13 |
| 115777 | AA424142 | Hs.39384 putative secreted ligand homologous to f | 2.13 |
| 123193 | AA489228 | Hs.136956 ESTs | 2.13 |
| 116875 | H67749 | Hs.161022 EST | 2.13 |
| 107271 | D60607 | Hs.34931 EST | 2.13 |
| 134551 | R44839 | Hs.8526 β -N-acetylglucosaminyltransfera | 2.13 |
| 113413 | T83739 | Hs.186512 ESTs | 2.13 |
| 120522 | AA258843 | Hs.258748 ESTs | 2.13 |
| 119965 | W87738 | Hs.59039 EST | 2.13 |
| 131283 | AA101601 | Hs.183986 herpesvirus entry mediator B (poliovirus | 2.13 |
| 107347 | U43628 | Hs.102598 mucosal vascular addressin cell adhesion | 2.13 |
| 116490 | C14265 | Hs.66450 ESTs | 2.13 |
| 100563 | HG2239-HT2324 | Potassium Channel Protein (Gb:Z11585) | 2.13 |
| 110441 | H50302 | Hs.19845 ESTs; Highly similar to protein phosphat | 2.13 |
| 101035 | J05158 | Hs.73858 carboxypeptidase N; polypeptide 2; 83kD | 2.13 |
| 132500 | AA047297 | Hs.50107 ESTs; Moderately similar to CDO [H.sapi | 2.13 |
| 129807 | L34820 | Hs.5299 aldehyde dehydrogenase 5 family; member | 2.13 |
| 106250 | AA430466 | Hs.28890 ESTs | 2.13 |
| 113569 | T91088 | Hs.162070 EST | 2.13 |
| 122911 | AA470087 | Hs.239726 ESTs | 2.13 |
| 107452 | W28988 | Hs.250746 ESTs | 2.12 |
| 111824 | R35661 | Hs.25006 EST | 2.12 |
| 132831 | U53442 | Hs.57732 mitogen-activated protein kinase 11 | 2.12 |
| 110244 | H26742 | Hs.25367 ESTs; Weakly similar to ALR [H.sapiens] | 2.12 |
| 128918 | H85347 | Hs.107164 spectrin; beta; non-erythrocytic 1 | 2.12 |
| 133728 | M10901 | Hs.75772 nuclear receptor subfamily 3; group C; m | 2.12 |
| 122476 | AA448211 | Hs.99164 ESTs | 2.12 |
| 132004 | L37360 | Hs.37054 ephrin-A3 | 2.12 |
| 113971 | W86760 | Hs.220682 ESTs | 2.12 |
| 103388 | X92972 | Hs.80324 protein phosphatase 6; catalytic subunit | 2.12 |
| 131120 | AA443576 | Hs.23133 ESTs; Weakly similar to alcohol sulfotra | 2.12 |
| 102186 | U20285 | G protein pathway suppressor 1 | 2.12 |
| 103694 | AA018541 | Hs.60580 zinc finger protein | 2.12 |
| 111995 | R42333 | Hs.20893 ESTs | 2.12 |
| 124436 | N39596 | Hs.182584 ESTs | 2.12 |
| 100306 | D50495 | Hs.80598 transcription elongation factor A (SII); | 2.12 |
| 103084 | X59932 | Hs.77793 c-src tyrosine kinase | 2.11 |
| 115092 | AA255903 | Hs.80975 CD39-like 4 | 2.11 |
| 121579 | AA416543 | Hs.111981 ESTs | 2.11 |
| 127101 | AI349351 | Hs.118944 ESTs | 2.11 |
| 121195 | AA400273 | Hs.97791 ESTs | 2.11 |
| 112721 | R91484 | Hs.30853 ESTs | 2.11 |
| 113253 | T64207 | Hs.55296 HLA-B associated transcript-1 | 2.11 |
| 120838 | AA348887 | Hs.98907 ESTs | 2.11 |
| 114122 | Z38582 | Hs.12751 ESTs | 2.11 |
| 112635 | R82298 | Hs.29497 ESTs | 2.11 |
| 103785 | AA095600 | Hs.225647 ESTs | 2.11 |
| 128250 | AA331445 | EST35277 Embryo, 8 week Homo sapiens c | 2.11 |
| 122987 | AA479155 | Hs.103364 ESTs | 2.11 |

| | | | | |
|--------|----------|-----------|---|------|
| 110374 | H42983 | Hs.227263 | ESTs | 2.11 |
| 116595 | D60625 | Hs.177656 | calmodulin 1 (phosphorylase kinase; delta yu26a08.r1 Soares fetal liver spleen 1NF | 2.11 |
| 126117 | H78617 | | | 2.11 |
| 116810 | D80448 | Hs.45177 | ESTs | 2.11 |
| 111430 | R01248 | Hs.19165 | ESTs | 2.11 |
| 106700 | AA463929 | Hs.28701 | ESTs | 2.11 |
| 120181 | Z40121 | Hs.65870 | ESTs; Weakly similar to Pro-Pol-dUTPase | 2.1 |
| 132545 | AA147218 | Hs.5105 | ESTs | 2.1 |
| 105005 | AA115253 | Hs.28805 | ESTs | 2.1 |
| 126702 | U54602 | Hs.2785 | keratin 17 | 2.1 |
| 124096 | H10060 | Hs.101687 | EST | 2.1 |
| 132720 | Z69881 | Hs.5541 | ATPase; Ca++ transporting; ubiquitous | 2.1 |
| 121926 | AA428559 | Hs.104895 | ESTs | 2.1 |
| 125734 | AA157445 | Hs.227391 | DKFZP547E1010 protein | 2.1 |
| 122368 | AA443963 | Hs.104964 | EST | 2.1 |
| 116910 | H72014 | Hs.161031 | ESTs; Weakly similar to SYNAPTOTAGMIN I | 2.1 |
| 113171 | T54613 | Hs.9761 | EST | 2.1 |
| 134629 | U00951 | Hs.87150 | Human clone A9A2BR11 (CAC)n(GTG)n repeat | 2.1 |
| 105712 | AA291293 | Hs.25219 | ESTs | 2.1 |
| 106931 | AA495918 | Hs.26714 | ESTs | 2.1 |
| 114278 | Z40424 | Hs.27728 | ESTs | 2.1 |
| 116615 | D80666 | Hs.45203 | ESTs | 2.09 |
| 100189 | D21089 | Hs.320 | xeroderma pigmentosum; complementation g | 2.09 |
| 119500 | W37694 | Hs.55561 | ESTs | 2.09 |
| 129605 | S72493 | Hs.115947 | keratin 16 (focal non-epidermolytic palm | 2.09 |
| 133912 | X62744 | Hs.77522 | major histocompatibility complex; class | 2.09 |
| 129636 | N34942 | Hs.11782 | ESTs | 2.09 |
| 106372 | AA443941 | Hs.4992 | tumor suppressing subtransferable candid | 2.09 |
| 101885 | M98539 | Hs.8272 | prostaglandin D2 synthase (21kD; brain) | 2.09 |
| 132749 | AA235989 | Hs.55967 | short stature homeobox 2 | 2.09 |
| 135042 | X91348 | Hs.83522 | putative non-coding transcript (DiGeorge | 2.09 |
| 109404 | AA224594 | Hs.86941 | ESTs | 2.09 |
| 101333 | L47738 | Hs.80313 | p53 Inducible protein | 2.09 |
| 100114 | D00596 | Hs.82962 | thymidylate synthetase | 2.09 |
| 130536 | T17045 | Hs.159492 | spastic ataxia of Charlevoix-Saguenay (s | 2.09 |
| 125772 | R83903 | Hs.78040 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 2.09 |
| 132192 | AA247569 | Hs.4209 | ESTs | 2.09 |
| 124697 | R06273 | Hs.186467 | ESTs; Moderately similar to !!! ALU SUB | 2.09 |
| 127694 | A1247780 | Hs.117036 | ESTs | 2.08 |
| 127895 | AA772600 | Hs.187998 | ESTs; Weakly similar to ATP-binding cass | 2.08 |
| 121315 | AA402883 | Hs.82269 | progesterone-associated endometrial prote | |
| | | | endometrial alpha-2-globulin; alpha utr | 2.08 |
| 112150 | R46576 | Hs.23239 | ESTs | 2.08 |
| 105054 | AA133584 | Hs.26333 | JM1 protein | 2.08 |
| 113151 | T51620 | Hs.9326 | EST | 2.08 |
| 118783 | N75285 | Hs.50593 | ESTs; Moderately similar to cytoplasmic | 2.08 |
| 126748 | AA249580 | Hs.239975 | ESTs; Moderately similar to CDO [H.sapi | 2.08 |
| 135160 | U77643 | Hs.95655 | secreted and transmembrane 1 | 2.08 |
| 107518 | X60152 | | zinc finger protein 2 | 2.08 |
| 126055 | N28990 | | yx39g04.r1 Soares melanocyte 2NbHM Homo | 2.08 |
| 116382 | H81933 | Hs.40317 | ESTs | 2.08 |
| 101756 | M77235 | Hs.169331 | sodium channel; voltage-gated; type V; a | 2.08 |
| 116935 | H75763 | Hs.53468 | ESTs | 2.08 |
| 118556 | N68408 | Hs.194637 | Homo sapiens mRNA; cDNA DKFZp554D113 (fr | 2.08 |
| 129812 | L07807 | Hs.166181 | dynamin 1 | 2.08 |
| 121946 | AA429411 | Hs.104888 | ESTs | 2.08 |
| 133843 | AA489045 | Hs.76691 | Homo sapiens clone 25100 mRNA sequence | 2.08 |
| 122170 | AA435744 | Hs.163913 | ESTs | 2.08 |
| 122399 | AA446449 | Hs.231112 | EST | 2.08 |
| 105775 | AA348274 | Hs.6664 | ESTs | 2.08 |
| 123943 | AA621553 | Hs.112998 | ESTs | 2.08 |
| 105771 | AA347957 | Hs.256267 | neuroblastoma RAS viral (v-ras) oncogene | 2.08 |
| 114454 | AA021091 | Hs.226208 | ESTs | 2.08 |
| 125802 | R78852 | Hs.151099 | ESTs | 2.08 |
| 131556 | AA442853 | Hs.2869 | cyclin-dependent kinase 5; regulatory su | 2.08 |
| 118837 | N79836 | Hs.216338 | ESTs | 2.08 |
| 107345 | U26209 | Hs.102307 | solute carrier family 13 (sodium-depende | 2.08 |
| 131324 | H58690 | Hs.25625 | ESTs | 2.08 |
| 105233 | AA216759 | Hs.191132 | ESTs | 2.07 |
| 112886 | T03864 | Hs.7436 | putative acyltransferase | 2.07 |
| 120252 | AA169400 | Hs.152701 | DKFZP434F124 protein | 2.07 |
| 114867 | AA235310 | Hs.52899 | ESTs; Moderately similar to !!! ALU SUB | 2.07 |
| 106715 | AA464955 | Hs.126052 | ESTs; Weakly similar to EPIDERMAL GROWTH | 2.07 |
| 125560 | R51281 | Hs.13692 | ESTs; Highly similar to PROTEIN TSG24 [M | 2.07 |
| 112270 | R53021 | Hs.203358 | ESTs | 2.07 |
| 134625 | S82198 | Hs.8709 | caldecacin (serum calcium decreasing fact | 2.07 |

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|--------|---------------|-----------|--|------|
| 115723 | AA417345 | Hs.54846 | ESTs | 2.07 |
| 123895 | AA621192 | Hs.112949 | EST | 2.07 |
| 119906 | W85818 | | ESTs; Moderately similar to !!! ALU SUB | 2.07 |
| 108559 | AA085161 | | zr12c5.s1 Stratagene hNT neuron (#937233) | |
| | | | IMAGE:54728 3' similar to TR:G1151228 G | 2.07 |
| 101246 | L33799 | Hs.202097 | procollagen C-endopeptidase enhancer | 2.07 |
| 100663 | HG2915-HT3059 | | Major Histocompatibility Complex, Class I, E (Gb:M20022) | 2.07 |
| 114178 | Z39063 | Hs.17930 | Human DNA seq fm clone 1033B10 on chr 6p | |
| | | | for GaT3 (beta3-Galactosyltransferase) | 2.07 |
| 125672 | AA152281 | Hs.78601 | uroporphyrinogen decarboxylase | 2.07 |
| 118052 | N53360 | Hs.165133 | ESTs | 2.07 |
| 102387 | U41163 | Hs.229731 | solute carrier family 6 (neurotransmitter | 2.07 |
| 127305 | AA535148 | Hs.255277 | ESTs | 2.07 |
| 101182 | L19711 | Hs.76111 | dystroglycan 1 (dystrophin-associated gl | 2.07 |
| 131111 | R33245 | Hs.23076 | ESTs; Weakly similar to putative [C.eleg | 2.07 |
| 112441 | R63388 | Hs.28412 | ESTs | 2.06 |
| 117796 | N48571 | Hs.46689 | EST | 2.06 |
| 116099 | AA456309 | Hs.58831 | regulator of Fas-induced apoptosis | 2.06 |
| 125559 | AA307550 | Hs.119571 | collagen; type III; alpha 1 (Ehlers-Danl | 2.06 |
| 135271 | AA397763 | Hs.97562 | ESTs | 2.06 |
| 106083 | AA418545 | Hs.31659 | thyroid hormone receptor-associated prot | 2.06 |
| 133419 | U67363 | Hs.73172 | growth factor independent 1 | 2.06 |
| 127816 | AA743646 | Hs.120604 | ESTs | 2.06 |
| 127502 | AA614422 | Hs.183502 | ESTs | 2.06 |
| 129371 | M10321 | Hs.110802 | von Willebrand factor | 2.06 |
| 108417 | AA075716 | | zm89e5.s1 Stratagene ovarian cancer (#93 | |
| | | | CLUSTERIN PRECURSOR (HUMAN); mRNA sequ | 2.06 |
| 102837 | U94585 | Hs.13495 | requiem; apoptosis response zinc finger | 2.06 |
| 124226 | H62396 | Hs.190266 | ESTs | 2.06 |
| 102254 | U28131 | | Human HMGI-C chimeric transcript mRNA, p | 2.06 |
| 128472 | X87212 | Hs.10029 | cathepsin C | 2.06 |
| 107545 | Z82022 | Hs.26433 | dolichyl-phosphate (UDP-N-acetylglucosam | 2.06 |
| 135311 | M36089 | Hs.98493 | X-ray repair complementing defective rep | 2.06 |
| 121727 | AA420973 | Hs.104234 | ESTs | 2.06 |
| 131846 | U02619 | Hs.331 | general transcription factor IIIC; polyp | 2.06 |
| 120415 | AA235810 | Hs.182522 | ESTs | 2.06 |
| 110529 | H57686 | Hs.37486 | ESTs | 2.06 |
| 104996 | AA112307 | Hs.105894 | Homo sapiens mRNA; cDNA DKFZp434G231 (fr | 2.06 |
| 110351 | H41222 | Hs.156459 | ESTs | 2.06 |
| 131261 | AA223746 | Hs.171776 | Inositol(myo)-1(or 4)-monophosphatase 1 | 2.06 |
| 110585 | H62223 | Hs.133526 | ESTs; Weakly similar to !!! ALU SUBFAMI | 2.06 |
| 129420 | AA234259 | Hs.99816 | ESTs | 2.06 |
| 103796 | AA112595 | Hs.31146 | Human DNA sequence from clone 1042K10 on | |
| | | | lyase (EC 4.3.2.2; Adenylosuccinate; AS | |
| | | | 3). Contains ESTs; STSs; GS | 2.06 |
| 119762 | W72982 | Hs.58262 | ESTs | 2.06 |
| 108641 | AA112059 | | ATP synthase; H+ transporting; mitochond | 2.06 |
| 134875 | U66672 | Hs.180513 | ATP-binding cassette; sub-family A (ABC1 | 2.06 |
| 106832 | AA482015 | Hs.30114 | ESTs; Highly similar to C8 [H.sapiens] | 2.06 |
| 109403 | AA224413 | Hs.86937 | ESTs | 2.06 |
| 115485 | AA287667 | Hs.188804 | ESTs | 2.06 |
| 102923 | X12517 | Hs.1063 | small nuclear ribonucleoprotein polypept | 2.06 |
| 123320 | AA495792 | Hs.139572 | EST | 2.05 |
| 111901 | R39066 | Hs.17638 | ESTs | 2.05 |
| 106558 | AA455111 | Hs.182447 | heterogeneous nuclear ribonucleoprotein | 2.05 |
| 126885 | AA293052 | Hs.10101 | ESTs; Weakly similar to coded for by C. | 2.05 |
| 113429 | T85190 | Hs.179808 | ESTs | 2.05 |
| 102270 | U30255 | Hs.75888 | phosphogluconate dehydrogenase | 2.05 |
| 103204 | X72475 | Hs.192989 | H.sapiens mRNA for rearranged Ig kappa I | 2.05 |
| 106666 | AA461072 | Hs.37916 | ESTs | 2.05 |
| 100947 | HG907-HT807 | | Mg44 | 2.05 |
| 102578 | U60666 | Hs.57693 | testis specific leucine rich repeat prot | 2.05 |
| 105827 | AA398255 | Hs.31520 | ESTs | 2.05 |
| 122324 | AA442830 | Hs.98921 | EST | 2.05 |
| 101025 | J04823 | Hs.81097 | cytochrome c oxidase subunit VIII | 2.05 |
| 115861 | AA431768 | Hs.90259 | ESTs; Weakly similar to alpha 1 [H.sapi | 2.05 |
| 108081 | AA045306 | Hs.42996 | ESTs | 2.05 |
| 133994 | X74929 | Hs.242463 | keratin 8 | 2.05 |
| 119131 | R46700 | Hs.129692 | ESTs; Moderately similar to !!! ALU SUB | 2.05 |
| 129793 | AA300151 | Hs.126857 | ESTs | 2.05 |
| 101653 | M60284 | Hs.161305 | tachykinin receptor 2 | 2.05 |
| 120300 | AA191648 | Hs.131476 | ESTs | 2.05 |
| 106519 | AA453415 | Hs.8763 | Hu DNA sequence from clone 889N15 on chr | |
| | | | Thymocyte Marker CTX; the possibly alte | 2.05 |
| 114291 | Z40690 | Hs.123666 | Homo sapiens mRNA full length insert cDN | 2.05 |
| 105747 | AA293719 | Hs.30251 | ESTs; Weakly similar to GLUCOSE-6-PHOSPH | 2.04 |

| | | | | |
|--------|----------|-----------|--|------|
| 125325 | AA332944 | Hs.8402 | adenylyl cyclase 3 | 2.04 |
| 119978 | W88623 | Hs.59190 | EST | 2.04 |
| 102449 | U48231 | Hs.46348 | bradykinin receptor B1 | 2.04 |
| 101454 | M21812 | Hs.50889 | myosin light chain 2 | 2.04 |
| 116086 | AA455904 | Hs.86023 | ESTs | 2.04 |
| 102297 | U32674 | Hs.198252 | G protein-coupled receptor 9 | 2.04 |
| 130889 | D57622 | Hs.20985 | sin3-associated polypeptide; 30kD | 2.04 |
| 100196 | D21853 | Hs.79768 | KIAA0111 gene product | 2.04 |
| 120957 | AA398111 | Hs.97503 | ESTs | 2.04 |
| 105735 | AA293096 | Hs.32417 | ESTs | 2.04 |
| 135031 | R41604 | Hs.9344 | ESTs; Weakly similar to III ALU SUBFAMI | 2.04 |
| 104882 | AA052954 | Hs.29546 | ESTs | 2.04 |
| 132819 | AA404565 | Hs.53447 | ESTs; Moderately similar to kinesin ligh | 2.04 |
| 127993 | AA847856 | Hs.124565 | ESTs | 2.04 |
| 116441 | AA620299 | Hs.91696 | ESTs | 2.04 |
| 102272 | U30610 | Hs.41682 | killer cell lectin-like receptor subfami | 2.04 |
| 119566 | W38209 | | Accession not listed in Genbank | 2.04 |
| 116622 | D81171 | Hs.45208 | ESTs; Weakly similar to collagen type VI | 2.04 |
| 127182 | AA248620 | Hs.166011 | catenin (cadherin-associated protein); d | 2.04 |
| 116870 | H57146 | Hs.38564 | ESTs | 2.04 |
| 115448 | AA284845 | Hs.165051 | ESTs | 2.04 |
| 127231 | AA343584 | | zw52c03.r1 Soares_total_fetus_Nb2HF8_9w | 2.04 |
| 103457 | X99728 | | H.sapiens NDUV3 gene, exon 3 | 2.04 |
| 134737 | U00802 | Hs.89434 | drebrin 1 | 2.04 |
| 117046 | H89505 | | yu8144.s1 Soares fetal liver spleen 1NFL to contains Alu repetitive element, mR | 2.04 |
| 124579 | N68345 | Hs.127179 | ESTs; Weakly similar to TERATOCARCINOMA- | 2.04 |
| 112132 | R45970 | Hs.236349 | EST | 2.04 |
| 132281 | AA133300 | Hs.43803 | leukocyte-associated Ig-like receptor 2 | 2.03 |
| 103668 | Z83741 | Hs.248174 | H2A histone family; member M | 2.03 |
| 113501 | T89107 | Hs.13262 | ESTs | 2.03 |
| 125021 | T70060 | Hs.163918 | ESTs | 2.03 |
| 115754 | AA420998 | Hs.178095 | ESTs | 2.03 |
| 123405 | AA521370 | Hs.191708 | ESTs | 2.03 |
| 102054 | U07695 | Hs.155227 | EphB4 | 2.03 |
| 115627 | AA401910 | Hs.119175 | ESTs; Weakly similar to ZINC FINGER PROT | 2.03 |
| 129252 | AA234663 | Hs.109773 | ESTs | 2.03 |
| 103417 | X96849 | | H.sapiens 5' mRNA of PECAM-1 molecule | 2.03 |
| 133721 | U11863 | Hs.75741 | amidoboride binding protein 1 (amine oxida | 2.03 |
| 114176 | Z39059 | Hs.27267 | ESTs; Weakly similar to tetraspan TM4SF | 2.03 |
| 123956 | C14068 | Hs.21806 | ESTs; Moderately similar to similar to N | 2.03 |
| 134236 | D45371 | Hs.80485 | adipose most abundant gene transcript 1 | 2.03 |
| 116381 | AA598614 | Hs.65394 | ESTs | 2.03 |
| 103711 | AA046737 | Hs.102792 | ESTs | 2.03 |
| 109316 | AA206914 | Hs.85322 | EST | 2.03 |
| 123793 | AA620343 | Hs.112853 | ESTs | 2.03 |
| 128462 | M69238 | Hs.166172 | aryl hydrocarbon receptor nuclear transl | 2.03 |
| 117690 | N40467 | Hs.93834 | ESTs | 2.03 |
| 113301 | T67452 | Hs.13104 | EST | 2.03 |
| 134563 | AA173430 | Hs.85335 | Homo sapiens mRNA; cDNA DKFZp564D1462 (fr | 2.03 |
| 108316 | AA070160 | | zm694.s1 Stratagene neuroepithelium (#9 | 2.03 |
| 135239 | AA454599 | Hs.19399 | Homo sapiens chromosome 19; fosmid 39554 | 2.03 |
| 120342 | AA207105 | Hs.45068 | Homo sapiens mRNA; cDNA DKFZp4341143 (fr | 2.02 |
| 103493 | Y08976 | Hs.234759 | H.sapiens mRNA for FEV protein | 2.02 |
| 114204 | Z39259 | Hs.26096 | ESTs | 2.02 |
| 125425 | H62307 | Hs.18575 | ESTs; Weakly similar to KIAA0246 (H.sapi | 2.02 |
| 133027 | AA402624 | Hs.63236 | synuclein; gamma (breast cancer-specific | 2.02 |
| 131323 | H54036 | Hs.25619 | death-associated protein kinase 3 | 2.02 |
| 121515 | AA412133 | Hs.104696 | ESTs | 2.02 |
| 129780 | AA291526 | Hs.124659 | ESTs | 2.02 |
| 131292 | AF005033 | Hs.20060 | secretory carrier membrane protein 3 | 2.02 |
| 132973 | AA035446 | Hs.214351 | ESTs | 2.02 |
| 103727 | AA059415 | Hs.6289 | growth factor receptor-bound protein 2 | 2.02 |
| 113174 | T54659 | Hs.9779 | ESTs | 2.02 |
| 120964 | AA398085 | Hs.142390 | ESTs | 2.02 |
| 134303 | AA457242 | Hs.8141 | etoposide-induced mRNA | 2.02 |
| 128118 | T81623 | Hs.21765 | hypothetical protein of unknown functio | 2.02 |
| 121087 | AA398751 | Hs.97304 | ESTs | 2.02 |
| 102806 | U90306 | | Human Iroquois-class homeodomain protein | 2.02 |
| 103195 | X70940 | Hs.2642 | eukaryotic translation elongation factor | 2.02 |
| 126767 | C17148 | | C17148 Clontech human aorta polyA+ mRNA | 2.02 |
| 105179 | AA189083 | Hs.21974 | ESTs; Moderately similar to mBOCT (M.mus | 2.02 |
| 116797 | H40486 | | yn87a08.s1 Soares adult brain N2b5HB55Y | 2.02 |
| | | | 3' similar to contains Alu repetitive e | 2.02 |
| 133268 | AA099404 | Hs.69307 | ESTs | 2.02 |
| 123951 | AA621721 | Hs.231130 | EST | 2.02 |

| | | | | |
|--------|---------------|-----------|--|------|
| 115463 | AA286819 | Hs.69485 | ESTs; Weakly similar to similar to other | 2.02 |
| 110603 | H65776 | Hs.222403 | ESTs | 2.02 |
| 101234 | L29277 | Hs.142258 | signal transducer and activator of trans | 2.02 |
| 121208 | AA400470 | Hs.97805 | ESTs | 2.02 |
| 122598 | AA453465 | Hs.99329 | ESTs | 2.02 |
| 110668 | H84882 | Hs.33791 | ESTs; Weakly similar to K-Cl cotransport | 2.02 |
| 117137 | H96670 | Hs.42221 | ESTs | 2.02 |
| 119389 | T88826 | Hs.90973 | ESTs | 2.01 |
| 102940 | X13956 | Hs.24998 | Human 12S RNA induced by poly(rI); poly/ | 2.01 |
| 100748 | HG3517-HT3711 | | Alpha-1-Antitrypsin, 5' End | 2.01 |
| 103012 | X52638 | Hs.739 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 2.01 |
| 132755 | AA609201 | Hs.182635 | ESTs | 2.01 |
| 130842 | H39589 | Hs.20159 | ESTs; Highly similar to CGI-92 protein [| 2.01 |
| 133599 | M64788 | Hs.75151 | RAP1; GTPase activating protein 1 | 2.01 |
| 117250 | N21081 | Hs.15299 | HMBA-inducible | 2.01 |
| 115124 | AA256666 | Hs.39155 | ESTs | 2.01 |
| 128155 | AA926843 | Hs.143302 | ESTs | 2.01 |
| 130574 | AA379087 | Hs.16178 | apoptosis antagonizing transcription fac | 2.01 |
| 132601 | R78838 | Hs.54943 | fracture callus 1 (rat) homolog | 2.01 |
| 117428 | N27366 | Hs.43933 | EST | 2.01 |
| 121108 | AA399053 | Hs.97529 | EST | 2.01 |
| 130518 | X69550 | Hs.159161 | Rho GDP dissociation inhibitor (GDI) alp | 2.01 |
| 110606 | H66049 | Hs.19085 | ESTs; Weakly similar to putative p150 [H | 2.01 |
| 120606 | AA282956 | | z15h4.s1 NCL_CGAP_GCB1 Homo sapiens cDN SW:CADR_MOUSE P3938 RETINAL_CADHERIN PR | 2.01 |
| 130070 | T47969 | Hs.194660 | ceroid-lipofuscinosis; neuronal 3; juven | 2.01 |
| 130331 | Z80783 | Hs.239884 | H2B histone family; member L | 2.01 |
| 109599 | F02602 | Hs.6749 | ESTs | 2.01 |
| 131749 | W78211 | Hs.31547 | ESTs; Highly similar to NADH:ubiquinone | 2.01 |
| 129463 | AA376905 | Hs.111742 | ESTs; Weakly similar to III ALU SUBFAMI | 2.01 |
| 114880 | AA235698 | Hs.65862 | ESTs | 2.01 |
| 114745 | AA135523 | Hs.139064 | EST | 2.01 |
| 115637 | AA402727 | Hs.76925 | ESTs; Highly similar to R31167_2; partia | 2.01 |
| 109043 | AA159605 | Hs.72580 | ESTs | 2.01 |
| 128901 | Z41411 | Hs.107040 | ESTs | 2.01 |
| 124427 | N36812 | Hs.178663 | ESTs | 2 |
| 100673 | HG3033-HT3194 | | Spliceosomal Protein Sap 62 | 2 |
| 108436 | AA078801 | | zm94a9.s1 Stratagene colon HT29 (#937221 | 2 |
| 123764 | AA610019 | Hs.112654 | ESTs | 2 |
| 129343 | N70791 | Hs.180060 | ESTs | 2 |
| 122794 | AA460254 | Hs.105043 | EST | 2 |
| 128688 | AA161469 | Hs.103755 | receptor-interacting serine-threonine ki | 2 |
| 115592 | AA399543 | Hs.48026 | ESTs | 2 |
| 111693 | R22007 | Hs.23321 | EST | 2 |
| 113353 | T79186 | Hs.14468 | ESTs | 2 |

Table 18: B survivor vs Mets – Up in Mets

| Pkey | Ex Accn | UniG ID | Complete Title | Ratio BS/Met |
|--------|---------------|-----------|--|--------------|
| 106024 | AA412059 | Hs.111742 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 0.17 |
| 110930 | N48603 | Hs.14947 | ESTs | 0.18 |
| 105772 | AA347973 | Hs.221132 | ESTs | 0.2 |
| 133271 | Z48633 | Hs.6940 | H.sapiens mRNA for retrotransposon | 0.2 |
| 107109 | AA609943 | Hs.32793 | ESTs | 0.24 |
| 108593 | F02506 | Hs.159591 | thyroid hormone receptor interactor 8 | 0.24 |
| 123016 | AA480103 | Hs.111730 | ESTs; Weakly similar to alternatively sp | 0.25 |
| 100739 | HG3484-HT3678 | | Protein Kinase (GbxM59287) | 0.25 |
| 130252 | U92014 | Hs.153527 | Human clone 121711 defective mariner tra | 0.26 |
| 105149 | AA169253 | Hs.8958 | ESTs | 0.26 |
| 115412 | AA283804 | Hs.193552 | ESTs | 0.27 |
| 105952 | AA405263 | Hs.181400 | ESTs | 0.28 |
| 106596 | AA456981 | Hs.35349 | ESTs | 0.28 |
| 120249 | AA167567 | Hs.133325 | ESTs | 0.28 |
| 111676 | R19414 | Hs.166459 | ESTs | 0.29 |
| 111161 | N66767 | Hs.124145 | ESTs | 0.29 |
| 109364 | AA215379 | Hs.50418 | ESTs | 0.29 |
| 132316 | U28831 | | Human protein immuno-reactive with anti- | 0.3 |
| 104030 | AA363131 | Hs.222992 | ESTs; Weakly similar to TRANSFORMATION-S | 0.3 |
| 109825 | F13653 | Hs.16798 | ESTs | 0.3 |
| 111110 | N63165 | Hs.23618 | ESTs | 0.31 |
| 135315 | W90583 | Hs.9853 | ESTs | 0.32 |
| 104792 | AA029288 | Hs.29147 | ESTs; Highly similar to ZINC FINGER PROT | 0.33 |
| 123562 | AA608893 | Hs.190065 | ESTs | 0.33 |
| 116079 | AA455286 | Hs.54982 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 0.33 |
| 110671 | H87770 | Hs.153800 | ESTs | 0.33 |
| 108819 | AA130986 | Hs.193253 | ESTs | 0.34 |
| 115558 | AA393808 | Hs.1010 | regulator of mitotic spindle assembly 1 | 0.34 |
| 104781 | AA026617 | Hs.21610 | ESTs; Highly similar to BAI1-associated | 0.34 |
| 111236 | N69324 | Hs.12526 | Homo sapiens clone 23903 mRNA sequence | 0.34 |
| 113341 | T77656 | Hs.189703 | ESTs | 0.35 |
| 125371 | AI084676 | Hs.133266 | ESTs; Moderately similar to Sqv-7-like p | 0.35 |
| 115890 | AA435853 | Hs.44114 | ESTs; Weakly similar to CGI-73 protein [| 0.35 |
| 113571 | T91116 | Hs.15713 | ESTs | 0.35 |
| 121683 | AA417911 | Hs.175663 | ESTs | 0.35 |
| 105489 | AA256157 | Hs.24115 | ESTs | 0.35 |
| 116320 | AA490866 | Hs.39429 | ESTs | 0.36 |
| 111917 | R39882 | Hs.21397 | ESTs | 0.36 |
| 127568 | T53722 | | ya91c06.r3 Stratagene placenta (#937225) | 0.36 |
| 123541 | AA608794 | Hs.112592 | ESTs | 0.36 |
| 123131 | AA487207 | Hs.193272 | ESTs | 0.36 |
| 125069 | T86914 | Hs.194485 | ESTs | 0.36 |
| 114757 | AA136725 | Hs.161990 | ESTs | 0.37 |
| 132778 | AA446695 | Hs.5671 | Homo sapiens clone 23926 mRNA sequence | 0.37 |
| 123132 | AA487233 | Hs.105711 | eukaryotic translation initiation factor | 0.37 |
| 134029 | AA378597 | Hs.143601 | ESTs; Moderately similar to 67A9.b [D.m. | 0.37 |
| 126956 | AI434405 | Hs.171957 | triple functional domain (PTPRF interact | 0.38 |
| 106869 | AA487563 | Hs.188813 | ESTs | 0.38 |
| 107818 | AA202957 | Hs.167948 | ESTs | 0.38 |
| 129974 | K00629 | Hs.19300 | Human kpnl repeat mma (cdna clone pcd-k | 0.38 |
| 129477 | D49728 | Hs.1119 | nuclear receptor subfamily 4; group A; m | 0.38 |
| 119359 | T78020 | Hs.245915 | ESTs; Weakly similar to kinase-related p | 0.39 |
| 114021 | W91995 | Hs.16145 | ESTs | 0.39 |
| 122024 | AA431296 | Hs.139433 | EST | 0.39 |
| 130014 | N50959 | Hs.143102 | amine oxidase; copper containing 2 (reti | 0.39 |
| 110163 | H19326 | Hs.22073 | ESTs; Highly similar to J KAPPA-RECOMBIN | 0.39 |
| 104641 | AA004652 | Hs.18564 | ESTs | 0.39 |
| 124777 | R41933 | Hs.140237 | ESTs | 0.39 |
| 125382 | AA713494 | Hs.194660 | ceroid-lipofuscinosis; neuronal 3; juven | 0.4 |
| 120406 | AA234999 | Hs.111279 | ESTs; Weakly similar to unnamed protein | 0.4 |
| 132734 | R23653 | Hs.164250 | ESTs | 0.4 |
| 117001 | H84719 | Hs.40721 | EST | 0.4 |
| 120905 | AA371602 | Hs.182930 | ESTs; Highly similar to PHOSPHATIDYLINOS.4 | 0.4 |
| 125488 | AA355158 | Hs.41181 | Homo sapiens mRNA; cDNA DKFZp727C191 (fr | 0.4 |

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|--------|---------------|--|--|------|
| 121989 | AA430044 | Hs.193784 | Homo sapiens mRNA; cDNA DKFZp586K1922 (f | 0.4 |
| 127921 | AA806616 | Hs.209523 | ESTs | 0.4 |
| 119830 | W74700 | Hs.53478 | ESTs | 0.41 |
| 106292 | AA435571 | Hs.148560 | ESTs | 0.41 |
| 102762 | U82303 | Hs.123080 | Homo sapiens unknown protein mRNA; parti | 0.41 |
| 113518 | T89731 | ye11R06.s1 | Stratagene lung (#937210) H s to contains Alu repetitive element;cont | 0.41 |
| 100635 | HG2724-HT2820 | Oncogene Tis/Chop, Fusion Activated | | 0.41 |
| 113319 | T70356 | Hs.193141 | ESTs; Weakly similar to coding sequence | 0.41 |
| 121319 | AA402935 | Hs.194242 | ESTs; Weakly similar to !!!! ALU CLASS B | 0.42 |
| 111818 | R34382 | Hs.24779 | ESTs | 0.42 |
| 104883 | AA052959 | Hs.177409 | ESTs; Highly similar to dJ1119D9.2 [H.sa | 0.42 |
| 129258 | W95592 | Hs.251946 | ESTs; Moderately similar to POLYADENYLAT | 0.42 |
| 130576 | T86475 | Hs.16193 | Homo sapiens mRNA; cDNA DKFZp586B211 (fr | 0.43 |
| 106354 | AA443271 | Hs.26764 | KIAA0546 protein | 0.43 |
| 108841 | AA132524 | Hs.70614 | ESTs | 0.43 |
| 113922 | W80741 | Hs.37890 | ESTs | 0.43 |
| 120997 | AA398285 | Hs.97598 | EST | 0.43 |
| 108158 | AA054597 | Hs.221935 | ESTs | 0.43 |
| 124516 | N58185 | Hs.131830 | ESTs | 0.43 |
| 114477 | AA032013 | Hs.144260 | EST | 0.43 |
| 104290 | C16652 | Hs.107205 | Homo sapiens mRNA; cDNA DKFZp434L2221 (f | 0.43 |
| 126700 | AI318412 | Hs.108258 | actin binding protein; macrophin (microf | 0.44 |
| 110887 | N38770 | Hs.4283 | ESTs | 0.44 |
| 116141 | AA460420 | Hs.44949 | ESTs | 0.44 |
| 110689 | H93046 | Hs.15571 | ESTs | 0.44 |
| 115314 | AA280583 | Hs.256501 | ESTs | 0.44 |
| 110904 | N39453 | Hs.27371 | Homo sapiens mRNA; cDNA DKFZp566J123 (fr | 0.44 |
| 109482 | AA233375 | Hs.78085 | ESTs | 0.44 |
| 102284 | U31449 | Hs.11881 | transmembrane 4 superfamily member 4 | 0.44 |
| 118654 | N70582 | Hs.49892 | ESTs | 0.44 |
| 115334 | AA281244 | Hs.65300 | ESTs | 0.44 |
| 113149 | T51588 | ESTs; Moderately similar to !!!! ALU SUB | 0.44 | |
| 113721 | T97831 | Hs.18190 | EST | 0.44 |
| 111299 | N73808 | Hs.24936 | ESTs | 0.44 |
| 103778 | AA094107 | Hs.7187 | ESTs; Weakly similar to similar to glyco | 0.44 |
| 113204 | T57865 | Hs.10310 | EST | 0.44 |
| 100315 | D50857 | Hs.82295 | dicator of cyto-kinesis 1 | 0.44 |
| 115254 | AA279024 | Hs.194437 | ESTs | 0.44 |
| 125500 | H46104 | Hs.244624 | ESTs | 0.44 |
| 117387 | N26011 | Hs.53810 | ESTs | 0.45 |
| 135113 | W42450 | Hs.206833 | ESTs | 0.45 |
| 124517 | N58204 | Hs.199945 | ESTs | 0.45 |
| 120379 | AA227849 | Hs.238380 | Human endogenous retroviral protease mRN | 0.45 |
| 119205 | R91954 | Hs.153699 | ESTs | 0.45 |
| 128266 | T70341 | Hs.131897 | ESTs | 0.45 |
| 104106 | AA422123 | Hs.42457 | ESTs | 0.45 |
| 115864 | AA432080 | Hs.81200 | ESTs | 0.45 |
| 113771 | W02695 | Hs.18714 | ESTs | 0.45 |
| 126515 | AI124649 | Hs.252708 | Homo sapiens mRNA; cDNA DKFZp586O031 (fr | 0.45 |
| 127823 | AA524806 | Hs.78859 | transcription elongation factor A (SII); | 0.45 |
| 116665 | F04405 | Hs.223654 | EST | 0.45 |
| 106355 | AA443272 | Hs.27836 | ESTs | 0.45 |
| 132693 | AA621429 | Hs.55075 | KIAA0410 gene product | 0.45 |
| 107388 | W01587 | Hs.173319 | ESTs | 0.45 |
| 110688 | H93021 | Hs.182937 | peptidylprolyl Isomerase A (cyclophilin | 0.46 |
| 116893 | H69569 | Hs.191316 | EST | 0.46 |
| 105375 | AA236542 | Hs.9512 | ESTs; Moderately similar to !!!! ALU SUB | 0.46 |
| 115601 | AA400277 | Hs.48849 | ESTs | 0.46 |
| 106696 | AA489707 | Hs.29896 | ESTs; Weakly similar to proline-rich pro | 0.46 |
| 111770 | R27975 | Hs.187469 | ESTs | 0.46 |
| 115663 | AA405838 | Hs.40507 | ESTs | 0.46 |
| 131404 | AA504744 | Hs.26461 | ESTs; Weakly similar to go-rich sequence | 0.46 |
| 108622 | AA101828 | Hs.189956 | ESTs | 0.46 |
| 128286 | AI025771 | Hs.144090 | ESTs | 0.46 |
| 105760 | AA338960 | Hs.28170 | ESTs | 0.46 |
| 100020 | | AFFX control: BioB-3 | | 0.46 |
| 105209 | AA205072 | Hs.227743 | KIAA0980 protein | 0.47 |
| 111975 | R41724 | Hs.149566 | ESTs | 0.47 |
| 114688 | AA121403 | Hs.144331 | ESTs | 0.47 |
| 116994 | H83918 | Hs.40528 | ESTs | 0.47 |
| 118401 | N64762 | Hs.49053 | EST | 0.47 |
| 110997 | N52540 | Hs.74316 | desmoplakin (DPI; DPL) | 0.47 |
| 123791 | AA620331 | Hs.245351 | EST | 0.47 |
| 109858 | H02266 | Hs.167451 | ESTs | 0.47 |
| 115470 | AA287122 | Hs.48391 | ESTs | 0.47 |

| | | | | |
|--------|----------|-----------|---|------|
| 130606 | AA402109 | Hs.16593 | ESTs | 0.47 |
| 116067 | AA454827 | Hs.124823 | ESTs | 0.47 |
| 125881 | AA775807 | Hs.150741 | 2';3'-cyclic nucleotide 3' phosphodiester | 0.47 |
| 124028 | F04112 | Hs.177178 | ESTs | 0.47 |
| 108995 | AA155574 | Hs.172702 | ESTs | 0.47 |
| 125102 | T95105 | Hs.173772 | ESTs | 0.47 |
| 110421 | H48462 | Hs.36093 | ESTs; Weakly similar to reverse transcript | 0.47 |
| 105658 | AA282914 | Hs.10176 | ESTs | 0.47 |
| 129046 | AA195678 | Hs.108258 | actin binding protein; macrophin (microf | 0.47 |
| 113639 | T95128 | Hs.17529 | ESTs | 0.48 |
| 132575 | AA045365 | Hs.5188 | ESTs; Weakly similar to 60S RIBOSOMAL PRO | 0.48 |
| 132592 | AA129390 | Hs.5285 | ESTs | 0.48 |
| 107619 | AA004955 | Hs.60015 | ESTs | 0.48 |
| 118684 | N70907 | Hs.230619 | EST | 0.48 |
| 127612 | AA917801 | Hs.116076 | ESTs | 0.48 |
| 112319 | R55615 | Hs.26432 | ESTs; Weakly similar to finger protein H | 0.48 |
| 113635 | T95087 | Hs.15543 | ESTs | 0.48 |
| 119344 | T62969 | Hs.193348 | ESTs | 0.48 |
| 121080 | AA398720 | Hs.177953 | ESTs | 0.48 |
| 133686 | X83378 | Hs.211614 | chloride channel 6 | 0.48 |
| 130395 | R54534 | Hs.87889 | helicase-moi | 0.49 |
| 127530 | AA563806 | Hs.145728 | ESTs | 0.49 |
| 132971 | AA033951 | Hs.61700 | ESTs | 0.49 |
| 127132 | AA721156 | Hs.190440 | ESTs | 0.49 |
| 129980 | T72661 | Hs.13969 | ESTs | 0.49 |
| 105323 | AA234112 | Hs.29075 | ESTs | 0.49 |
| 114439 | AA018937 | Hs.128629 | ESTs | 0.49 |
| 107632 | AA007242 | Hs.60179 | EST | 0.49 |
| 130952 | AB002296 | Hs.21560 | Human mRNA for KIAA0298 gene; complete cDNA | 0.49 |
| 127595 | AA927308 | Hs.130464 | ESTs | 0.49 |
| 124276 | H83465 | Hs.221934 | ESTs | 0.49 |
| 125935 | H30721 | Hs.30172 | ESTs | 0.49 |
| 131275 | U45974 | Hs.25156 | Human phosphatidylinositol (4;5) bisphos | 0.49 |
| 131186 | C20633 | Hs.24129 | ESTs | 0.49 |
| 125505 | AH127843 | Hs.155071 | ESTs | 0.5 |
| 113327 | T71776 | Hs.12097 | ESTs | 0.5 |
| 104709 | AA017146 | Hs.34579 | ESTs; Moderately similar to !!!! ALU SUB | 0.5 |
| 115772 | AA423972 | Hs.8154 | ESTs | 0.5 |
| 118286 | N63150 | Hs.48723 | ESTs | 0.5 |
| 131453 | C20596 | Hs.26985 | KIAA0457 protein | 0.5 |
| 104734 | AA019528 | Hs.32677 | ESTs | 0.5 |
| 119358 | T70550 | Hs.193651 | ESTs; Weakly similar to alternatively sp | 0.5 |

Table 19: B survivor vs Mets – Up in B survivor

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

| Pkey | Ex Accn | UniG_ID | Complete Title | Ratio BS/Met |
|--------|----------|-----------|--|--------------|
| 333601 | | | CH22_FGENES.213_4 | 5.5 |
| 325300 | | | CH.11_hs g 5866908 | 4.67 |
| 333642 | | | CH22_FGENES.231_2 | 4.64 |
| 333591 | | | CH22_FGENES.208_4 | 4.46 |
| 332859 | | | CH22_FGENES.27_2 | 4.39 |
| 304013 | AW518573 | Hs.156110 | immunoglobulin kappa variable 1D-8 | 4.23 |
| 333791 | | | CH22_FGENES.274_10 | 4.18 |
| 327641 | | | CH.04_hs g 5867890 | 4.03 |
| 321172 | H49160 | Hs.133472 | ESTs | 3.9 |
| 334125 | | | CH22_FGENES.334_4 | 3.88 |
| 333646 | | | CH22_FGENES.234_2 | 3.88 |
| 326554 | | | CH.19_hs g 5867308 | 3.84 |
| 333650 | | | CH22_FGENES.238_3 | 3.82 |
| 333647 | | | CH22_FGENES.235_2 | 3.79 |
| 333626 | | | CH22_FGENES.224_2 | 3.68 |
| 314671 | AW236550 | Hs.131914 | ESTs | 3.68 |
| 310847 | AI420523 | Hs.161282 | ESTs | 3.67 |
| 333657 | | | CH22_FGENES.241_2 | 3.65 |
| 338522 | | | CH22_EM:AC005500.GENSCAN.395-36 | 3.64 |
| 329464 | | | CH.Y_hs g 6456788 | 3.6 |
| 328868 | | | CH.07_hs g 531930 | 3.6 |
| 333637 | | | CH22_FGENES.229_2 | 3.59 |
| 329737 | | | CH.14_p2 g 5865779 | 3.5 |
| 317828 | AI791749 | Hs.128896 | ESTs | 3.44 |
| 330520 | M96995 | Hs.6289 | growth factor receptor-bound protein 2 | 3.44 |
| 339271 | | | CH22_BA354112.GENSCAN.11-2 | 3.44 |
| 314927 | AI735482 | Hs.159580 | ESTs | 3.42 |
| 334782 | | | CH22_FGENES.432_7 | 3.42 |
| 313138 | AW138842 | Hs.196669 | ESTs | 3.4 |
| 332650 | H51595 | Hs.5541 | ATPase; Ca++ transporting; ubiquitous | 3.38 |
| 338648 | | | CH22_EM:AC005500.GENSCAN.460-6 | 3.38 |
| 325677 | | | CH.14_hs g 5867017 | 3.34 |
| 312639 | H50648 | Hs.213221 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 3.33 |
| 326545 | | | CH.19_hs g 5867307 | 3.32 |
| 318364 | R44616 | Hs.138280 | ESTs; Moderately similar to !!!! ALU SUB | 3.3 |
| 308385 | AI625428 | | EST singleton (not in UniGene) with exon | 3.26 |
| 328569 | | | CH.07_hs g 5004480 | 3.26 |
| 328582 | | | CH.07_hs g 5006033 | 3.24 |
| 310975 | AI492857 | Hs.170940 | ESTs | 3.24 |
| 336883 | | | CH22_FGENES.322-2 | 3.21 |
| 324425 | AW236939 | Hs.172154 | ESTs | 3.2 |
| 337870 | | | CH22_EM:AC005500.GENSCAN.48-3 | 3.19 |
| 306524 | AI001043 | | EST singleton (not in UniGene) with exon | 3.17 |
| 319091 | Z45264 | | EST cluster (not in UniGene) | 3.16 |
| 335247 | | | CH22_FGENES.516_8 | 3.12 |
| 324945 | AA088768 | | EST cluster (not in UniGene) | 3.1 |
| 319468 | R06504 | | EST cluster (not in UniGene) | 3.09 |
| 301635 | AI590720 | Hs.192682 | ESTs; Weakly similar to ZINC FINGER PROT | 3.08 |
| 321215 | AW378128 | Hs.120243 | ESTs; Weakly similar to CGI-56 protein [| 3.04 |
| 328507 | | | CH.07_hs g 5868473 | 3.03 |
| 330266 | | | CH.05_p2 g 58671885 | 3.02 |
| 326249 | | | CH.17_hs g 5867263 | 3.01 |
| 325649 | | | CH.14_hs g 5888011 | 2.99 |
| 304575 | AA496437 | | EST singleton (not in UniGene) with exon | 2.98 |
| 304559 | AA488050 | | EST singleton (not in UniGene) with exon | 2.97 |
| 338412 | | | CH22_EM:AC005500.GENSCAN.341-25 | 2.96 |
| 308707 | AI769997 | | EST singleton (not in UniGene) with exon | 2.95 |
| 313027 | N34307 | Hs.184003 | ESTs; Weakly similar to !!!! ALU SUBFAMI | 2.95 |
| 306590 | AI000246 | | EST singleton (not in UniGene) with exon | 2.95 |
| 306183 | AA922622 | | EST singleton (not in UniGene) with exon | 2.94 |
| 308611 | AI735372 | Hs.203820 | EST; Moderately similar to TRANSLATIONAL | 2.94 |
| 332454 | T63265 | Hs.11186 | ESTs; Weakly similar to transformation-r | 2.94 |

| | | | | | |
|--------|----------|-----------|--|------------|------|
| 330061 | | CH.17_p2 | gi 6721261 | 2.94 | |
| 317671 | AW138139 | Hs.244598 | ESTs | 2.93 | |
| 338705 | | | CH22_EM:AC005500.GENSCAN.480-4 | 2.93 | |
| 333737 | | | CH22_FGENES.261_1 | 2.9 | |
| 337756 | | | CH22_EM:AC000097.GENSCAN.109-3 | 2.9 | |
| 333572 | | | CH22_FGENES.189_1 | 2.89 | |
| 335349 | | | CH22_FGENES.539_2 | 2.89 | |
| 328835 | | | CH.07_hs | gi 5868339 | 2.89 |
| 319886 | AA984628 | | EST cluster (not in UniGene) | 2.88 | |
| 311247 | AI655313 | Hs.197692 | ESTs | 2.87 | |
| 303887 | R72672 | Hs.193484 | ESTs; Weakly similar to Similarity with | 2.86 | |
| 337564 | | | CH22_C65E1.GENSCAN.1-7 | 2.85 | |
| 333225 | | | CH22_FGENES.107_3 | 2.84 | |
| 314938 | AA515635 | | EST cluster (not in UniGene) | 2.83 | |
| 305803 | AA846052 | | EST singleton (not in UniGene) with exon | 2.83 | |
| 305264 | AA579505 | | EST singleton (not in UniGene) with exon | 2.83 | |
| 332646 | AA386284 | Hs.5337 | isocitrate dehydrogenase 2 (NADP+); mito | 2.81 | |
| 338508 | | | CH22_EM:AC005500.GENSCAN.391-1 | 2.81 | |
| 308097 | AI475411 | | EST singleton (not in UniGene) with exon | 2.81 | |
| 301130 | AW194167 | Hs.149418 | ESTs; Weakly similar to salivary proline | 2.8 | |
| 325571 | | | CH.12_hs | gi 5552439 | 2.8 |
| 307054 | AI148181 | Hs.176835 | EST | 2.8 | |
| 337456 | | | CH22_FGENES.777-2 | 2.79 | |
| 317870 | AI797066 | Hs.201995 | ESTs | 2.79 | |
| 303171 | AA065003 | Hs.64179 | hypothetical protein | 2.78 | |
| 333717 | | | CH22_FGENES.253_3 | 2.76 | |
| 303778 | AW505368 | | EST cluster (not in UniGene) with exon h | 2.76 | |
| 304918 | AA602697 | | EST singleton (not in UniGene) with exon | 2.76 | |
| 319373 | R00371 | | EST cluster (not in UniGene) | 2.75 | |
| 335072 | | | CH22_FGENES.685_4 | 2.74 | |
| 306023 | AA897764 | | EST singleton (not in UniGene) with exon | 2.74 | |
| 336127 | | | CH22_FGENES.701_15 | 2.74 | |
| 337355 | | | CH22_FGENES.728-1 | 2.73 | |
| 337885 | | | CH22_EM:AC005500.GENSCAN.54-3 | 2.73 | |
| 308506 | AI686791 | Hs.119598 | ribosomal protein L3 | 2.73 | |
| 300629 | AA152119 | Hs.155101 | ATP synthase; H+ transporting; mitochond | 2.73 | |
| 333043 | | | CH22_FGENES.70_4 | 2.72 | |
| 327736 | | | CH.05_hs | gi 5867940 | 2.72 |
| 333007 | | | CH22_FGENES.60_4 | 2.72 | |
| 321966 | AL122111 | | EST cluster (not in UniGene) | 2.72 | |
| 323179 | AW452576 | Hs.156875 | ESTs | 2.72 | |
| 332459 | AA609625 | Hs.112933 | Homo sapiens Tax interaction protein 40 | 2.71 | |
| 326224 | | | CH.17_hs | gi 5867230 | 2.71 |
| 329114 | | | CH.X_hs | gi 5868650 | 2.7 |
| 333577 | | | CH22_FGENES.196_2 | 2.69 | |
| 300413 | AW090347 | Hs.243443 | ESTs | 2.67 | |
| 304055 | R07994 | | EST singleton (not in UniGene) with exon | 2.67 | |
| 301013 | AI935304 | Hs.125262 | DKFZP586G1624 protein | 2.67 | |
| 337848 | | | CH22_EM:AC005500.GENSCAN.33-1 | 2.66 | |
| 327946 | | | CH.06_hs | gi 5868206 | 2.66 |
| 308380 | AA937573 | | EST singleton (not in UniGene) with exon | 2.66 | |
| 331071 | R01646 | Hs.200538 | ESTs | 2.65 | |
| 304841 | AA587541 | | EST singleton (not in UniGene) with exon | 2.65 | |
| 301321 | AI860987 | Hs.189097 | ESTs | 2.65 | |
| 311280 | AI767957 | Hs.197737 | ESTs; Weakly similar to Y38A8.1 gene pro | 2.65 | |
| 338843 | | | CH22_DJ246D7.GENSCAN.8-1 | 2.64 | |
| 335720 | | | CH22_FGENES.599_23 | 2.64 | |
| 333670 | | | CH22_FGENES.245_4 | 2.64 | |
| 313588 | AI803591 | Hs.209667 | ESTs | 2.64 | |
| 335750 | | | CH22_FGENES.602_4 | 2.63 | |
| 333240 | | | CH22_FGENES.111_4 | 2.63 | |
| 332721 | R70212 | Hs.79630 | CD79A antigen (immunoglobulin-associated | 2.62 | |
| 338747 | | | CH22_EM:AC005500.GENSCAN.511-1 | 2.62 | |
| 303582 | AA377444 | | EST cluster (not in UniGene) with exon h | 2.62 | |
| 336898 | | | CH22_FGENES.330-1 | 2.62 | |
| 325835 | | | CH.16_hs | gi 5552452 | 2.62 |
| 301660 | F13112 | | EST cluster (not in UniGene) with exon h | 2.61 | |
| 335968 | | | CH22_FGENES.652_1 | 2.61 | |
| 336705 | | | CH22_FGENES.63-2 | 2.6 | |
| 309815 | AW292760 | | EST singleton (not in UniGene) with exon | 2.6 | |
| 339220 | | | CH22_FF113D11.GENSCAN.6-15 | 2.6 | |
| 308582 | AI709056 | | EST singleton (not in UniGene) with exon | 2.6 | |
| 334260 | | | CH22_FGENES.357_8 | 2.6 | |
| 309963 | AW449073 | | EST singleton (not in UniGene) with exon | 2.6 | |
| 300178 | AI282665 | Hs.166969 | ESTs | 2.59 | |
| 335690 | | | CH22_FGENES.596_5 | 2.59 | |

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|--------|---------------|-----------|--|------|--|
| 308127 | AJ492187 | | EST singleton (not in UniGene) with exon | 2.59 | |
| 337835 | | | CH22_EM:AC005500.GENSCAN.22-4 | 2.58 | |
| 333251 | | | CH22_FGENES.116_3 | 2.58 | |
| 330319 | | | CH.08_p2 g 5932415 | 2.58 | |
| 314490 | AJ758114 | Hs.197032 | ESTs | 2.57 | |
| 305934 | AA878815 | Hs.75442 | albumin | 2.57 | |
| 329665 | | | CH.14_p2 g 6272129 | 2.57 | |
| 328558 | | | CH.07_hs g 5868489 | 2.57 | |
| 336094 | | | CH22_FGENES.691_3 | 2.57 | |
| 307899 | AJ380270 | | EST singleton (not in UniGene) with exon | 2.57 | |
| 339312 | | | CH22_BA35412.GENSCAN.22-10 | 2.57 | |
| 336442 | | | CH22_FGENES.827_8 | 2.57 | |
| 317894 | R60848 | | EST cluster (not in UniGene) | 2.56 | |
| 330435 | HG2689-HT2785 | | Mucin 5b, Tracheobronchial (Gb:X74955) | 2.56 | |
| 327304 | | | CH.01_hs g 5867494 | 2.56 | |
| 308859 | AJ830787 | | EST singleton (not in UniGene) with exon | 2.55 | |
| 30224 | AJ951549 | Hs.161166 | KIAA1094 protein | 2.55 | |
| 304324 | AA137045 | | EST singleton (not in UniGene) with exon | 2.54 | |
| 338090 | | | CH22_EM:AC005500.GENSCAN.176-3 | 2.53 | |
| 334797 | | | CH22_FGENES.434_5 | 2.52 | |
| 303535 | AL043430 | | EST cluster (not in UniGene) with exon h | 2.52 | |
| 339037 | | | CH22_DA59H18.GENSCAN.26-5 | 2.52 | |
| 327846 | | | CH.05_hs g 56531962 | 2.52 | |
| 325271 | | | CH.11_hs g 5866901 | 2.52 | |
| 312385 | R4285 | Hs.215555 | ESTs | 2.51 | |
| 302816 | AJ733918 | Hs.204112 | ESTs; Weakly similar to alternatively sp | 2.51 | |
| 316941 | AW449871 | Hs.124591 | ESTs | 2.5 | |
| 300184 | AJ285912 | Hs.254515 | ESTs | 2.5 | |
| 333762 | | | CH22_FGENES.270_2 | 2.5 | |
| 317028 | AA962623 | Hs.189144 | ESTs; Weakly similar to RENAL SODIUM-DEP | 2.5 | |
| 326266 | | | CH.17_hs g 5867264 | 2.49 | |
| 326005 | | | CH.16_hs g 5867112 | 2.49 | |
| 301971 | AJ003125 | Hs.120330 | a disintegrin-like and metalloprotease (| 2.48 | |
| 326539 | | | CH.19_hs g 5867307 | 2.48 | |
| 338896 | | | CH22_DJ3210.GENSCAN.9-4 | 2.48 | |
| 306773 | AJ040750 | | EST singleton (not in UniGene) with exon | 2.47 | |
| 336279 | | | CH22_FGENES.763_3 | 2.47 | |
| 321017 | AL050345 | Hs.227637 | hypothetical protein | 2.47 | |
| 306090 | AA908609 | | EST singleton (not in UniGene) with exon | 2.47 | |
| 333216 | | | CH22_FGENES.104_8 | 2.46 | |
| 338593 | | | CH22_EM:AC005500.GENSCAN.435-2 | 2.46 | |
| 333587 | | | CH22_FGENES.205_2 | 2.46 | |
| 300396 | AW295466 | Hs.232051 | ESTs | 2.45 | |
| 304693 | AA554263 | | EST singleton (not in UniGene) with exon | 2.45 | |
| 338934 | | | CH22_DJ3210.GENSCAN.18-2 | 2.45 | |
| 325751 | | | CH.14_hs g 56582474 | 2.45 | |
| 334137 | | | CH22_FGENES.337_1 | 2.45 | |
| 333581 | | | CH22_FGENES.200_1 | 2.45 | |
| 302083 | AJ422807 | Hs.134012 | C1q-related factor | 2.44 | |
| 307318 | AJ208577 | | EST singleton (not in UniGene) with exon | 2.44 | |
| 302181 | AW374284 | Hs.157732 | Homo sapiens chromosome 19; cosmid R2689 | 2.44 | |
| 337425 | | | CH22_FGENES.761-1 | 2.44 | |
| 336227 | | | CH22_FGENES.730_2 | 2.44 | |
| 314657 | AI015953 | Hs.125265 | ESTs | 2.44 | |
| 338529 | | | CH22_EM:AC005500.GENSCAN.398-10 | 2.44 | |
| 333680 | | | CH22_FGENES.247_7 | 2.43 | |
| 324834 | AJ003258 | Hs.250891 | ESTs | 2.43 | |
| 305093 | AA642917 | | EST singleton (not in UniGene) with exon | 2.43 | |
| 335787 | | | CH22_FGENES.611_3 | 2.43 | |
| 311704 | AI655206 | Hs.121512 | ESTs; Moderately similar to kinesin like | 2.43 | |
| 329382 | | | CH.X_hs g 5868868 | 2.42 | |
| 334785 | | | CH22_FGENES.432_10 | 2.42 | |
| 330130 | | | CH.21_p2 g 5602196 | 2.42 | |
| 327206 | | | CH.01_hs g 5867447 | 2.41 | |
| 319235 | F11330 | Hs.177633 | ESTs | 2.41 | |
| 334691 | | | CH22_FGENES.420_4 | 2.4 | |
| 327610 | | | CH.04_hs g 5867868 | 2.4 | |
| 327646 | | | CH.04_hs g 5867894 | 2.4 | |
| 337093 | | | CH22_FGENES.465-18 | 2.4 | |
| 335081 | | | CH22_FGENES.488_4 | 2.4 | |
| 333576 | | | CH22_FGENES.193_2 | 2.4 | |
| 337604 | | | CH22_C20H12.GENSCAN.16-5 | 2.4 | |
| 329879 | | | CH.15_p2 g 56466518 | 2.4 | |
| 328444 | | | CH.07_hs g 5868420 | 2.39 | |
| 335700 | | | CH22_FGENES.598_1 | 2.39 | |
| 331255 | Z41009 | Hs.21446 | ESTs; Weakly similar to HYPOTHETICAL PRO | 2.39 | |

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|--------|----------|--|------|
| 327927 | | CH.06_hs g 5868173 | 2.39 |
| 334354 | | CH22_FGENES.377_1 | 2.39 |
| 308517 | AI689279 | EST singleton (not in UniGene) with exon | 2.39 |
| 303669 | AW499648 | Hs.233750 copine V | 2.39 |
| 333648 | | CH22_FGENES.237_2 | 2.38 |
| 318318 | AI653893 | Hs.174463 ESTs; Weakly similar to alpha3b subunit | 2.38 |
| 338336 | | CH22_EM:AC005500.GENSCAN.310-8 | 2.38 |
| 304125 | H40976 | EST singleton (not in UniGene) with exon | 2.38 |
| 304983 | AA617786 | EST singleton (not in UniGene) with exon | 2.38 |
| 334935 | | CH22_FGENES.484_3 | 2.38 |
| 314326 | AW170057 | Hs.133179 ESTs | 2.38 |
| 330406 | D49490 | Hs.76901 for protein disulfide isomerase-related | 2.38 |
| 307646 | AI302236 | EST singleton (not in UniGene) with exon | 2.38 |
| 338911 | | CH22_DJ32 10.GENSCAN.11-3 | 2.38 |
| 319952 | T79532 | Hs.225725 ESTs; Moderately similar to CGI-101 prot | 2.37 |
| 336878 | | CH22_FGENES.318-5 | 2.37 |
| 338140 | | CH22_EM:AC005500.GENSCAN.203-6 | 2.37 |
| 300564 | AI383878 | Hs.225588 ESTs | 2.37 |
| 304635 | AA523976 | EST singleton (not in UniGene) with exon | 2.37 |
| 334091 | | CH22_FGENES.327_47 | 2.37 |
| 336328 | | CH22_FGENES.812_7 | 2.37 |
| 325310 | | CH.11_hs g 5866864 | 2.37 |
| 338043 | | CH22_EM:AC005500.GENSCAN.153-2 | 2.37 |
| 307090 | AI161024 | EST singleton (not in UniGene) with exon | 2.37 |
| 335768 | | CH22_FGENES.607_2 | 2.37 |
| 334989 | | CH22_FGENES.466_2 | 2.37 |
| 333640 | | CH22_FGENES.230_2 | 2.36 |
| 330002 | | CH.16_p2 g 5623963 | 2.36 |
| 338829 | | CH22_DJ246D7.GENSCAN.5-12 | 2.36 |
| 323808 | AW250114 | EST cluster (not in UniGene) | 2.36 |
| 327755 | | CH.05_hs g 5867955 | 2.35 |
| 306426 | AA975039 | EST singleton (not in UniGene) with exon | 2.35 |
| 336481 | | CH22_FGENES.830_1 | 2.35 |
| 335163 | | CH22_FGENES.502_7 | 2.35 |
| 322012 | AL137357 | EST cluster (not in UniGene) | 2.35 |
| 337345 | | CH22_FGENES.723-1 | 2.35 |
| 334625 | | CH22_FGENES.414_3 | 2.35 |
| 320957 | AI878933 | EST cluster (not in UniGene) | 2.35 |
| 334915 | | CH22_FGENES.457_4 | 2.35 |
| 336295 | | CH22_FGENES.787_1 | 2.35 |
| 321556 | N46402 | Hs.14570 ESTs | 2.35 |
| 338491 | | CH22_EM:AC005500.GENSCAN.385-2 | 2.35 |
| 335517 | | CH22_FGENES.571_34 | 2.34 |
| 330639 | X90872 | Hs.75854 SULT1C sulfotransferase | 2.34 |
| 310383 | AI263102 | Hs.145596 ESTs | 2.34 |
| 331526 | N49957 | Hs.46624 ESTs | 2.34 |
| 334396 | | CH22_FGENES.381_2 | 2.34 |
| 332993 | | CH22_FGENES.57_2 | 2.34 |
| 327487 | | CH.02_hs g 5867785 | 2.34 |
| 335920 | | CH22_FGENES.836_16 | 2.33 |
| 336463 | | CH22_FGENES.829_22 | 2.33 |
| 319000 | Z44318 | EST cluster (not in UniGene) | 2.33 |
| 332992 | | CH22_FGENES.57_1 | 2.33 |
| 332920 | | CH22_FGENES.37_6 | 2.33 |
| 337590 | | CH22_C20H12.GENSCAN.6-5 | 2.33 |
| 327059 | | CH.21_hs g 5531965 | 2.33 |
| 334399 | | CH22_FGENES.382_5 | 2.33 |
| 300982 | AA837754 | EST cluster (not in UniGene) with exon h | 2.32 |
| 327430 | | CH.02_hs g 5867754 | 2.32 |
| 326808 | | CH.20_hs g 56682504 | 2.32 |
| 309324 | AW015373 | EST singleton (not in UniGene) with exon | 2.32 |
| 329779 | | CH.14_p2 g 5002090 | 2.32 |
| 330492 | M25809 | Hs.64173 ATPase; H+ transporting; lysosomal (vacu | 2.31 |
| 330080 | | CH.19_p2 g 5015314 | 2.31 |
| 334342 | | CH22_FGENES.375_20 | 2.31 |
| 336306 | | CH22_FGENES.793_5 | 2.31 |
| 336400 | | CH22_FGENES.823_15 | 2.31 |
| 323735 | AA323714 | EST cluster (not in UniGene) | 2.31 |
| 334496 | | CH22_FGENES.397_12 | 2.31 |
| 336075 | | CH22_FGENES.687_1 | 2.31 |
| 335566 | | CH22_FGENES.580_1 | 2.31 |
| 337657 | | CH22_EM:AC000097.GENSCAN.32-9 | 2.31 |
| 327816 | | CH.05_hs g 5867958 | 2.3 |
| 308465 | AI672480 | EST singleton (not in UniGene) with exon | 2.3 |
| 330112 | | CH.19_p2 g 5015238 | 2.3 |
| 304465 | AA421948 | EST singleton (not in UniGene) with exon | 2.3 |

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| 308449 | AI660854 | | EST singleton (not in UniGene) with exon | 2.3 | |
| 328171 | | | CH.06_hs gj 5868071 | 2.3 | |
| 328271 | | | CH.06_hs gj 5552415 | 2.3 | |
| 328803 | | | CH.07_hs gj 6004475 | 2.3 | |
| 330063 | | | CH.19_p2 gj 5165044 | 2.29 | |
| 312281 | H11643 | | EST cluster (not in UniGene) | 2.29 | |
| 328974 | | | CH.09_hs gj 5868520 | 2.29 | |
| 333859 | | | CH22_FGENES.290_18 | 2.29 | |
| 326253 | | | CH.17_hs gj 5887263 | 2.29 | |
| 325703 | | | CH.14_hs gj 5867028 | 2.29 | |
| 338925 | | | CH22_DJ32I10.GENSCAN.14-3 | 2.29 | |
| 328552 | | | CH.07_hs gj 5868489 | 2.29 | |
| 337244 | | | CH22_FGENES.646-8 | 2.29 | |
| 314770 | AJ732722 | Hs.187694 | ESTs | 2.29 | |
| 324560 | AW502208 | | EST cluster (not in UniGene) | 2.29 | |
| 310603 | AW376860 | Hs.156398 | ESTs | 2.29 | |
| 337363 | | | CH22_FGENES.733-2 | 2.29 | |
| 308015 | AI440174 | Hs.228907 | EST; Weakly similar to GUANINE NUCLEOTID | 2.28 | |
| 309206 | AI961962 | | EST singleton (not in UniGene) with exon | 2.28 | |
| 337455 | | | CH22_FGENES.777-1 | 2.28 | |
| 327605 | | | CH.03_hs gj 6004463 | 2.28 | |
| 301611 | W22172 | Hs.59038 | ESTs | 2.28 | |
| 317222 | AI206964 | Hs.130051 | ESTs | 2.28 | |
| 338278 | | | CH22_EM:AC005500.GENSCAN.290-3 | 2.28 | |
| 337291 | | | CH22_FGENES.673-2 | 2.27 | |
| 337913 | | | CH22_EM:AC005500.GENSCAN.59-10 | 2.27 | |
| 306406 | AA971973 | | EST singleton (not in UniGene) with exon | 2.27 | |
| 332947 | | | CH22_FGENES.47_10 | 2.27 | |
| 321763 | W01148 | | EST cluster (not in UniGene) | 2.27 | |
| 304424 | AA283494 | | EST singleton (not in UniGene) with exon | 2.27 | |
| 303782 | T64737 | | EST cluster (not in UniGene) with exon h | 2.27 | |
| 326943 | | | CH.21_hs gj 6004446 | 2.27 | |
| 324977 | R14439 | Hs.209194 | ESTs | 2.27 | |
| 325480 | | | CH.12_hs gj 5866957 | 2.27 | |
| 327743 | | | CH.05_hs gj 5867944 | 2.27 | |
| 333221 | | | CH22_FGENES.105_1 | 2.26 | |
| 336498 | | | CH22_FGENES.833_3 | 2.26 | |
| 321583 | H84421 | | EST cluster (not in UniGene) | 2.26 | |
| 334191 | | | CH22_FGENES.352_6 | 2.26 | |
| 327089 | | | CH.21_hs gj 6531965 | 2.26 | |
| 310001 | F18939 | Hs.153827 | ESTs | 2.26 | |
| 304056 | R08577 | | EST singleton (not in UniGene) with exon | 2.25 | |
| 324700 | AW504745 | Hs.103913 | ESTs; Moderately similar to !!! ALU SUB | 2.25 | |
| 330637 | X86371 | Hs.95659 | lethal giant larvae (Drosophila) homolog | 2.25 | |
| 307642 | AI302103 | | EST singleton (not in UniGene) with exon | 2.25 | |
| 336985 | | | CH22_FGENES.402-6 | 2.25 | |
| 334425 | | | CH22_FGENES.384_13 | 2.25 | |
| 321216 | AI078042 | Hs.126691 | ESTs | 2.25 | |
| 315785 | AW205946 | Hs.150319 | ESTs | 2.25 | |
| 305809 | AA853998 | Hs.124580 | EST | 2.25 | |
| 331334 | AA284658 | Hs.89134 | ESTs | 2.25 | |
| 317131 | AI991125 | Hs.189109 | ESTs | 2.25 | |
| 334216 | | | CH22_FGENES.358_1 | 2.24 | |
| 330330 | | | CH.08_p2 gj 5670267 | 2.24 | |
| 326923 | | | CH.21_hs gj 6456782 | 2.24 | |
| 333774 | | | CH22_FGENES.272_5 | 2.24 | |
| 324311 | AA443061 | Hs.202520 | ESTs | 2.24 | |
| 338551 | | | CH22_EM:AC005500.GENSCAN.413-2 | 2.24 | |
| 305716 | AI024916 | Hs.251354 | ESTs | 2.24 | |
| 337689 | | | CH22_EM:AC000097.GENSCAN.77-5 | 2.24 | |
| 300079 | AI192520 | Hs.147178 | EST | 2.23 | |
| 334617 | | | CH22_FGENES.411_16 | 2.23 | |
| 336890 | | | CH22_FGENES.326-10 | 2.23 | |
| 334495 | | | CH22_FGENES.397_10 | 2.23 | |
| 327301 | | | CH.01_hs gj 5867493 | 2.23 | |
| 337856 | | | CH22_EM:AC005500.GENSCAN.41-3 | 2.23 | |
| 307072 | AI150424 | Hs.146817 | EST | - 2.23 | |
| 330515 | M85247 | | H.sapiens dopamine D1A receptor gene, co | 2.22 | |
| 325943 | | | CH.16_hs gj 5867138 | 2.22 | |
| 338947 | | | CH22_DJ32I10.GENSCAN.21-4 | 2.22 | |
| 317465 | AW197361 | Hs.131360 | ESTs | 2.22 | |
| 332458 | M33493 | Hs.184504 | tryptase, alpha | 2.22 | |
| 333195 | | | CH22_FGENES.98_17 | 2.22 | |
| 304837 | AA587139 | | EST singleton (not in UniGene) with exon | 2.22 | |
| 307602 | AI288843 | Hs.231239 | EST | 2.22 | |
| 337078 | | | CH22_FGENES.457-1 | 2.22 | |

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| 335862 | | CH22_FGENES.629_7 | 2.22 | |
| 301979 | L28168 | Hs.121495 | potassium voltage-gated channel; Isk-rel | 2.22 |
| 335668 | | CH22_FGENES.590_19 | 2.22 | |
| 305068 | AA639618 | | EST singleton (not in UniGene) with exon | 2.21 |
| 329034 | | CH.X_hs gj 5868561 | 2.21 | |
| 318403 | AI131241 | Hs.143234 | ESTs | 2.21 |
| 328058 | | CH.06_hs gj 5902482 | 2.21 | |
| 335513 | | CH22_FGENES.571_28 | 2.21 | |
| 330803 | AA004699 | Hs.150580 | putative translation initiation factor | 2.21 |
| 331427 | H54764 | Hs.237339 | EST | 2.21 |
| 338973 | | CH22_DJ32110.GENSCAN.27-6 | 2.2 | |
| 336723 | | CH22_FGENES.85-3 | 2.2 | |
| 327290 | | CH.01_hs gj 5867483 | 2.2 | |
| 337240 | | CH22_FGENES.644-1 | 2.2 | |
| 306201 | AA926818 | | EST singleton (not in UniGene) with exon | 2.2 |
| 303659 | AA868464 | Hs.126263 | ESTs; Highly similar to FIBRILLARIN [H.s | 2.2 |
| 334517 | | CH22_FGENES.399_7 | 2.2 | |
| 334189 | | CH22_FGENES.352_4 | 2.2 | |
| 335199 | | CH22_FGENES.508_8 | 2.2 | |
| 333705 | | CH22_FGENES.250_19 | 2.2 | |
| 305794 | AA845324 | | EST singleton (not in UniGene) with exon | 2.2 |
| 303273 | AA316069 | | EST cluster (not in UniGene) with exon h | 2.2 |
| 313384 | W85694 | Hs.118335 | ESTs | 2.2 |
| 329158 | | CH.X_hs gj 5868687 | 2.2 | |
| 337551 | | CH22_FGENES.847-8 | 2.2 | |
| 328792 | | CH.07_hs gj 5868309 | 2.2 | |
| 303737 | AW502711 | | EST cluster (not in UniGene) with exon h | 2.19 |
| 324529 | AW502486 | | EST cluster (not in UniGene) | 2.19 |
| 323103 | Z45529 | Hs.92030 | ESTs | 2.19 |
| 333773 | | CH22_FGENES.272_4 | 2.19 | |
| 337806 | | CH22_EM:AC005500.GENSCAN.56-19 | 2.19 | |
| 327129 | | CH.21_hs gj 6531976 | 2.19 | |
| 305710 | AA826544 | | EST singleton (not in UniGene) with exon | 2.19 |
| 335595 | | CH22_FGENES.581_34 | 2.19 | |
| 323646 | AA310926 | Hs.154412 | ESTs | 2.19 |
| 328368 | | CH.07_hs gj 5868388 | 2.19 | |
| 325802 | | CH.14_hs gj 6552451 | 2.19 | |
| 337167 | | CH22_FGENES.562-27 | 2.19 | |
| 305059 | AA635756 | | EST singleton (not in UniGene) with exon | 2.18 |
| 321445 | AW245524 | Hs.121590 | ESTs; Weakly similar to ZINC FINGER PROT | 2.18 |
| 332790 | | CH22_FGENES.2_4 | 2.18 | |
| 336750 | | CH22_FGENES.128-4 | 2.18 | |
| 310999 | AI520706 | Hs.171012 | ESTs | 2.18 |
| 329798 | | CH.14_p2_gj 6523160 | 2.18 | |
| 327012 | | CH.21_hs gj 5867664 | 2.18 | |
| 304599 | AA506638 | | EST singleton (not in UniGene) with exon | 2.18 |
| 335351 | | CH22_FGENES.539_4 | 2.18 | |
| 310661 | AI354717 | Hs.223908 | ESTs | 2.18 |
| 332791 | | CH22_FGENES.3_1 | 2.17 | |
| 333022 | | CH22_FGENES.65_1 | 2.17 | |
| 310502 | AI458973 | Hs.170422 | ESTs | 2.17 |
| 324963 | AA853440 | | EST cluster (not in UniGene) | 2.17 |
| 325275 | | CH.11_hs gj 5866902 | 2.17 | |
| 328338 | | CH.07_hs gj 5868377 | 2.17 | |
| 333063 | | CH22_FGENES.75_6 | 2.17 | |
| 308895 | AI858423 | | EST singleton (not in UniGene) with exon | 2.17 |
| 338885 | | CH22_EM:AC005500.GENSCAN.472-4 | 2.16 | |
| 325655 | | CH.14_hs gj 5867007 | 2.16 | |
| 332420 | H49570 | Hs.108074 | ESTs; Weakly similar to CEREBELLIN 1 PRE | 2.16 |
| 337216 | | CH22_FGENES.613-10 | 2.16 | |
| 335660 | | CH22_FGENES.590_11 | 2.16 | |
| 337145 | | CH22_FGENES.542-2 | 2.16 | |
| 335753 | | CH22_FGENES.604_2 | 2.16 | |
| 301766 | R02224 | | EST cluster (not in UniGene) with exon h | 2.16 |
| 303442 | AI953998 | Hs.152510 | ESTs; Weakly similar to L-SERINE DEHYDRA | 2.16 |
| 311009 | AI949701 | Hs.210589 | ESTs | 2.16 |
| 307093 | AI167606 | | EST singleton (not in UniGene) with exon | 2.16 |
| 300262 | AI874402 | Hs.170810 | ESTs | 2.16 |
| 337989 | | CH22_EM:AC005500.GENSCAN.112-7 | 2.16 | |
| 326263 | | CH.17_hs gj 5867264 | 2.16 | |
| 319402 | W21298 | | EST cluster (not in UniGene) | 2.16 |
| 321010 | Y17456 | Hs.227150 | Homo sapiens LSFR2 gene; last exon | 2.16 |
| 301706 | AI929150 | Hs.241496 | ESTs | 2.16 |
| 307412 | AI241753 | Hs.241507 | ribosomal protein S6 | 2.16 |
| 335662 | | CH22_FGENES.590_13 | 2.15 | |
| 332480 | AA092932 | Hs.12570 | tubulin-specific chaperone d | 2.15 |

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| 329273 | CH.X_hs gl 5868762 | 2.15 |
| 339383 | CH22_BA232E17.GENSCAN.3-20 | 2.15 |
| 332795 | CH22_FGENES.5_1 | 2.15 |
| 335227 | CH22_FGENES.513_13 | 2.15 |
| 326925 | CH.21_hs gl 6456782 | 2.15 |
| 332403 AA424199 Hs.106529 | ESTs; Highly similar to CGI-65 protein [| 2.15 |
| 317786 AI859605 Hs.155686 | ESTs | 2.15 |
| 326582 | CH.19_hs gl 5867318 | 2.15 |
| 336494 | CH22_FGENES.832_11 | 2.15 |
| 329656 | CH.14_p2 gl 6448516 | 2.15 |
| 307581 AI284415 | EST singleton (not in UniGene) with exon | 2.15 |
| 335670 | CH22_FGENES.591_2 | 2.14 |
| 332452 AA040369 Hs.11170 | SYT interacting protein | 2.14 |
| 309387 AW079943 Hs.156110 | Immunoglobulin kappa variable 1D-8 | 2.14 |
| 308427 AI652677 Hs.195055 | EST | 2.14 |
| 322027 NM_004551 | EST cluster (not in UniGene) | 2.14 |
| 301693 Z45023 | EST cluster (not in UniGene) with exon h | 2.14 |
| 334308 | CH22_FGENES.373_11 | 2.14 |
| 301131 AW134518 Hs.131807 | ESTs | 2.13 |
| 338495 | CH22_EMAC005500.GENSCAN.387-1 | 2.13 |
| 329600 | CH.10_p2 gl 3962481 | 2.13 |
| 307980 AI431696 | EST singleton (not in UniGene) with exon | 2.13 |
| 337260 | CH22_FGENES.652-15 | 2.13 |
| 304655 AA527887 | EST singleton (not in UniGene) with exon | 2.13 |
| 303141 AF195951 | EST cluster (not in UniGene) with exon h | 2.13 |
| 327957 | CH.06_hs gl 5868210 | 2.13 |
| 334317 | CH22_FGENES.374_1 | 2.13 |
| 302870 AF011407 | EST cluster (not in UniGene) with exon h | 2.13 |
| 333806 | CH22_FGENES.278_2 | 2.13 |
| 329947 | CH.16_p2 gl 5540101 | 2.13 |
| 309602 AW182523 | EST singleton (not in UniGene) with exon | 2.13 |
| 322790 AI700273 Hs.122162 | ESTs; Weakly similar to KIAA0557 protein | 2.13 |
| 337706 | CH22_EMAC000097.GENSCAN.87-11 | 2.13 |
| 306894 AI092731 | EST singleton (not in UniGene) with exon | 2.13 |
| 325530 | CH.12_hs gl 5625289 | 2.12 |
| 321087 AL110227 Hs.241533 | Homo sapiens mRNA; cDNA DKFZp434J194 (fr | 2.12 |
| 309853 AW298169 Hs.57553 | tousled-like kinase 2 | 2.12 |
| 326822 | CH.20_hs gl 5117831 | 2.12 |
| 328776 | CH.07_hs gl 5868309 | 2.12 |
| 335112 | CH22_FGENES.494_20 | 2.12 |
| 334564 | CH22_FGENES.405_4 | 2.12 |
| 333455 | CH22_FGENES.157_4 | 2.12 |
| 317395 R55044 Hs.124130 | ESTs | 2.12 |
| 334221 | CH22_FGENES.360_1 | 2.12 |
| 331374 AA442134 Hs.70573 | ESTs; Weakly similar to HINT PROTEIN [H. | 2.12 |
| 304473 AA428343 Hs.140 | immunoglobulin gamma 3 (Gm marker) | 2.12 |
| 328907 | CH.08_hs gl 5868493 | 2.12 |
| 319448 R05539 Hs.108738 | ESTs | 2.12 |
| 333676 | CH22_FGENES.247_3 | 2.12 |
| 324767 AA630931 Hs.34348 | Homo sapiens mRNA; cDNA DKFZp434P0235 (f | 2.12 |
| 318585 Z43405 | EST cluster (not in UniGene) | 2.12 |
| 331732 AA251192 Hs.177708 | ESTs | 2.12 |
| 329553 | CH.10_p2 gl 3962492 | 2.12 |
| 336910 | CH22_FGENES.343-6 | 2.12 |
| 326959 | CH.21_hs gl 6469836 | 2.12 |
| 305417 AA725228 | EST singleton (not in UniGene) with exon | 2.11 |
| 301573 AI150328 Hs.226402 | ESTs; Weakly similar to mitochondrial ci | 2.11 |
| 326935 | CH.21_hs gl 6004446 | 2.11 |
| 335176 | CH22_FGENES.504_6 | 2.11 |
| 337210 | CH22_FGENES.603-5 | 2.11 |
| 311284 AW027025 Hs.239262 | ESTs | 2.11 |
| 330240 | CH.05_p2 gl 6671858 | 2.11 |
| 327463 | CH.02_hs gl 6004455 | 2.11 |
| 332938 | CH22_FGENES.41_3 | 2.11 |
| 332785 | CH22_FGENES.1_1 | 2.11 |
| 301035 AI358105 Hs.123164 | ESTs | 2.1 |
| 305712 AA826701 | EST singleton (not in UniGene) with exon | 2.1 |
| 318651 AW003150 Hs.240165 | ESTs | 2.1 |
| 302753 M74299 | EST cluster (not in UniGene) with exon h | 2.1 |
| 334635 | CH22_FGENES.417_2 | 2.1 |
| 319447 AA456745 | EST cluster (not in UniGene) | 2.1 |
| 301204 AW008544 Hs.239994 | ESTs | 2.1 |
| 333950 | CH22_FGENES.303_6 | 2.1 |
| 325947 | CH.16_hs gl 5867138 | 2.1 |
| 337683 | CH22_EMAC000097.GENSCAN.76-1 | 2.1 |
| 328962 | CH.08_hs gl 5655775 | 2.1 |

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| 336655 | | CH22_FGENES.34-3 | 2.1 |
| 336596 | | CH22_FGENES.163_2 | 2.1 |
| 330486 | M13755 | Hs.833 interferon-stimulated protein; 15 kDa | 2.1 |
| 314356 | AA531607 | Hs.125143 ESTs | 2.09 |
| 314976 | AA524725 | Hs.162108 ESTs | 2.09 |
| 336650 | | CH22_FGENES.29-6 | 2.09 |
| 339026 | | CH22_DA59H18.GENSCAN.22-6 | 2.09 |
| 302395 | AW297357 | Hs.114606 ESTs | 2.09 |
| 323280 | AI910263 | EST cluster (not in UniGene) | 2.09 |
| 338857 | | CH22_DJ32I10.GENSCAN.1-1 | 2.09 |
| 335374 | | CH22_FGENES.543_12 | 2.09 |
| 308766 | AI808510 | EST singleton (not in UniGene) with exon | 2.09 |
| 331027 | N48584 | Hs.6168 KIAA0703 gene product | 2.09 |
| 337853 | | CH22_EM:AC005500.GENSCAN.37-1 | 2.09 |
| 302498 | NM_002991 | EST cluster (not in UniGene) with exon h | 2.09 |
| 312607 | AI337440 | Hs.169375 ESTs | 2.09 |
| 314309 | Z44049 | Hs.184352 ESTs; Weakly similar to cDNA EST EMBL:D3 | 2.09 |
| 311695 | AI142078 | Hs.135562 ESTs | 2.09 |
| 333280 | | CH22_FGENES.126_2 | 2.09 |
| 333518 | | CH22_FGENES.173_3 | 2.09 |
| 337199 | | CH22_FGENES.583-11 | 2.09 |
| 337819 | | CH22_EM:AC005500.GENSCAN.13-9 | 2.08 |
| 300546 | AA214450 | Hs.250913 ESTs | 2.08 |
| 322577 | AA354452 | Hs.59075 ESTs; Weakly similar to WD40 protein Cla | 2.08 |
| 336028 | | CH22_FGENES.572_1 | 2.08 |
| 300238 | AI394673 | Hs.254030 ESTs | 2.08 |
| 307429 | AI243573 | EST singleton (not in UniGene) with exon | 2.08 |
| 326444 | | CH.19_hs g 5867385 | 2.08 |
| 310641 | AI345597 | Hs.254727 ESTs | 2.08 |
| 337633 | | CH22_C20H12.GENSCAN.32-1 | 2.08 |
| 336008 | | CH22_FGENES.668_6 | 2.08 |
| 339030 | | CH22_DA59H18.GENSCAN.24-1 | 2.08 |
| 333952 | | CH22_FGENES.303_8 | 2.08 |
| 329149 | | CH.X_hs g 5868685 | 2.08 |
| 335192 | | CH22_FGENES.507_7 | 2.08 |
| 308225 | AI557713 | Hs.177592 ribosomal protein; large; P1 | 2.08 |
| 330519 | M94172 | Hs.69949 calcium channel; voltage-dependent; L ty | 2.08 |
| 331809 | AA402482 | Hs.97312 ESTs | 2.07 |
| 324837 | AJ003669 | Hs.246171 ESTs | 2.07 |
| 332608 | D00749 | Hs.36972 CD7 antigen (p41) | 2.07 |
| 327291 | | CH.01_hs g 5867483 | 2.07 |
| 315936 | AW069807 | Hs.247094 ESTs; Moderately similar to !!!! ALU SUB | 2.07 |
| 317917 | AI143593 | Hs.129419 ESTs | 2.07 |
| 328674 | | CH.07_hs g 5868254 | 2.07 |
| 338654 | | CH22_EM:AC005500.GENSCAN.460-55 | 2.07 |
| 320828 | AJ012590 | Hs.194728 hexose-6-phosphate dehydrogenase (glucos | 2.07 |
| 337896 | | CH22_EM:AC005500.GENSCAN.58-3 | 2.07 |
| 335310 | | CH22_FGENES.532_3 | 2.07 |
| 300076 | AW074835 | Hs.145223 ESTs | 2.07 |
| 303588 | AI046182 | EST cluster (not in UniGene) with exon h | 2.07 |
| 328648 | | CH.07_hs g 5381921 | 2.07 |
| 318723 | C18060 | EST cluster (not in UniGene) | 2.07 |
| 335352 | | CH22_FGENES.539_5 | 2.07 |
| 339316 | | CH22_BA35412.GENSCAN.22-15 | 2.06 |
| 335873 | | CH22_FGENES.631_1 | 2.06 |
| 335261 | | CH22_FGENES.520_2 | 2.06 |
| 322032 | AL079807 | EST cluster (not in UniGene) | 2.06 |
| 308771 | AI809301 | EST singleton (not in UniGene) with exon | 2.06 |
| 310024 | AI252661 | Hs.145224 ESTs | 2.06 |
| 320555 | R36212 | Hs.235534 ESTs | 2.06 |
| 319314 | T74062 | EST cluster (not in UniGene) | 2.06 |
| 334642 | | CH22_FGENES.417_9 | 2.06 |
| 335767 | | CH22_FGENES.607_1 | 2.06 |
| 336159 | | CH22_FGENES.707_3 | 2.06 |
| 336358 | | CH22_FGENES.818_1 | 2.06 |
| 334687 | | CH22_FGENES.419_12 | 2.06 |
| 339389 | | CH22_BA232E17.GENSCAN.4-7 | 2.06 |
| 335898 | | CH22_FGENES.635_6 | 2.06 |
| 328847 | | CH.07_hs g 5381920 | 2.06 |
| 313431 | W91884 | EST cluster (not in UniGene) | 2.06 |
| 313270 | AI374993 | Hs.159611 ESTs | 2.06 |
| 339211 | | CH22_FF113D11.GENSCAN.6-6 | 2.06 |
| 333860 | | CH22_FGENES.290_19 | 2.06 |
| 308852 | AI868157 | Hs.224226 EST | 2.06 |
| 305471 | AA743947 | EST singleton (not in UniGene) with exon | 2.06 |
| 300619 | AA991438 | Hs.233293 ESTs | 2.06 |

| | | | | |
|--------|----------|-----------|---|------|
| 302962 | AI693349 | Hs.228981 | EST | 2.06 |
| 332446 | AA112799 | Hs.238756 | ESTs; Weakly similar to unknown [H.sapiens] | 2.06 |
| 334972 | | | CH22_FGENES.468_2 | 2.05 |
| 330195 | | | CH.05_p2 g j5165140 | 2.05 |
| 304754 | AA579795 | | EST singleton (not in UniGene) with exon h | 2.05 |
| 309726 | AW248521 | Hs.195188 | glyceraldehyde-3-phosphate dehydrogenase | 2.05 |
| 333939 | | | CH22_FGENES.301_5 | 2.05 |
| 304836 | AA587008 | | EST singleton (not in UniGene) with exon h | 2.05 |
| 302087 | AA324163 | | EST cluster (not in UniGene) with exon h | 2.05 |
| 308424 | AI650714 | | EST singleton (not in UniGene) with exon h | 2.05 |
| 304347 | AA176914 | | EST singleton (not in UniGene) with exon h | 2.05 |
| 333141 | | | CH22_FGENES.85_1 | 2.05 |
| 310573 | AW292180 | Hs.156142 | ESTs | 2.05 |
| 337565 | | | CH22_C65E1.GENSCAN.1-11 | 2.05 |
| 304295 | AA084082 | | EST singleton (not in UniGene) with exon h | 2.05 |
| 326624 | | | CH.20_hs g j5867553 | 2.05 |
| 326443 | | | CH.19_hs g j5867385 | 2.04 |
| 339012 | | | CH22_DA59H18.GENSCAN.19-2 | 2.04 |
| 337384 | | | CH22_FGENES.745-1 | 2.04 |
| 332326 | T79623 | Hs.111787 | ESTs | 2.04 |
| 303706 | AW501525 | | EST cluster (not in UniGene) with exon h | 2.04 |
| 336046 | | | CH22_FGENES.679_8 | 2.04 |
| 301770 | R05887 | | EST cluster (not in UniGene) with exon h | 2.04 |
| 326726 | | | CH.20_hs g j5867597 | 2.04 |
| 330485 | M11186 | Hs.113216 | oxytocin; prepro-(neurophysin I) | 2.04 |
| 332956 | | | CH22_FGENES.48_13 | 2.04 |
| 300021 | M97935 | | AFFX control: STAT1 | 2.04 |
| 306872 | AI086920 | | EST singleton (not in UniGene) with exon h | 2.03 |
| 302744 | L03151 | | EST cluster (not in UniGene) with exon h | 2.03 |
| 338507 | | | CH22_EMAC005500.GENSCAN.390-11 | 2.03 |
| 334020 | | | CH22_FGENES.317_1 | 2.03 |
| 333870 | | | CH22_FGENES.291_3 | 2.03 |
| 330552 | U40223 | Hs.248157 | pyrimidinergic receptor P2Y; G-protein c | 2.03 |
| 335486 | | | CH22_FGENES.570_18 | 2.03 |
| 339374 | | | CH22_BA232E17.GENSCAN.2-5 | 2.03 |
| 328384 | | | CH.07_hs g j5868392 | 2.03 |
| 334690 | | | CH22_FGENES.420_3 | 2.03 |
| 310318 | AI733942 | Hs.145338 | ESTs | 2.03 |
| 325893 | | | CH.16_hs g j5867088 | 2.03 |
| 331373 | AA435513 | Hs.178170 | ESTs; Weakly similar to DUAL SPECIFICITY | 2.03 |
| 329784 | | | CH.14_p2 g j5912597 | 2.03 |
| 335087 | | | CH22_FGENES.488_11 | 2.03 |
| 310582 | AI336563 | Hs.254585 | ESTs | 2.03 |
| 332611 | R06751 | Hs.1600 | chaperonin containing TCP1; subunit 5 (e | 2.03 |
| 339258 | | | CH22_BA354112.GENSCAN.8-3 | 2.03 |
| 336851 | | | CH22_FGENES.274-1 | 2.03 |
| 305596 | AA780684 | Hs.8734 | ESTs; Moderately similar to !!! ALU CLA | 2.03 |
| 330364 | | | CH.X_p2 g j3126882 | 2.03 |
| 302940 | AL137619 | | EST cluster (not in UniGene) with exon h | 2.03 |
| 317349 | AA923657 | Hs.126359 | ESTs; Weakly similar to !!! ALU SUBFAM1 | 2.03 |
| 309869 | AW300314 | | EST singleton (not in UniGene) with exon h | 2.03 |
| 334222 | | | CH22_FGENES.147_2 | 2.03 |
| 325233 | | | CH.10_hs g j6381943 | 2.03 |
| 330586 | U77968 | Hs.79564 | neuronal PAS domain protein 1 | 2.03 |
| 336725 | | | CH22_FGENES.88-1 | 2.02 |
| 334157 | | | CH22_FGENES.340_7 | 2.02 |
| 303357 | AW006352 | Hs.159643 | ESTs; Weakly similar to MLD [H.sapiens] | 2.02 |
| 328533 | | | CH.07_hs g j5868482 | 2.02 |
| 309210 | AI862817 | | EST singleton (not in UniGene) with exon h | 2.02 |
| 327412 | | | CH.02_hs g j5867750 | 2.02 |
| 333172 | | | CH22_FGENES.94_7 | 2.02 |
| 334869 | | | CH22_FGENES.447_3 | 2.02 |
| 301047 | AA971485 | Hs.116136 | ESTs | 2.02 |
| 329394 | | | CH.X_hs g j6478817 | 2.02 |
| 301736 | F12128 | | EST cluster (not in UniGene) with exon h | 2.02 |
| 335591 | | | CH22_FGENES.581_30 | 2.02 |
| 338234 | | | CH22_EMAC005500.GENSCAN.260-7 | 2.02 |
| 334433 | | | CH22_FGENES.385_8 | 2.02 |
| 334904 | | | CH22_FGENES.452_18 | 2.02 |
| 318443 | AI939323 | Hs.157714 | ESTs; Weakly similar to NEUR ACETYLCHOLI | 2.02 |
| 300151 | AI243445 | Hs.189654 | ESTs | 2.01 |
| 310348 | AI478563 | Hs.145519 | ESTs | 2.01 |
| 310898 | AI439868 | Hs.165742 | ESTs | 2.01 |
| 332860 | | | CH22_FGENES.27_3 | 2.01 |
| 301699 | AI879117 | | EST cluster (not in UniGene) with exon h | 2.01 |
| 332554 | W96450 | Hs.23111 | phenylalanine-tRNA synthetase-like | 2.01 |

| | | |
|---------------------------|--|------|
| 327994 | CH.06_hs glj5868218 | 2.01 |
| 315613 AW137420 Hs.192311 | ESTs | 2.01 |
| 335356 | CH22_FGENES.541_3 | 2.01 |
| 334028 | CH22_FGENES.318_7 | 2.01 |
| 335277 | CH22_FGENES.523_3 | 2.01 |
| 308657 AJ749855 Hs.236497 | EST; Weakly similar to GLANDULAR KALLIKR | 2.01 |
| 305913 AA876109 | EST singleton (not in UniGene) with exon | 2.01 |
| 323681 AW247730 Hs.102548 | glucocorticoid receptor DNA binding fact | 2.01 |
| 333533 | CH22_FGENES.175_20 | 2.01 |
| 328753 | CH.07_hs glj5868298 | 2.01 |
| 302397 L01694 Hs.211523 | guanine nucleotide binding protein (G pr | 2.01 |
| 304643 AA526588 | EST singleton (not in UniGene) with exon | 2.01 |
| 333065 | CH22_FGENES.75_8 | 2.01 |
| 316192 AA804441 Hs.221286 | ESTs | 2 |
| 302533 L35149 Hs.248116 | chemokine (C motif) XC receptor 1 | 2 |
| 312988 AA813689 Hs.123436 | ESTs | 2 |
| 333612 | CH22_FGENES.217_7 | 2 |
| 333615 | CH22_FGENES.217_10 | 2 |
| 316085 AJ027959 Hs.132300 | ESTs | 2 |
| 337936 | CH22_EM:AC005500.GENSCAN.85-7 | 2 |
| 330972 H18467 Hs.118983 | ESTs; Weakly similar to diaphanous 1 [H. | 2 |

Table 20: B survivor vs Mets – Up in Mets

| Pkey | Ex Accn | UniG_ID | Complete Title | Ratio BS/Met |
|--------|----------|--|--|--------------|
| 316625 | AA780307 | Hs.122156 | ESTs | 0.28 |
| 316076 | AW297895 | Hs.116424 | ESTs | 0.3 |
| 315943 | AA699756 | Hs.117335 | ESTs | 0.38 |
| 317198 | AI810384 | Hs.128025 | ESTs | 0.38 |
| 320082 | AA487678 | Hs.189738 | ESTs | 0.39 |
| 313510 | AI147291 | Hs.154006 | ESTs | 0.39 |
| 323683 | AI380045 | Hs.225033 | ESTs | 0.39 |
| 318558 | AW402677 | Hs.90372 | ESTs | 0.4 |
| 310264 | AI915771 | Hs.148867 | ESTs | 0.4 |
| 314945 | AW276866 | Hs.192715 | ESTs | 0.41 |
| 313403 | W86995 | Hs.113157 | ESTs | 0.42 |
| 321505 | H73183 | Hs.129885 | ESTs | 0.43 |
| 312171 | AW444619 | Hs.138211 | ESTs | 0.43 |
| 324585 | AI823969 | Hs.132678 | ESTs | 0.44 |
| 316695 | AA809844 | EST cluster (not in UniGene) | | 0.44 |
| 319818 | AA825819 | Hs.136952 | ESTs | 0.44 |
| 337522 | | CH22_FGENES.819-1 | | 0.45 |
| 324714 | AA574312 | Hs.245737 | ESTs | 0.45 |
| 315080 | AA551104 | Hs.189048 | ESTs | 0.46 |
| 300548 | AI026836 | Hs.114689 | ESTs | 0.47 |
| 304483 | AA431441 | EST singleton (not in UniGene) with exon | | 0.47 |
| 313096 | AI422367 | Hs.163533 | ESTs | 0.47 |
| 306501 | AA987294 | EST singleton (not in UniGene) with exon | | 0.47 |
| 329086 | | CH.X_hsgI 5868604 | | 0.47 |
| 320176 | AA167566 | Hs.133325 | ESTs | 0.47 |
| 320418 | AI674481 | Hs.199638 | ESTs | 0.47 |
| 302982 | W92391 | Hs.198222 | ESTs; Weakly similar to C2H2-type zinc f | 0.48 |
| 315609 | AW207535 | Hs.224012 | ESTs | 0.48 |
| 317056 | AA904908 | Hs.250643 | ESTs | 0.48 |
| 314361 | AI038765 | Hs.161304 | ESTs | 0.49 |
| 315169 | AI371390 | Hs.158667 | ESTs | 0.49 |
| 323743 | AA324992 | Hs.257168 | ESTs | 0.49 |
| 313903 | AW167439 | Hs.190651 | ESTs | 0.49 |
| 315061 | AA551196 | Hs.188952 | ESTs | 0.49 |
| 300969 | AI140799 | Hs.76230 | ribosomal protein S10 | 0.5 |
| 331950 | AA454595 | Hs.99369 | ESTs | 0.5 |
| 315076 | AI623817 | Hs.168457 | ESTs | 0.5 |
| 300975 | AI283548 | Hs.149668 | ESTs | 0.5 |

TABLE 1-20A

Table 1-20A, shows the accession numbers for those pkeys lacking unigeneID's for Tables 1-20. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|-----------------|--|-----------|
| 108446 112224_1 | AA085383 AA126091 AA074174 AA075373 AA079120 AA070831 AA075978 AA075372 AA128503 | |
| 108474 116896_1 | AA115179 AA073667 AA115897 AA079771 | |
| 100635 10605_34 | BE259039 W29128 AW410299 X72990 BE246492 NM_005243 X66899 AJ909006 AW248151 AL031186 AA012966 BE273549 BE311429 BE253102 Y07848 BE538102 BE26863 BE261240 BE312156 BE618412 BE257322 BE620446 AW806629 AA376777 AA325384 BE256808 BE251031 BE257878 BE275352 AA357169 AW403562 AA204995 AA093259 W95953 BE256279 BE336683 BE252465 AA380754 BE294942 AA380941 AA380999 BE297164 BE249995 BE294719 BE295372 AI270673 BE305132 BE563752 BE295357 AI525421 BE263980 AA057505 AA020915 BE266318 BE206948 AI474020 BE296420 BE297374 BE408545 BE019366 BE407372 BE266180 BE279437 R52233 T19567 BE300738 AW381179 AA357571 AW361285 AA436908 AA301019 AA301022 N20202 BE408777 BE548638 BE167415 AA071260 BE088429 BE280092 W23117 T19568 R51681 AW402216 W22784 BE185607 AI457224 BE544120 AL134874 S72620 AA375079 D51319 AW81820 BE514686 AW853024 BE563744 AA300469 TD7592 BE622190 BE272834 W21781 BE315450 BE542367 BE393120 AA988441 H55137 BE562296 BE622502 BE39590 AA329733 AA332348 JE68317 AA456866 AI497832 AW878437 AA857042 U18018 BE621418 AJ818790 AI949507 BE397693 AA885545 AI858854 AI355147 BE169028 S62138 AW732191 AA856891 BE266060 XT1427 BE266557 AF095690 AW001288 AJ799634 AI623498 AA071346 BE547662 BE261446 AI564543 BE559759 U35622 BE314249 BE264915 AI638591 AI538385 AW90025 BE384754 AI888893 AW778800 AI925273 AA075797 AW949130 AV660275 AW438697 AJ587137 AI524121 AA806249 AW628247 AA808241 BE244388 AI761125 AW117672 AA911782 AI129250 AA654447 H55291 BE258050 BE260162 W95867 AA857187 AI871378 AI650103 AW103827 AI220929 AW149949 BE465561 AI302857 AW168841 D82190 AW249814 AI623432 AI687358 AW951077 R51592 W60458 AI092853 AW474693 D12765 AI911646 D82208 D82187 AW074031 AI358527 AW338497 AA970893 AW072573 AA205364 AB58886 AA012830 AW148763 AB630356 AA464656 BE250329 AI016939 AI664005 BE046122 AI497746 C75340 R56898 D82141 AW168240 C19048 AT741090 A1222365 AA948284 AI583522 AW572212 AI031290 AA582727 AA579897 AA570629 W60883 AW516989 AL038160 AA577334 AA865872 AA994043 AA922583 AA464778 AA209178 AI829479 AI370235 BE246529 AA438177 AA455255 AI699730 W60654 AL035744 AA862042 R32756 AI886888 AA993087 AI289479 AA627840 AA446184 AI619503 R32755 AW075358 AA432315 AA457024 AA020865 R92132 AA54629 AA746059 AA454643 AA456240 AA826984 BE163738 AJ806470 AJ991074 AJ802560 AA587095 AA558714 AA968521 N87780 AI538246 NT1794 AV661738 AI368903 AA362570 AI989445 AI674962 S75762 BE245204 AA975296 D20123 AW005704 AA693328 AA582270 AI918474 AW205707 AI696299 AA220990 AA101538 T29030 H27201 AW262526 AI610530 AA126840 AA126790 X92120 AW367868 BE299644 BE299451 AA476561 BE300044 AA134363 BE295222 AA307504 NA23237 AA319098 N35502 AW964461 N57241 BE299049 N86332 R51156 AA085859 T75212 AA133939 AA147129 AA156161 BE543953 BE538848 AA133676 BE299745 AA135050 AA218535 AW405401 AW411287 BE410528 C01410 NM_04083 BE314959 AA836413 AA085862 AW024370 AA471059 AW467508 AA001025 AI820231 AA633221 T95517 AA147038 AA476447 AW027012 AW078627 BE513200 AI192297 AA886279 AW081806 AA316185 AA010506 AI269329 W93139 AI682935 AA609555 AA378028 AI093877 AA999997 AA730698 AI143923 AW575315 AA890550 AA494335 AW76601 AI796336 AA826130 AA609207 AI539618 AI088539 AI089090 AA825505 AA632978 AA015892 AW204713 AA156495 AA824613 AA133630 N29826 AA527476 AI633352 T27908 AA134364 AA133940 AW043601 H37775 AA772375 AA057871 AA047888 AA054225 H86568 AA001511 H25718 AW189507 AA165589 AA054433 H85549 AA165486 AA058972 AA454911 AA464064 AA493802 AA428253 R85508 AW302469 AI61812 BE162582 F11073 T95518 N26811 AI783929 H40669 AW1658830 R51042 AA528386 AA782875 AW880218 AL138391 AA314536 AW949338 AA149468 AA149552 AI346513 AA216776 BE349131 AW007654 AI141803 AA622688 AI185131 AW057635 AA101539 AA627986 H27202 AI536847 W93084 AI973148 AI246788 AW572108 AI469414 AA454835 AA612707 AA430746 AI084991 AA010400 AA856536 AA463928 AI248310 R07170 AA834033 D12244 AI655670 AA054350 AA639480 AI702067 AI475389 | |
| 100643 3931_1 | NM_005032 M34427 AA332167 AW409711 AL119718 BE297581 BE299855 AA082284 AA226855 AA149568 AW391953 M22299 BE163594 AW847881 AW366993 BE142871 AW847885 AW604137 AW847753 AW847886 AW376442 U48350 AW607478 AA373011 AA334080 BE294177 AL121355 AA302236 BE540666 BE170588 AA346884 BE541512 AA226818 AA082001 AA366490 AW604122 AA205784 AW607791 BE168496 AA058497 T64373 BE165633 AW802804 AW847878 AA187408 AA088397 AI751745 AA344103 AA034463 AI906008 AA363580 AA379193 AI32642 AI143569 W52748 W52754 AA385532 AA085967 F05943 AA363422 AA133444 AA133477 AA029541 AA8387 N83348 AA376066 AA147671 W70187 AA316255 BE174987 AA452776 AA089605 AL047776 BE162673 H39532 BE168406 AA357654 AA328728 AW813442 D57844 AW839748 AW839663 D57357 AA334536 AW268674 AW950788 AW409888 AI160544 D57821 AW664382 D25884 AI755101 AW130365 AI609094 AI984064 AI806523 AA492516 AI755258 BE157210 AA374884 AI983923 AI831088 AA706501 AI754957 | |

AI688651 AI088623 AI336114 N38752 T56004 AA845200 AA858377 BE157397 AW069347 AA045366 AW316918 AW130372
 AI355398 BE157396 AI751746 AI375820 AA129935 W60002 N24781 AI80524 W60009 AA044283 AA121161 AI539277
 AA301885 AW019944 AA133445 AA101108 AA033559 W70060 AA617751 AI986261 AI023234 D82235 AA085846 AW754181
 D82093 D82100 AA147653 AA600256 D57884 AI753982 AI568050 AI146490 AW302280 AI433051 AA329188 AW572150
 AW166345 AI337981 AA778973 N67577 AA227207 AA83281 C06190 AL046997 AI217682 AI752979 AW627538 AI127171
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 BE152850 BE149052 BE149084 AA866868 BE149064 BE149032 AA044093 AA129934 AA303976 BE157211 AA187291
 BE152830 AA046552 BE149079 BE149033 BE149065 BE149044 BE149076 BE149053 BE149085 BE149034
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 100670 22023_1 AA332178 BE259177 BE545625 T09105 S62076 M16424 NM_000520 BE244309 F13516 BE251567 BE514981 AL119537
 AA336739 BE261801 AA276642 N32708 T77034 W24621 W42478 AW630382 AW856214 AA134234 M13520 BE379212
 AA287459 BE019379 BE297192 BE162970 AW40568 AW403322 BE272280 BE208703 BE304428 BE162807 BE162828
 BE162887 BE078944 BE163025 BE162878 BE162898 BE162891 BE162880 BE073563 BE163086 BE162896
 BE162770 BE073565 BE162906 BE162913 BE162947 BE162803 BE262199 BE162811 BE08097 BE315095 AW206024
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 100673 21517_2 AW403342 AW248986 BE561709 AA357312 BE31834 BE389496 BE294887 AW732696 BE047868 AI702383 BE019155
 AI702357 BE048956 BE280458 BE313759 BE513492 BE535404 BE280258 AC005263 NM_007165 L21990 AW732711
 AI564920 AW249094 BE265365 AW607186 AW607346 BE005217 H27211 U46230 BE260066 BE207043 BE545782 AW248659
 AA085228 AA085161
 AA082885 AA114265 AA085398 AA113184
 AA932794 BE540417 AW409802 AW410765 BE296651 BE294197 BE164813 AW381886 AW381806 AL048654 AW403058
 BE207228 AA464654 AW966967 BE326831 BE407277 BE408669 AA476527 AA115576 AA359697 AA476357 AA449939
 BE263719 AL045304 W21442 R28919 BE395990 AA252273 AI346812 BE538487 AA507160 W93950 N42025 AI088439
 AL134931 AA031524 AI887287 AW470017 AA476423 AA464553 AW410766 AI569421 AA577476 AI248935 AI912371
 AW615674 AA824237 AA807746 AA827377 AA890268 AA476309 AI086424 AW409698 AA031553 AW451901 AI520934
 AW050554 RA9825 N30302 AA532541 W94004 N93402 AA115549 AA31202 L25665 NM_005275 AA436745 AI122671 R49779
 R18508
 100734 35197_1 AI807481 AI500404 AI092260 BE348982 AI143675 AA772399 AI772398 AI368565 AI379172 AI083781 AI871363 AA843793
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 W07463 BE551725 R28404 AW206461 W580506 AI885536 N96800 R34967 R25381 AA443093 AI143063 AI284647 AI703144
 AA309032 AA309031 AW949426 AW949428 AI638387 AI638386 R77173 R38513 T89263 F0190 H87979 R70205 AA664355
 AA235910 AA033657 AI436212 N50463 AI43805 AI081876 AI421090 AW020818 AI559529 AI887420 BE154202 AA889062
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 AI84363 AI338070 N57307 AA608928 T94993 AI514184 AA724695 N66630 AI379538 AI274671 AW628470 AA235346
 AA687581 AI073906 AI263602 AI685963 AI243808 AI076491 AI374640 H82967 AA776567 AA256191 T29856
 AA953584 AI140801 AI805484 AA984329 R33497 AI017114 AI263355 N81103 AW418776 D57474 AI918460 AA256152
 AI683268 AI042628 AW196650 CD0195 AI918567 T28903 N95383 R13671 T94939 AI275235 AA235751 T84335
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 100748 41861_1 X06098 X05826
 100760 1334_7 AW794626 M27126 M27014
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AI475389

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| 330855 | 111881_1 | AA070316 AA079318 |
| 332099 | genbank_AA608983 | AA608983 |
| 332240 | genbank_N54803 | N54803 |

TABLE 1-20B

Table 1-20B, shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Tables 1-20. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

| Pkey: | Unique number corresponding to an Eos probeset | | |
|--------------|---|--------|-----------------|
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA | | |
| Strand: | sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495. | | |
| Nt_position: | Indicates DNA strand from which exons were predicted. | | |
| Pkey | Ref | Strand | Nt_position |
| 332792 | Dunham, I. et.al. | Plus | 73381-73768 |
| 332843 | Dunham, I. et.al. | Plus | 1142859-1143494 |
| 332909 | Dunham, I. et.al. | Plus | 1946582-1946735 |
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| 332947 | Dunham, I. et.al. | Plus | 2431726-2432006 |
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| 332958 | Dunham, I. et.al. | Plus | 2516164-2516310 |
| 332992 | Dunham, I. et.al. | Plus | 2699997-2701093 |
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| 330086 | 6015293 | Plus | 29518-29652 |
| 330080 | 6015314 | Minus | 4890-4972 |
| 330082 | 6015314 | Plus | 27158-27296 |
| 330064 | 6165044 | Minus | 5619-5696 |
| 330063 | 6165044 | Minus | 948-1025 |
| 330065 | 6165044 | Minus | 9876-9948 |
| 326646 | 5867552 | Plus | 100426-100608 |
| 326688 | 5867582 | Plus | 104875-105531 |
| 326708 | 5867593 | Minus | 39203-39310 |
| 326710 | 5867593 | Minus | 80204-80468 |
| 326746 | 5867611 | Plus | 129366-129565 |
| 326793 | 5867631 | Plus | 136295-136518 |
| 326603 | 6056312 | Minus | 50323-50575 |
| 326806 | 6469835 | Plus | 101628-102149 |
| 326783 | 6525298 | Plus | 196378-196863 |
| 326668 | 6552455 | Plus | 146726-146838 |
| 326725 | 6552456 | Minus | 223005-223125 |
| 326857 | 6552460 | Minus | 120142-120345 |
| 326763 | 6598307 | Plus | 239690-239902 |
| 326808 | 6682504 | Minus | 65107-65214 |
| 326874 | 6682507 | Minus | 4543-4888 |
| 326876 | 6682507 | Minus | 46203-46499 |
| 326884 | 6682511 | Plus | 33403-33479 |
| 326997 | 5867660 | Minus | 71389-72147 |
| 327009 | 5867664 | Plus | 933145-933266 |
| 327015 | 5867664 | Plus | 1030457-1030534 |
| 326942 | 6004446 | Minus | 88675-88785 |
| 326943 | 6004446 | Minus | 89242-89427 |
| 326957 | 6469836 | Plus | 37529-37694 |
| 327049 | 6531965 | Minus | 1924026-1924110 |
| 327051 | 6531965 | Plus | 2222592-2222717 |
| 327056 | 6531965 | Plus | 2374323-2374751 |
| 327059 | 6531965 | Plus | 2421032-2421799 |
| 327067 | 6531965 | Minus | 3726023-3726668 |
| 327089 | 6531965 | Plus | 5238983-5239187 |
| 327037 | 6531965 | Minus | 387854-388045 |
| 327123 | 6531971 | Minus | 23980-24340 |
| 327125 | 6531971 | Plus | 48884-48975 |
| 326981 | 6588016 | Plus | 105091-106038 |
| 330139 | 4210430 | Plus | 112089-112450 |
| 330153 | 4325335 | Plus | 146951-147475 |
| 330130 | 6002196 | Minus | 241903-241967 |
| 327203 | 5867447 | Plus | 36485-36577 |
| 327206 | 5867447 | Plus | 177855-178031 |
| 327259 | 5867454 | Plus | 87268-87438 |
| 327264 | 5867461 | Plus | 47014-47367 |

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|--------|---------|-------|---------------|
| 327273 | 5867466 | Plus | 73451-73549 |
| 327274 | 5867470 | Minus | 84027-84128 |
| 327277 | 5867473 | Minus | 165616-165715 |
| 327278 | 5867473 | Minus | 166350-166439 |
| 327289 | 5867481 | Plus | 49256-49536 |
| 327304 | 5867494 | Plus | 20664-20850 |
| 327315 | 5867508 | Minus | 78409-79245 |
| 327246 | 5867547 | Plus | 136212-136325 |
| 327155 | 5867549 | Plus | 90343-90876 |
| 327159 | 5867550 | Minus | 8219-8331 |
| 327334 | 5902477 | Minus | 142655-142745 |
| 327341 | 6017016 | Minus | 122306-123014 |
| 327185 | 6117805 | Minus | 3287-3451 |
| 327309 | 6456757 | Minus | 10219-10457 |
| 327263 | 6525274 | Minus | 153814-154920 |
| 327362 | 6552412 | Minus | 62459-62805 |
| 327413 | 5867750 | Plus | 101410-101508 |
| 327418 | 5867750 | Minus | 153453-153547 |
| 327430 | 5867754 | Plus | 1320-1403 |
| 327431 | 5867754 | Plus | 1853-1958 |
| 327472 | 5867775 | Plus | 74628-74937 |
| 327487 | 5867785 | Minus | 146220-146326 |
| 327379 | 5867795 | Plus | 1368-1820 |
| 327461 | 6004455 | Plus | 209031-209210 |
| 327532 | 6469818 | Plus | 71994-72137 |
| 330170 | 6648220 | Plus | 103280-103849 |
| 330166 | 6648220 | Plus | 86542-86687 |
| 327544 | 5867797 | Minus | 18105-18332 |
| 327564 | 5867811 | Plus | 13850-14018 |
| 327566 | 5867811 | Plus | 33383-33901 |
| 327581 | 5867825 | Plus | 5318-5434 |
| 327585 | 5867825 | Plus | 85660-85764 |
| 327605 | 6004463 | Plus | 199214-199579 |
| 327710 | 5867860 | Minus | 131012-131790 |
| 327610 | 5867868 | Minus | 174109-174278 |
| 327624 | 5867871 | Minus | 37699-37788 |
| 327641 | 5867890 | Plus | 13583-13702 |
| 327646 | 5867894 | Minus | 3043-3258 |
| 327614 | 6525283 | Plus | 3634-4001 |
| 327736 | 5867940 | Minus | 37781-37887 |
| 327739 | 5867942 | Minus | 182187-182548 |
| 327740 | 5867943 | Plus | 25716-26077 |
| 327743 | 5867944 | Minus | 155930-156098 |
| 327755 | 5867955 | Minus | 61959-62145 |
| 327772 | 5867964 | Minus | 28185-26285 |
| 327774 | 5867964 | Minus | 127659-127899 |
| 327823 | 5867968 | Minus | 170359-170433 |
| 327827 | 5867968 | Minus | 201918-202048 |
| 327833 | 5867968 | Minus | 303618-303732 |
| 327805 | 5867968 | Plus | 19952-20019 |
| 327809 | 5867968 | Plus | 54610-54761 |
| 327816 | 5867968 | Minus | 79202-79552 |
| 327790 | 5867977 | Plus | 19822-19985 |
| 327791 | 5867977 | Plus | 22491-22610 |
| 327793 | 5867979 | Plus | 18874-18254 |
| 327845 | 6531982 | Plus | 193402-193549 |
| 327846 | 6531982 | Plus | 195216-195373 |
| 330204 | 6013606 | Plus | 86663-86811 |
| 330189 | 6165182 | Minus | 26732-26991 |
| 330239 | 6671857 | Plus | 117484-118092 |
| 330266 | 6671885 | Minus | 129505-129832 |
| 330275 | 6671904 | Plus | 103585-103716 |
| 330280 | 6671910 | Plus | 2109-2377 |
| 330286 | 6671913 | Minus | 31050-31171 |
| 327999 | 5867994 | Plus | 94710-94841 |
| 328109 | 5868020 | Minus | 353895-354525 |
| 328098 | 5868020 | Minus | 261745-261920 |
| 328134 | 5868039 | Plus | 72354-72487 |
| 328171 | 5868071 | Plus | 101102-101224 |
| 328221 | 5868099 | Minus | 37489-37829 |
| 328224 | 5868101 | Plus | 105563-105832 |
| 328228 | 5868105 | Minus | 21488-21595 |
| 328236 | 5868117 | Plus | 13864-14371 |
| 327864 | 5868130 | Plus | 59139-59358 |
| 327888 | 5868149 | Minus | 51964-52120 |
| 327899 | 5868156 | Minus | 102288-102697 |

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|--------|---------|-------|-----------------|
| 327925 | 5868172 | Minus | 118396-118490 |
| 327927 | 5868173 | Plus | 50989-51246 |
| 327937 | 5868192 | Minus | 33127-33485 |
| 327946 | 5868206 | Plus | 44102-44319 |
| 327982 | 5868216 | Plus | 30307-30527 |
| 327990 | 5868218 | Minus | 36225-36503 |
| 328015 | 5902482 | Minus | 477679-47813 |
| 328016 | 5902482 | Minus | 507572-508519 |
| 328025 | 5902482 | Minus | 931937-932171 |
| 328031 | 5902482 | Plus | 1176372-1177283 |
| 328053 | 5902482 | Minus | 2709850-2710010 |
| 328243 | 6056292 | Plus | 1-243 |
| 328271 | 6552415 | Plus | 39015-39098 |
| 328592 | 5868227 | Minus | 252407-252565 |
| 328570 | 5868231 | Plus | 89210-89816 |
| 328507 | 5868233 | Minus | 246798-246944 |
| 328620 | 5868241 | Minus | 15651-15788 |
| 328524 | 5868246 | Minus | 120666-120836 |
| 328791 | 5868309 | Plus | 171592-171929 |
| 328810 | 5868327 | Plus | 101730-101914 |
| 328820 | 5868330 | Plus | 80446-90602 |
| 328835 | 5868339 | Plus | 88053-88461 |
| 328282 | 5868353 | Plus | 72692-72819 |
| 328314 | 5868371 | Minus | 288397-288505 |
| 328328 | 5868375 | Plus | 169210-169407 |
| 328420 | 5868411 | Plus | 53812-53886 |
| 328428 | 5868417 | Plus | 13589-13780 |
| 328436 | 5868417 | Plus | 203760-203904 |
| 328444 | 5868420 | Plus | 65393-66103 |
| 328462 | 5868433 | Plus | 49649-49768 |
| 328457 | 5868434 | Minus | 15954-16073 |
| 328474 | 5868446 | Minus | 128777-128970 |
| 328484 | 5868454 | Minus | 21974-22140 |
| 328504 | 5868471 | Plus | 47084-47217 |
| 328506 | 5868471 | Plus | 60716-60830 |
| 328507 | 5868473 | Minus | 199637-199990 |
| 328544 | 5868486 | Plus | 145659-145829 |
| 328552 | 5868489 | Plus | 47328-47607 |
| 328557 | 5868489 | Plus | 138094-138161 |
| 328558 | 5868489 | Plus | 143648-144108 |
| 328276 | 6004471 | Plus | 13282-13450 |
| 328277 | 6004471 | Minus | 279901-280181 |
| 328662 | 6004473 | Plus | 1184773-1184855 |
| 328636 | 6004473 | Plus | 192484-192543 |
| 328803 | 6004475 | Minus | 291716-291948 |
| 328305 | 6004478 | Minus | 34730-34851 |
| 328569 | 6004480 | Plus | 232896-233243 |
| 328581 | 6006033 | Minus | 121249-121400 |
| 328582 | 6006033 | Minus | 134177-134282 |
| 328768 | 6017031 | Minus | 223741-224238 |
| 328770 | 6017031 | Minus | 363933-364166 |
| 328841 | 6381920 | Minus | 5214-5479 |
| 328851 | 6381923 | Plus | 2502-2606 |
| 328859 | 6381928 | Plus | 69045-69138 |
| 328860 | 6381928 | Plus | 83265-83366 |
| 328863 | 6381929 | Minus | 29313-29506 |
| 328868 | 6381930 | Plus | 112825-112893 |
| 328976 | 6525286 | Plus | 94053-94165 |
| 328886 | 6588003 | Plus | 31068-31429 |
| 328888 | 6588003 | Minus | 111901-111999 |
| 328936 | 5868500 | Minus | 1352202-1352259 |
| 328938 | 5868500 | Plus | 1522923-1522986 |
| 328971 | 6478806 | Minus | 23976-24105 |
| 330338 | 5457162 | Plus | 48406-48518 |
| 330327 | 5919194 | Plus | 121561-121683 |
| 330319 | 5932415 | Plus | 49095-50132 |
| 328974 | 5868520 | Plus | 31557-31668 |
| 328981 | 5868527 | Minus | 105677-105764 |
| 328989 | 5868535 | Plus | 182088-182198 |
| 330363 | 3126882 | Minus | 61838-61901 |
| 330370 | 6580495 | Plus | 10826-11669 |
| 329041 | 5868564 | Plus | 141592-141785 |
| 328078 | 5868597 | Plus | 326798-326860 |
| 328097 | 5868624 | Plus | 12002-12170 |
| 329107 | 5868626 | Plus | 101063-101190 |
| 329114 | 5868650 | Minus | 23792-23910 |

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|--------|---------|-------|---------------|
| 329116 | 5868650 | Minus | 43389-43493 |
| 329164 | 5868691 | Plus | 62305-62517 |
| 329187 | 5868713 | Plus | 29909-30175 |
| 329201 | 5868718 | Plus | 79266-79539 |
| 329221 | 5868727 | Minus | 105837-105894 |
| 329246 | 5868732 | Minus | 250541-250792 |
| 329254 | 5868733 | Plus | 4133-4214 |
| 329326 | 5868806 | Plus | 155884-155992 |
| 329330 | 5868806 | Minus | 340278-340403 |
| 329382 | 5868868 | Plus | 41401-41655 |
| 329384 | 5868869 | Minus | 116524-116662 |
| 329386 | 6004484 | Plus | 160502-161110 |
| 329140 | 6017060 | Plus | 290842-290905 |
| 329182 | 6056331 | Minus | 662206-663423 |
| 329018 | 6249620 | Plus | 103950-104034 |
| 329319 | 6381976 | Plus | 721390-721470 |
| 329392 | 6478815 | Plus | 109786-109854 |
| 329029 | 6525302 | Plus | 281445-282490 |
| 329401 | 6682544 | Plus | 21342-24014 |
| 329406 | 6682547 | Plus | 47249-47395 |
| 329411 | 6682549 | Minus | 84558-84835 |
| 329429 | 5868882 | Minus | 97008-97091 |
| 329436 | 5868883 | Plus | 230265-230528 |
| 329464 | 6456788 | Minus | 4437-4538 |

TABLE 21:
**310 GENES UP-REGULATED IN COLON CANCER DERIVED LIVER
 METASTASES COMPARED TO NORMAL COLON TISSUE**

Table 21 shows 310 genes up-regulated in colon cancer derived liver metastases compared to normal colon tissue. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" normal colon tissues was greater than or equal to 3.0. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" normal colon tissue level was set to the 50th percentile.

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
|--------|----------|---------------|---|-------|
| 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 26.72 |
| 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 16.36 |
| 409041 | AB033026 | Hs.50081 | KIAA1199 protein | 13.94 |
| 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypothetical | 13.90 |
| 432314 | AA533447 | Hs.312989 | ESTs | 12.24 |
| 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrixin, | 11.60 |
| 443162 | T49951 | Hs.9029 | DKFZP434G032 protein | 9.52 |
| 436385 | BE551618 | Hs.144097 | ESTs | 9.20 |
| 418652 | AI801098 | Hs.151500 | ESTs | 9.00 |
| 433312 | AI241331 | Hs.131765 | ESTs, Moderately similar to I38937 DNA/R | 8.90 |
| 412093 | BE242691 | Hs.14947 | ESTs | 8.74 |
| 442369 | AI565071 | Hs.159983 | ESTs | 8.40 |
| 426101 | AL049987 | Hs.166361 | Homo sapiens mRNA; cDNA DKFZp564F112 (fr | 8.39 |
| 435937 | AA830893 | Hs.119769 | ESTs | 8.22 |
| 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 8.22 |
| 432572 | AI660840 | Hs.191202 | ESTs, Weakly similar to ALUE_HUMAN !!! | 7.96 |
| 440524 | R71264 | Hs.16798 | ESTs | 7.94 |
| 424878 | H57111 | Hs.221132 | ESTs | 7.88 |
| 430433 | AA478883 | Hs.273766 | ESTs | 7.82 |
| 410245 | C17908 | Hs.194125 | ESTs | 7.78 |
| 417315 | AI080042 | Hs.336901 | ribosomal protein S24 | 7.76 |
| 430685 | BE350122 | Hs.157367 | ESTs, Weakly similar to I78885 serine/th | 7.76 |
| 432435 | BE218886 | Hs.282070 | ESTs | 7.74 |
| 426818 | AA554827 | Hs.289115 | DKFZp434A0131 protein | 7.58 |
| 419145 | N99638 | gbza39g11.r1 | Soares fetal liver spleen | 7.56 |
| 444838 | AV651680 | Hs.208558 | ESTs | 7.54 |
| 428046 | AW812795 | Hs.155381 | ESTs, Moderately similar to I38022 hypot | 7.48 |
| 446682 | AW205632 | Hs.211198 | ESTs | 7.26 |
| 421221 | AW276914 | Hs.326714 | Homo sapiens clone IMAGE:713177, mRNA se | 7.19 |
| 440116 | AI798851 | Hs.283108 | hemoglobin, gamma G | 7.12 |
| 450230 | AW016607 | Hs.201582 | ESTs | 7.08 |
| 456332 | AA228357 | gbznc39d05.r1 | NCI_CGAP_Pr2 Homo sapiens | 7.04 |
| 421814 | L12350 | Hs.108623 | thrombospondin 2 | 6.89 |
| 440774 | AI420611 | Hs.127832 | ESTs | 6.86 |
| 428065 | AI634046 | Hs.157313 | ESTs | 6.78 |
| 422330 | D30783 | Hs.115263 | epiregulin | 6.72 |
| 413950 | AA249096 | Hs.32793 | ESTs | 6.67 |
| 438011 | BE466173 | Hs.145696 | splicing factor (CC1.3) | 6.62 |
| 421057 | T58283 | Hs.10450 | Homo sapiens cDNA: FLJ22063 fis, clone H | 6.58 |
| 428698 | AA852773 | Hs.334838 | KIAA1866 protein | 6.40 |
| 408806 | AW847814 | Hs.289005 | Homo sapiens cDNA: FLJ21532 fis, clone C | 6.38 |
| 425787 | AA363867 | Hs.155029 | ESTs | 6.38 |
| 435812 | AA700439 | Hs.188490 | ESTs | 6.32 |
| 448974 | AL049390 | Hs.22689 | Homo sapiens mRNA; cDNA DKFZp586O1318 (f | 6.28 |
| 418875 | W19971 | Hs.233459 | ESTs | 6.22 |
| 407284 | AI539227 | Hs.214039 | hypothetical protein FLJ23556 | 6.17 |
| 408243 | Y00787 | Hs.624 | interleukin 8 | 6.12 |
| 434936 | AI285970 | Hs.183817 | ESTs | 6.12 |

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|--------|-----------|----------------------------|--|------|
| 412088 | AI689496 | Hs.108932 | ESTs | 6.04 |
| 450377 | AB033091 | Hs.74313 | KIAA1265 protein | 6.00 |
| 407618 | AW054922 | Hs.53478 | Homo sapiens cDNA FLJ12366 fis, clone MA | 5.98 |
| 408298 | AL117452 | Hs.44155 | DKFZp586G1517 protein | 5.94 |
| 456999 | AA319798 | Hs.298581 | eukaryotic translation elongation factor | 5.90 |
| 432559 | AW452948 | Hs.257631 | ESTs | 5.88 |
| 423349 | AF010258 | Hs.127428 | homeo box A9 | 5.84 |
| 436100 | AA704806 | Hs.143842 | ESTs, Weakly similar to 2004399A chromos | 5.84 |
| 453204 | R10799 | Hs.191990 | ESTs | 5.84 |
| 429183 | AB014604 | Hs.197955 | KIAA0704 protein | 5.78 |
| 427882 | AA640987 | Hs.193767 | ESTs | 5.72 |
| 447033 | AI357412 | Hs.157601 | ESTs | 5.70 |
| 428054 | AI948688 | Hs.266619 | ESTs | 5.66 |
| 414504 | AW069181 | Hs.115175 | sterile-alpha motif and leucine zipper c | 5.64 |
| 442806 | AW294522 | Hs.149991 | ESTs | 5.64 |
| 418259 | AA215404 | Hs.137289 | ESTs | 5.60 |
| 434963 | AW974957 | Hs.288719 | Homo sapiens cDNA FLJ12142 fis, clone MA | 5.60 |
| 419999 | AI760942 | Hs.191754 | ESTs | 5.58 |
| 431749 | AL049263 | Hs.306292 | Homo sapiens mRNA; cDNA DKFZp564F133 (fr | 5.58 |
| 422790 | AA809875 | Hs.259393 | ESTs | 5.56 |
| 440980 | AL042005 | Hs.1117 | tripeptidyl peptidase II | 5.48 |
| 432451 | AW972771 | Hs.292471 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.46 |
| 438578 | AA811244 | Hs.164168 | ESTs | 5.44 |
| 410467 | AF102546 | Hs.63931 | dachshund (<i>Drosophila</i>) homolog | 5.42 |
| 426317 | AA312350 | Hs.165294 | transcription factor 7 (T-cell specific, | 5.42 |
| 450164 | AI239923 | Hs.30098 | ESTs | 5.40 |
| 438899 | AF085833 | Hs.135624 | ESTs | 5.38 |
| 432945 | AL043683 | Hs.8173 | hypothetical protein FLJ10803 | 5.36 |
| 437176 | AW176909 | Hs.42346 | calcineurin-binding protein calsarcin-1 | 5.34 |
| 419829 | AI924228 | Hs.115185 | ESTs, Moderately similar to PC4259 ferr | 5.33 |
| 407966 | AA295052 | Hs.38516 | Homo sapiens, clone MGC:15887, mRNA, com | 5.30 |
| 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 5.26 |
| 419682 | H13139 | Hs.22282 | paired-like homeodomain transcription fa | 5.26 |
| 421097 | AI280112 | Hs.125232 | Homo sapiens cDNA FLJ13266 fis, clone OV | 5.22 |
| 443373 | AI792868 | Hs.135365 | ESTs | 5.22 |
| 412059 | AA317962 | Hs.249721 | ESTs, Moderately similar to PC4259 ferr | 5.21 |
| 443651 | W22152 | Hs.282929 | ESTs | 5.21 |
| 411274 | NM_002776 | Hs.69423 | kallikrein 10 | 5.17 |
| 421999 | U50535 | Hs.110630 | Human BRCA2 region, mRNA sequence CG006 | 5.17 |
| 426981 | AL044675 | Hs.173081 | KIAA0530 protein | 5.14 |
| 431319 | AA873350 | Hs.302232 | ESTs | 5.10 |
| 434966 | AA657494 | gb:mt66R04.s1 NCI_CGAP_Pr3 | Homo sapiens | 5.10 |
| 418830 | BE513731 | Hs.88959 | hypothetical protein MGC4816 | 5.08 |
| 428290 | AI932995 | Hs.183475 | Homo sapiens clone 25061 mRNA sequence | 5.07 |
| 408784 | AW971350 | Hs.63386 | ESTs | 5.04 |
| 411975 | AI916058 | Hs.144583 | ESTs | 5.02 |
| 409760 | AA302840 | gb:EST10534 | Adipose tissue, white Homo | 4.97 |
| 420717 | AA284447 | Hs.271887 | ESTs | 4.96 |
| 417035 | AA192455 | Hs.22968 | Homo sapiens clone IMAGE:451939, mRNA se | 4.95 |
| 434442 | AA737415 | Hs.152826 | ESTs | 4.94 |
| 441328 | AI982794 | Hs.159473 | ESTs | 4.92 |
| 438962 | BE046594 | gb:hn41c11x1 NCI_CGAP_RDF2 | Homo sapiens | 4.92 |
| 451277 | AK001123 | Hs.26176 | hypothetical protein FLJ10261 | 4.92 |
| 438408 | BE273296 | Hs.254467 | Homo sapiens cDNA FLJ13255 fis, clone OV | 4.90 |
| 424950 | AA602917 | Hs.156974 | ESTs | 4.88 |
| 436823 | AW749865 | Hs.293645 | ESTs, Weakly similar to I38022 hypotheti | 4.87 |
| 444783 | AK001468 | Hs.62180 | anillin (<i>Drosophila</i> Scraps homolog), act | 4.82 |
| 444301 | AK000136 | Hs.10760 | asporin (LRR class 1) | 4.80 |
| 445390 | AI222165 | Hs.144923 | ESTs | 4.80 |
| 439608 | AW864696 | Hs.301732 | hypothetical protein MGC5306 | 4.78 |
| 450506 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 4.78 |
| 432682 | AI376400 | Hs.159588 | ESTs | 4.76 |
| 426086 | T94907 | Hs.188572 | ESTs | 4.76 |
| 435981 | H74319 | Hs.188620 | ESTs | 4.74 |
| 432340 | AA534222 | gb:nj21d02.s1 NCI_CGAP_AA1 | Homo sapiens | 4.72 |
| 435756 | AI418466 | Hs.33665 | ESTs | 4.72 |
| 447982 | H22953 | Hs.137551 | ESTs | 4.72 |
| 449509 | AA001615 | Hs.84561 | ESTs | 4.72 |
| 407946 | AA226495 | Hs.154292 | ESTs | 4.70 |
| 426215 | AW963419 | Hs.155223 | stanniocalcin 2 | 4.70 |
| 414783 | AW069569 | Hs.278270 | unactive progesterone receptor, 23 kD | 4.68 |
| 417601 | NM_014735 | Hs.82292 | KIAA0215 gene product | 4.68 |
| 438461 | AW075485 | Hs.286049 | phosphoserine aminotransferase | 4.68 |
| 449032 | AA045573 | Hs.22900 | nuclear factor (erythroid-derived 2)-like | 4.68 |
| 426501 | AW043782 | Hs.293616 | ESTs | 4.67 |
| 409024 | AW883529 | Hs.173830 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 4.67 |

| | | | | |
|--------|-----------|---|------|------|
| 439848 | AW979249 | gb:EST391359 MAGE resequences, MAGP | Homo | 4.66 |
| 424762 | AL119442 | Hs.183684 eukaryotic translation initiation factor | | 4.66 |
| 442007 | AA301116 | Hs.142838 nucleolar phosphoprotein Nopp34 | | 4.62 |
| 409632 | W74001 | Hs.55279 serine (or cysteine) proteinase inhibitor | | 4.62 |
| 432409 | AA806538 | Hs.130732 KIAA1575 protein | | 4.60 |
| 452220 | BE158006 | Hs.212296 ESTs | | 4.60 |
| 442577 | AA292998 | Hs.163900 ESTs | | 4.58 |
| 434001 | AW950905 | Hs.3697 serine (or cysteine) proteinase inhibitor | | 4.58 |
| 414271 | AK000275 | Hs.75871 protein kinase C binding protein 1 | | 4.58 |
| 433854 | AA610649 | Hs.333239 ESTs | | 4.56 |
| 431315 | AW972227 | Homo sapiens cDNA: FLJ22765 fts, clone K | | 4.53 |
| 434220 | AI174777 | Hs.283039 Homo sapiens PRO2492 mRNA, complete cds | | 4.50 |
| 457752 | AI821270 | Hs.285643 Homo sapiens cDNA FLJ14364 fts, clone HE | | 4.50 |
| 449941 | AW450536 | Hs.209260 ESTs | | 4.48 |
| 415116 | AA160363 | Hs.269956 ESTs | | 4.47 |
| 414386 | X00442 | Hs.75990 haptoglobin | | 4.47 |
| 422956 | BE545072 | Hs.122579 hypothetical protein FLJ10461 | | 4.44 |
| 423974 | AL118754 | gb:DKFZp761P1910_r1 761 (synonym: hamy2) | | 4.44 |
| 449618 | AI076459 | Hs.15978 KIAA1272 protein | | 4.44 |
| 428279 | AA425310 | Hs.155766 ESTs, Weakly similar to A47582 B-cell gr | | 4.42 |
| 430573 | AA744550 | Hs.136345 ESTs | | 4.42 |
| 430929 | AA489166 | Hs.156933 ESTs | | 4.40 |
| 433530 | BE349534 | Hs.281789 ESTs | | 4.40 |
| 446099 | T93096 | Hs.17128 hypothetical protein MGC15912 | | 4.40 |
| 447082 | T85314 | Hs.42644 thioredoxin-like | | 4.39 |
| 407168 | R45175 | Hs.117183 ESTs | | 4.38 |
| 417067 | AJ001417 | Hs.81086 solute carrier family 22 (extraneuronal | | 4.38 |
| 408380 | AF123050 | Hs.44532 ubiquitin | | 4.36 |
| 431379 | AA504264 | Hs.182937 peptidylprolyl isomerase A (cyclophilin | | 4.36 |
| 405671 | AA129547 | Hs.285754 met proto-oncogene (hepatocyte growth fa | | 4.34 |
| 419317 | AA235282 | Hs.172318 ESTs | | 4.32 |
| 450295 | AI766732 | Hs.210628 ESTs | | 4.32 |
| 423578 | AW960454 | Hs.222830 ESTs | | 4.31 |
| 419553 | N34145 | Hs.250614 ESTs, Moderately similar to ZN91_HUMAN Z | | 4.31 |
| 429512 | AA453987 | Hs.144802 ESTs | | 4.30 |
| 426848 | H72531 | Hs.36190 ESTs | | 4.30 |
| 429831 | AA564489 | Hs.137526 ESTs | | 4.30 |
| 433735 | AA608955 | Hs.109653 ESTs | | 4.30 |
| 450546 | AA010200 | Hs.175551 ESTs | | 4.27 |
| 421059 | AI654133 | Hs.30212 thyroid receptor interacting protein 15 | | 4.27 |
| 413243 | AA769266 | Hs.193657 ESTs | | 4.26 |
| 433230 | AW136134 | Hs.220277 ESTs | | 4.22 |
| 439717 | W94472 | Hs.59529 ESTs, Moderately similar to ALU1_HUMAN A | | 4.20 |
| 439362 | AI954880 | Hs.134604 ESTs | | 4.19 |
| 450157 | AW961576 | Hs.60178 ESTs | | 4.17 |
| 451690 | AW451469 | Hs.209980 ESTs | | 4.17 |
| 418661 | NM_001949 | Hs.1189 E2F transcription factor 3 | | 4.16 |
| 443135 | AI376331 | Hs.156103 ESTs | | 4.16 |
| 443148 | AI034357 | Hs.211194 ESTs, Weakly similar to ALU8_HUMAN ALU S | | 4.16 |
| 407765 | AW076027 | Hs.257711 ESTs, Moderately similar to ALU8_HUMAN A | | 4.14 |
| 428825 | AI084336 | Hs.126783 ESTs, Weakly similar to I38022 hypotheti | | 4.14 |
| 447519 | U46258 | Hs.339665 ESTs | | 4.14 |
| 439451 | AF086270 | Hs.278554 heterochromatin-like protein 1 | | 4.12 |
| 450219 | AI826999 | Hs.224624 ESTs | | 4.12 |
| 431451 | AA761378 | Hs.192013 ESTs | | 4.11 |
| 432917 | NM_014125 | Hs.279812 PRO0327 protein | | 4.10 |
| 431328 | AA502999 | Hs.291591 ESTs | | 4.09 |
| 425992 | AA367069 | Hs.100636 ESTs | | 4.08 |
| 404571 | | | | 4.06 |
| 420911 | U77413 | Hs.100293 O-linked N-acetylglucosamine (GlcNAc) tr | | 4.06 |
| 421114 | AW975051 | Hs.293156 ESTs, Weakly similar to I78885 serine/th | | 4.06 |
| 432731 | R31178 | Hs.287820 fibronectin 1 | | 4.06 |
| 433588 | AI056872 | Hs.133386 ESTs | | 4.06 |
| 434658 | AI624436 | Hs.310286 ESTs | | 4.06 |
| 444040 | AF204231 | Hs.182982 golgin-67 | | 4.06 |
| 444984 | H15474 | Hs.132898 fatty acid desaturase 1 | | 4.06 |
| 438543 | AA810141 | Hs.192182 ESTs | | 4.05 |
| 413497 | BE177661 | gb:RC1-HT0598-020300-011-h02 HT0598 Homo | | 4.04 |
| 434575 | AI133446 | Hs.299964 Homo sapiens clone FLB7723 PRO2055 mRNA, | | 4.04 |
| 430256 | AA4470152 | Hs.192195 ESTs | | 4.04 |
| 424839 | AA740632 | Hs.120850 ESTs, Weakly similar to ALU1_HUMAN ALU S | | 4.02 |
| 429048 | AI372949 | Hs.44241 Homo sapiens cDNA: FLJ21447 fts, clone C | | 4.02 |
| 449429 | AA054224 | Hs.59847 ESTs | | 4.02 |
| 410762 | AF226053 | Hs.66170 HSKM-B protein | | 4.00 |
| 418876 | AA740616 | gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens | | 4.00 |
| 425905 | AB032959 | Hs.318584 novel C3HC4 type Zinc finger (ring finger | | 4.00 |

| | | | | |
|--------|-----------|-----------|---|------|
| 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytотактин) | 4.00 |
| 431393 | AW971493 | Hs.134269 | ESTs, Highly similar to cytokine receptor | 4.00 |
| 435008 | AF150262 | Hs.162898 | ESTs | 4.00 |
| 431361 | AW971375 | Hs.292921 | ESTs | 3.97 |
| 444816 | Z48633 | Hs.283742 | H.sapiens mRNA for retrotransposon | 3.96 |
| 434701 | AA460479 | Hs.321707 | KIAA0742 protein | 3.96 |
| 413886 | AW958264 | Hs.103832 | similar to yeast Upf3, variant B | 3.95 |
| 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 3.92 |
| 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 3.91 |
| 435714 | AA699325 | Hs.269880 | ESTs | 3.86 |
| 447514 | AI809314 | Hs.208501 | ESTs, Weakly similar to B34087 hypotheti | 3.86 |
| 453818 | BE256832 | Hs.10711 | hypothetical protein FLJ13449 | 3.85 |
| 433586 | T85301 | | gbyd78d06.s1 Soares fetal liver spleen | 3.85 |
| 440638 | AI376551 | | gbta64e10.x1 Soares_NFL_T_GBC_S1 Homo s | 3.85 |
| 417819 | AI253112 | Hs.133540 | ESTs | 3.84 |
| 409596 | BE244200 | Hs.55075 | KIAA0410 gene product | 3.83 |
| 423129 | L44396 | Hs.124106 | Homo sapiens cDNA FLJ11941 fis, clone HE | 3.83 |
| 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 3.83 |
| 431193 | AW749505 | Hs.296770 | KIAA1719 protein | 3.81 |
| 409262 | AK000631 | Hs.52256 | hypothetical protein FLJ20624 | 3.80 |
| 425568 | AW963118 | Hs.161784 | ESTs | 3.78 |
| 441085 | AW136551 | Hs.181245 | Homo sapiens cDNA FLJ12532 fis, clone NT | 3.77 |
| 428079 | AA421020 | Hs.208919 | ESTs | 3.77 |
| 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 3.76 |
| 435354 | AA678267 | Hs.117115 | ESTs | 3.75 |
| 436535 | AW295687 | Hs.254420 | ESTs | 3.74 |
| 420439 | AW270041 | Hs.193053 | eukaryotic translation initiation factor | 3.72 |
| 436090 | AI640635 | Hs.116468 | EST | 3.71 |
| 416265 | AA177088 | Hs.190065 | ESTs | 3.70 |
| 417715 | AW869587 | Hs.86366 | ESTs | 3.67 |
| 435577 | AA694142 | Hs.293726 | ESTs, Weakly similar to TSGA RAT TESTIS | 3.67 |
| 438607 | AW080237 | Hs.252884 | ESTs | 3.66 |
| 408194 | AA601038 | Hs.191797 | ESTs, Weakly similar to S65657 alpha-1C- | 3.65 |
| 417211 | T97617 | Hs.269092 | ESTs | 3.60 |
| 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 3.59 |
| 410390 | AA876905 | Hs.125286 | ESTs | 3.58 |
| 438818 | AW979008 | Hs.222487 | ESTs | 3.57 |
| 431416 | AA532718 | Hs.178604 | ESTs | 3.57 |
| 433517 | AW022133 | Hs.189838 | ESTs | 3.56 |
| 428355 | BE256452 | Hs.2257 | vitronectin (serum spreading factor, som | 3.56 |
| 432954 | AI076345 | Hs.214199 | ESTs | 3.53 |
| 434466 | AB037829 | Hs.3862 | regulator of nonsense transcripts 2; DKF | 3.53 |
| 421933 | R98881 | Hs.109655 | sex comb on midleg (<i>Drosophila</i>)-like 1 | 3.52 |
| 422082 | AA016188 | Hs.111244 | hypothetical protein | 3.52 |
| 437135 | AL038624 | Hs.208752 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 3.49 |
| 424723 | BE409813 | Hs.152337 | protein arginine N-methyltransferase 3(h | 3.49 |
| 434280 | AB005398 | | gb:CM1-BN0116-150400-189-h02 BN0116 Homo | 3.49 |
| 407289 | AA135159 | Hs.203349 | Homo sapiens cDNA FLJ12149 fis, clone MA | 3.48 |
| 417670 | R07785 | | gbtyff15c06.r1 Soares fetal liver spleen | 3.48 |
| 431615 | AW295859 | Hs.235860 | ESTs | 3.48 |
| 429355 | AW973253 | Hs.292689 | ESTs | 3.45 |
| 430068 | AA464964 | | gbzx80f10.s1 Soares ovary tumor NbHOT H | 3.45 |
| 432929 | AW207166 | Hs.191265 | ESTs | 3.44 |
| 437763 | AA469369 | Hs.5831 | tissue inhibitor of metalloproteinase 1 | 3.44 |
| 445674 | BE410347 | Hs.13063 | transcription factor CA150 | 3.42 |
| 408113 | T82427 | Hs.194101 | Homo sapiens cDNA: FLJ20869 fis, clone A | 3.42 |
| 408808 | BE295227 | Hs.250822 | serine/threonine kinase 15 | 3.41 |
| 432235 | AA531129 | Hs.190297 | ESTs | 3.41 |
| 453985 | N44545 | Hs.251865 | ESTs | 3.41 |
| 415736 | AA827082 | Hs.291872 | ESTs | 3.38 |
| 430220 | BE378277 | Hs.152230 | ESTs | 3.37 |
| 426510 | AW861225 | Hs.194637 | BANP homolog, SMAR1 homolog | 3.37 |
| 412104 | AW205197 | Hs.240951 | Homo sapiens, Similar to RIKEN cDNA 2210 | 3.36 |
| 411573 | AB029000 | Hs.70823 | KIAA1077 protein | 3.33 |
| 413816 | AW958181 | Hs.189998 | ESTs | 3.32 |
| 428057 | AI343641 | Hs.185798 | ESTs | 3.32 |
| 436280 | AI690734 | Hs.131740 | Homo sapiens cDNA: FLJ22562 fis, clone H | 3.31 |
| 449365 | AW968261 | Hs.118913 | ESTs, Moderately similar to T46371 hypot | 3.31 |
| 440659 | AF134160 | Hs.7327 | claudin 1 | 3.30 |
| 436110 | AA704899 | Hs.291651 | ESTs, Weakly similar to I38022 hypotheti | 3.29 |
| 433862 | D86960 | Hs.3610 | KIAA0205 gene product | 3.29 |
| 424624 | AB032947 | Hs.151301 | Ca2+-dependent activator protein for secr | 3.29 |
| 439955 | AW203959 | Hs.149532 | ESTs | 3.28 |
| 417333 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 3.28 |
| 436150 | AW510927 | Hs.125243 | ESTs | 3.27 |
| 414900 | AW452420 | Hs.248678 | ESTs | 3.26 |

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|--------|-----------|-----------|---|------|
| 439349 | AI660898 | Hs.195602 | ESTs | 3.25 |
| 428255 | AI627478 | Hs.187670 | ESTs | 3.24 |
| 436217 | T53925 | Hs.107 | fibrinogen-like 1 | 3.24 |
| 429083 | Y09397 | Hs.227817 | BCL2-related protein A1 | 3.24 |
| 422244 | Y08890 | Hs.113503 | karyopherin (importin) beta 3 | 3.22 |
| 430178 | AW449612 | Hs.152475 | ESTs | 3.21 |
| 413810 | AW197644 | Hs.19107 | ESTs | 3.20 |
| 428728 | NM_016625 | Hs.191381 | hypothetical protein | 3.20 |
| 437151 | AA745618 | Hs.194637 | BANP homolog, SMAR1 homolog | 3.19 |
| 427051 | BE178110 | Hs.173374 | <i>Homo sapiens</i> cDNA FLJ10500 fts, clone NT | 3.19 |
| 438378 | AW970529 | Hs.86434 | hypothetical protein FLJ21816 | 3.19 |
| 439943 | AW083789 | Hs.124620 | ESTs | 3.18 |
| 439280 | AI125436 | Hs.48752 | ESTs | 3.18 |
| 452336 | AA960961 | Hs.305953 | zinc finger protein 83 (HPF1) | 3.17 |
| 433713 | AW976511 | Hs.112592 | ESTs | 3.16 |
| 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 3.14 |
| 407328 | AA508857 | Hs.187748 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.14 |
| 432722 | AA830532 | Hs.326150 | ESTs | 3.14 |
| 419457 | AA243146 | Hs.209334 | ESTs, Moderately similar to S23A_HUMAN P | 3.11 |
| 449987 | AW079749 | Hs.184719 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.11 |
| 418522 | AA605038 | Hs.7149 | <i>Homo sapiens</i> cDNA: FLJ21950 fts, clone H | 3.09 |
| 409969 | AW514668 | Hs.194258 | ESTs, Moderately similar to ALU5_HUMAN A | 3.08 |
| 436299 | AK000767 | Hs.5111 | hypothetical protein FLJ20729 | 3.08 |
| 406687 | M31126 | Hs.272620 | pregnancy specific beta-1-glycoprotein 9 | 3.07 |
| 408242 | AA251594 | Hs.43913 | PIBF1 gene product | 3.07 |
| 444614 | R44284 | Hs.2730 | heterogeneous nuclear ribonucleoprotein | 3.06 |
| 459407 | N92114 | | gb:za22h11.r1 Soares fetal liver spleen | 3.05 |
| 433972 | AI878910 | Hs.3688 | cisplatin resistance-associated overexpr | 3.04 |
| 427704 | AW971063 | Hs.292882 | ESTs | 3.03 |
| 440255 | AI932285 | Hs.160569 | ESTs | 3.03 |
| 424542 | AI860558 | Hs.272009 | ESTs, Weakly similar to ALU2_HUMAN ALU S | 3.03 |
| 413822 | R08950 | Hs.272044 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.02 |
| 433944 | AL117518 | Hs.3686 | KIAA0978 protein | 3.01 |
| 440428 | BE560954 | | gb:601347719P1 NIH_MGC_8 <i>Homo sapiens</i> cD | 3.00 |

TABLE 21A

Table 21A shows the accession numbers for those pkeys lacking unigeneID's for Table 21A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|---|
| 409760 | 115373_1 | AA302840 T93016 T92950 AA077551 |
| 413497 | 1373771_1 | BE177661 H06215 BE144709 BE144829 |
| 417670 | 1692163_1 | R07785 T85948 T86972 |
| 418876 | 179960_1 | AA740616 AA654854 AA229923 |
| 419145 | 182217_1 | N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815 |
| 423974 | 233842_1 | AL118754 AA333202 H38001 |
| 430068 | 312849_1 | AA464984 M85405 AA947566 |
| 432340 | 345248_1 | AA534222 AA632632 T81234 |
| 433586 | 370470_1 | T85301 AW517087 AA601054 BE073959 |
| 434280 | 382816_1 | BE005398 AA628622 AA994155 |
| 434966 | 396504_1 | AA657494 AI582663 AI581639 |
| 438962 | 467390_1 | BE046594 BE046667 AA828585 AI207343 |
| 439848 | 477806_1 | AW879249 D63277 AA846968 |
| 440428 | 49370_-1 | BE560954 |
| 440638 | 499025_1 | AI376551 T87714 AA897445 |
| 456332 | 179104_1 | AA228357 AW841786 AW841716 |

TABLE 21B

| | |
|--------------|--|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| Nt_position: | Indicates nucleotide positions of predicted exons. |

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|---------------|
| 404571 | 7249169 | Minus | 112450-112648 |

TABLE 22: 177 GENES DOWN-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO NORMAL COLON TISSUE

Table 22 shows 177 genes down-regulated in colon cancer derived liver metastases compared to normal colon tissue. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" normal colon tissues was less than or equal to 0.25. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" normal adult tissue level was set to the 50th percentile.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Genes down mets vs. normal

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
|--------|-----------|-----------|--|------|
| 425196 | AL037915 | Hs.155097 | carbonic anhydrase II | 0.03 |
| 414522 | AW518944 | Hs.76325 | step II splicing factor SLU7 | 0.03 |
| 409153 | W03754 | Hs.50813 | hypothetical protein FLJ20022 | 0.03 |
| 452594 | AU076405 | Hs.29981 | solute carrier family 26 (sulfate transp | 0.03 |
| 424326 | NM_014479 | Hs.145296 | disintegrin protease | 0.04 |
| 414798 | AI286323 | Hs.97411 | hypothetical protein MGC12335 | 0.04 |
| 432150 | AK000224 | Hs.272789 | hypothetical protein FLJ20217 | 0.04 |
| 425206 | NM_002153 | Hs.155109 | hydroxysteroid (17-beta) dehydrogenase 2 | 0.05 |
| 437145 | AF007216 | Hs.5462 | solute carrier family 4, sodium bicarbon | 0.05 |
| 447513 | AW955776 | Hs.313500 | ESTs, Moderately similar to ALU7_HUMAN A | 0.05 |
| 414807 | AI738616 | Hs.77348 | hydroxyprostaglandin dehydrogenase 15-N | 0.06 |
| 428934 | AF039401 | Hs.194659 | chloride channel, calcium activated, fam | 0.06 |
| 432251 | AW972983 | Hs.232165 | polyclathrinium rubra vera 1; cell surface | 0.07 |
| 431727 | AW293464 | Hs.162031 | ESTs | 0.07 |
| 421515 | Y11339 | Hs.105352 | GalNAc alpha-2, 6-sialyltransferase I, I | 0.07 |
| 414555 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, | 0.08 |
| 412047 | AA934589 | Hs.49596 | ESTs | 0.08 |
| 412056 | T28160 | Hs.778 | guanylate cyclase activator 1B (retina) | 0.08 |
| 422440 | NM_004812 | Hs.116724 | aldo-keto reductase family 1, member B10 | 0.08 |
| 450684 | AA872605 | Hs.25333 | interleukin 1 receptor, type II | 0.09 |
| 418935 | T28499 | Hs.89485 | carbonic anhydrase IV | 0.09 |
| 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant | 0.09 |
| 422260 | AA315993 | Hs.105484 | regenerating gene type IV | 0.09 |
| 433336 | AF017986 | Hs.31386 | secreted frizzled-related protein 2 | 0.09 |
| 426784 | U03749 | Hs.172216 | chromogranin A (parathyroid secretory pr | 0.09 |
| 441888 | AI733306 | Hs.128071 | hypothetical protein FLJ21302 | 0.10 |
| 440624 | AF017987 | Hs.7306 | secreted frizzled-related protein 1 | 0.10 |
| 420929 | AI694143 | Hs.296251 | programmed cell death 4 | 0.10 |
| 429970 | AK000072 | Hs.227059 | chloride channel, calcium activated, fam | 0.10 |
| 417233 | W25005 | Hs.24395 | small inducible cytokine subfamily B (Cy | 0.10 |
| 414802 | AI793107 | Hs.27018 | Ris | 0.10 |
| 424566 | M16801 | Hs.1790 | nuclear receptor subfamily 3, group C, m | 0.11 |
| 421996 | AW583807 | Hs.1460 | glucagon | 0.11 |
| 423371 | AU076819 | Hs.1650 | solute carrier family 26, member 3 | 0.11 |
| 406741 | AA058357 | Hs.74466 | carcinoembryonic antigen-related cell ad | 0.11 |
| 414176 | BE140638 | Hs.75794 | endothelial differentiation, lysophospha | 0.11 |
| 408741 | M73720 | Hs.646 | carboxypeptidase A3 (mast cell) | 0.11 |
| 424527 | AW138558 | Hs.267158 | ESTs, Weakly similar to I54374 gene NF2 | 0.12 |
| 426682 | AV680038 | Hs.2056 | UDF glycosyltransferase 1 family, polype | 0.12 |
| 453967 | AW009077 | Hs.232947 | ESTs | 0.12 |
| 425920 | AL049977 | Hs.162209 | claudin 8 | 0.13 |
| 408134 | AK000184 | Hs.42945 | acid sphingomyelinase-like phosphodiester | 0.13 |
| 457407 | AA505035 | Hs.195651 | ESTs | 0.13 |
| 446500 | U78093 | Hs.15154 | sushi-repeat-containing protein, X chrom | 0.14 |
| 422487 | AJ010901 | Hs.198267 | mucin 4, tracheobronchial | 0.14 |
| 409196 | NM_001874 | Hs.334873 | carboxypeptidase M | 0.14 |
| 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 0.14 |
| 406636 | L12064 | | gb:Homo sapiens (clone WR4.12VL) anti-th | 0.14 |

| | | | | |
|--------|--------------------|-----------|---|------|
| 457982 | AW856093 | Hs.183617 | ESTs | 0.14 |
| 407744 | AB020629 | Hs.38095 | ATP-binding cassette, sub-family A (ABC1 | 0.14 |
| 430378 | Z29572 | Hs.2556 | tumor necrosis factor receptor superfamily | 0.14 |
| 424885 | AB333771 | Hs.82204 | ESTs | 0.14 |
| 423555 | AW958201 | Hs.178589 | hepatocellular carcinoma antigen gene 52 | 0.14 |
| 444237 | AA336878 | Hs.9842 | Human DNA sequence from clone RP4-788L20 | 0.14 |
| 445848 | AA774824 | Hs.13377 | Homo sapiens clone 23649 and 23755 unkno | 0.14 |
| 451062 | AL110125 | Hs.25910 | Homo sapiens mRNA; cDNA DKFZp564C1416 (f | 0.14 |
| 436485 | X59135 | Hs.156110 | immunoglobulin kappa constant | 0.14 |
| 423655 | AA722425 | Hs.182785 | ESTs, Moderately similar to 1207289A rev | 0.15 |
| 417332 | AW972717 | Hs.288462 | hypothetical protein FLJ21511 | 0.15 |
| 427506 | AK000134 | Hs.179100 | hypothetical protein FLJ20127 | 0.15 |
| 430712 | AW044647 | Hs.196284 | ESTs | 0.15 |
| 421666 | AL035250 | Hs.1408 | endothelin 3 | 0.16 |
| 425692 | D80041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acetyl | 0.16 |
| 429412 | NM_006235Hs.2407 | Hs.4 | POU domain, class 2, associating factor | 0.16 |
| 433745 | AF075320 | Hs.28980 | hypothetical protein FLJ14540 | 0.16 |
| 450085 | AW293791 | Hs.60162 | Homo sapiens cDNA: FLJ21528 fs, clone C | 0.16 |
| 417820 | D87449 | Hs.82635 | UDP-glucuronic acid/UDP-N-acetyl/galactos | 0.16 |
| 406722 | H27498 | Hs.293441 | Homo sapiens SNC73 protein (SNC73) mRNA, | 0.16 |
| 426488 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 0.16 |
| 436327 | AA813075 | Hs.120181 | ESTs | 0.16 |
| 408873 | AL046017 | Hs.182278 | calmodulin 2 (phosphorylase kinase, delta | 0.16 |
| 429524 | AB033037 | Hs.205293 | KIAA1211 protein | 0.16 |
| 447023 | AA356764 | Hs.17109 | Integral membrane protein 2A | 0.17 |
| 424264 | D80400 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 0.17 |
| 410310 | J02931 | Hs.62192 | coagulation factor III (thromboplastin, | 0.17 |
| 432563 | NM_013261Hs.198468 | Hs.231958 | peroxisome proliferative activated recep | 0.17 |
| 406897 | M57417 | Hs.198468 | gb:Homo sapiens mucin (mucin) mRNA, part | 0.17 |
| 451095 | BE383224 | Hs.25925 | Homo sapiens, clone MGC:15393, mRNA, com | 0.17 |
| 447726 | AL137638 | Hs.19368 | matrilin 2 | 0.17 |
| 409549 | AB029015 | Hs.54866 | phospholipase C, epsilon 2 | 0.17 |
| 433334 | AI927208 | Hs.231958 | matrix metalloproteinase 28 | 0.17 |
| 425849 | AJ000512 | Hs.296323 | serum/glucocorticoid regulated kinase | 0.17 |
| 407360 | X13075 | Hs.296323 | gb:Human 2a12 mRNA for kappa-immunoglobu | 0.17 |
| 430627 | U81148 | Hs.247685 | ataxin homolog 1 (<i>Drosophila</i>) | 0.17 |
| 418807 | NM_004944Hs.88646 | Hs.4 | deoxyribonuclease I-like 3 | 0.18 |
| 453399 | Z70295 | Hs.32966 | guanylate cyclase activator 2B (uroguany | 0.18 |
| 422994 | AW891802 | Hs.296276 | ESTs | 0.18 |
| 432134 | AI816782 | Hs.122583 | hypothetical protein FLJ21934 | 0.18 |
| 400417 | X72475 | Hs.192124 | ESTs, Weakly similar to I38022 hypothet | 0.18 |
| 443506 | H10661 | Hs.192124 | ESTs, Weakly similar to I38022 hypothet | 0.18 |
| 428470 | AC002301 | Hs.184507 | Homo sapiens Chromosome 16 BAC clone CIT | 0.18 |
| 451928 | AI823801 | Hs.30315 | CTCL tumor antigen se57-1 | 0.18 |
| 429576 | BE242628 | Hs.209061 | sudD (suppressor of bimD6, <i>Aspergillus</i> n | 0.18 |
| 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 0.19 |
| 430304 | AL122071 | Hs.238927 | Homo sapiens mRNA; cDNA DKFZp43H1235 (f | 0.19 |
| 452852 | AK001972 | Hs.30822 | hypothetical protein FLJ11110 | 0.19 |
| 421904 | BE143533 | Hs.109309 | hypothetical protein FLJ20035 | 0.19 |
| 417165 | R80137 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fs, clone C | 0.19 |
| 417771 | AA804693 | Hs.82547 | retinoic acid receptor responder (tazaro | 0.19 |
| 452802 | AL076403 | Hs.323468 | electron-transferring-flavoprotein dehyd | 0.19 |
| 450680 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 0.19 |
| 420061 | AW024937 | Hs.29410 | ESTs | 0.19 |
| 426828 | NM_000020Hs.172670 | Hs.1 | activin A receptor type II-like 1 | 0.19 |
| 408190 | AB032963 | Hs.43577 | ATPase, Class I, type 8B, member 2 | 0.19 |
| 437682 | AA476652 | Hs.94952 | Homo sapiens cDNA: FLJ23371 fs, clone H | 0.19 |
| 449110 | H56112 | Hs.94952 | gb:yq95f07.r1 Soares fetal liver spleen | 0.19 |
| 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 0.19 |
| 408395 | BE072425 | Hs.44579 | hypothetical protein FLJ20199 | 0.20 |
| 423541 | AA256922 | Hs.129778 | gastrointestinal peptide | 0.20 |
| 410850 | AW362867 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fs, clone C | 0.20 |
| 412420 | AL035661 | Hs.73853 | bone morphogenetic protein 2 | 0.20 |
| 423942 | AF209704 | Hs.135723 | glycolipid transfer protein | 0.20 |
| 421832 | NM_016098Hs.108725 | Hs.1 | HSPC040 protein | 0.20 |
| 459046 | AA910339 | Hs.26216 | LOC50627 | 0.20 |
| 421360 | AA297012 | Hs.103839 | erythrocyte membrane protein band 4.1-ii | 0.20 |
| 438091 | AW373062 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 0.20 |
| 403047 | | | | 0.20 |
| 421712 | AK000140 | Hs.107139 | hypothetical protein | 0.20 |
| 427333 | AF067797 | Hs.176658 | aquaporin 8 | 0.20 |
| 421984 | X73079 | Hs.288579 | polymeric immunoglobulin receptor | 0.20 |
| 438089 | W05391 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 0.21 |
| 445200 | AA084460 | Hs.12409 | somatostatin | 0.21 |
| 404854 | | | | 0.21 |
| 426390 | AA377299 | Hs.80431 | ESTs | 0.21 |

| | | | | |
|--------|-----------|-----------|---|------|
| 403381 | | | 0.21 | |
| 449833 | R82252 | Hs.105106 | protein kinase (cAMP-dependent, catalytic) | 0.21 |
| 457718 | F18572 | Hs.22978 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 0.21 |
| 435730 | AB020635 | Hs.4984 | KIAA0828 protein | 0.21 |
| 431518 | AA743462 | Hs.165337 | ESTs | 0.21 |
| 412589 | R28650 | Hs.24305 | ESTs | 0.21 |
| 432584 | AA928829 | Hs.47099 | hypothetical protein FLJ21212 | 0.21 |
| 426088 | AF038007 | Hs.166196 | ATPase, Class I, type 8B, member 1 | 0.21 |
| 429143 | AA333327 | Hs.197333 | plasma glutamate carboxypeptidase | 0.21 |
| 414429 | R51494 | Hs.71818 | ESTs | 0.22 |
| 439570 | AF088076 | Hs.55507 | ESTs, Weakly similar to AC004858 3 U1 sm | 0.22 |
| 406697 | M21388 | Hs.123017 | Human unproductively rearranged Ig mu-ch | 0.22 |
| 406663 | U24683 | Hs.302063 | immunoglobulin heavy constant mu | 0.22 |
| 407811 | AW190902 | Hs.40098 | cysteine knot superfamily 1, BMP antagonist | 0.22 |
| 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule) | 0.22 |
| 430107 | AA465293 | Hs.105069 | ESTs | 0.22 |
| 424273 | W40460 | Hs.144442 | phospholipase A2, group X | 0.22 |
| 419559 | Y07828 | Hs.91096 | ring finger protein | 0.22 |
| 413517 | N76712 | Hs.44829 | ESTs, Weakly similar to I38022 hypothetical | 0.22 |
| 407243 | AA058357 | Hs.74466 | carcinoembryonic antigen-related cell ad | 0.22 |
| 433906 | AI167816 | Hs.43355 | ESTs | 0.22 |
| 446203 | Z47553 | Hs.14286 | flavin containing monooxygenase 5 | 0.22 |
| 403740 | | | 0.22 | |
| 405701 | | | 0.22 | |
| 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 0.22 |
| 419577 | L36531 | Hs.91296 | integrin, alpha 8 | 0.23 |
| 451820 | AW058357 | Hs.337353 | ESTs | 0.23 |
| 424897 | D63216 | Hs.153684 | frizzled-related protein | 0.23 |
| 422880 | AF228704 | Hs.121524 | glutathione reductase | 0.23 |
| 430832 | AI073913 | Hs.100866 | ESTs, Weakly similar to JE0350 Anterior | 0.23 |
| 430753 | AI432401 | Hs.2659 | fibrinogen-like 2 | 0.23 |
| 409060 | AI815867 | Hs.50130 | necidin (mouse) homolog | 0.23 |
| 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 0.24 |
| 414171 | AA360328 | Hs.865 | RAP1A, member of RAS oncogene family | 0.24 |
| 417916 | NM_006416 | Hs.82921 | solute carrier family 35 (CMP-sialic acid) | 0.24 |
| 414589 | AA149791 | Hs.68864 | ESTs, Weakly similar to phosphatidyseri | 0.24 |
| 427167 | AI239507 | Hs.59196 | hypothetical protein MGC11324 | 0.24 |
| 440630 | BE561430 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 0.24 |
| 423044 | AA320829 | Hs.97266 | protocadherin 18 | 0.24 |
| 441931 | BE564830 | Hs.23744 | hypothetical protein FLJ12899 | 0.24 |
| 443060 | D78874 | Hs.8944 | procollagen C-endopeptidase enhancer 2 | 0.24 |
| 405441 | | | 0.24 | |
| 407241 | M34516 | | gb3-Human omega light chain protein 14.1 | 0.24 |
| 415165 | AW887604 | Hs.78065 | complement component 7 | 0.24 |
| 426447 | AV655843 | Hs.169919 | electron-transfer-flavoprotein, alpha pol | 0.24 |
| 410748 | BE383816 | Hs.12532 | chromosome 1 open reading frame 21 | 0.24 |
| 436032 | AA150797 | Hs.109276 | latexin protein | 0.24 |
| 414256 | AW410035 | Hs.75862 | MAD (mothers against decapentaplegic, Dr | 0.24 |
| 414197 | W44877 | Hs.55501 | ESTs | 0.24 |
| 406836 | AW514501 | Hs.155110 | immunoglobulin kappa constant | 0.24 |
| 437083 | AW082597 | Hs.244862 | ESTs | 0.25 |
| 421709 | AA159394 | Hs.107056 | CED-6 protein | 0.25 |
| 426512 | AW511656 | Hs.170177 | Meis1 (mouse) homolog | 0.25 |

TABLE 22A

Table 22A shows the accession numbers for those pkeys lacking unigeneID's for Tables 21A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|-------------------------------|
| 449110 | 798430_1 | H56112 H58047 A1630710 N58742 |

TABLE 22B

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., *Nature* (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|---------------|
| 403047 | 3540153 | Minus | 59793-59968 |
| 403381 | 9438267 | Minus | 26009-26178 |
| 403740 | 7630882 | Plus | 86504-87227 |
| 404854 | 7143420 | Plus | 14260-14537 |
| 405441 | 7408124 | Plus | 100952-101283 |
| 405701 | 4263751 | Plus | 93243-93364 |

TABLE 23: 175 GENES UP-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO COLON CANCER PRIMARY TUMOR SAMPLES CLASSIFIED AS DUKE'S B SURVIVOR

Table 23 shows 175 genes up-regulated in colon cancer derived liver metastases compared to colon cancer primary tumor samples classified as Duke's B stage with a positive survival outcome (Duke's B survivor). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" Duke's B survivor was greater than or equal to 3.0. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" Duke's B survivor level was set to the 50th percentile.

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
|--------|----------|-----------|---|------|
| 426101 | AI049987 | Hs.166361 | Homo sapiens mRNA; cDNA DKFZp564F112 (fr 9.08 | |
| 432572 | AI660840 | Hs.191202 | ESTs, Weakly similar to ALUE_HUMAN !!! | 7.96 |
| 424878 | H57111 | Hs.221132 | ESTs | 7.88 |
| 428046 | AW812795 | Hs.155381 | ESTs, Moderately similar to I38022 hypot | 7.48 |
| 407284 | AI539227 | Hs.214039 | hypothetical protein FLJ23556 | 7.45 |
| 439943 | AW083789 | Hs.124620 | ESTs | 7.00 |
| 442369 | AI565071 | Hs.159983 | ESTs | 7.00 |
| 415116 | AA160363 | Hs.269956 | ESTs | 6.98 |
| 433517 | AW022133 | Hs.189838 | ESTs | 6.70 |
| 437176 | AW176909 | Hs.42346 | calcineurin-binding protein calsarcin-1 | 6.68 |
| 440524 | R71284 | Hs.16798 | ESTs | 6.62 |
| 408806 | AW847814 | Hs.289005 | Homo sapiens cDNA: FLJ21532 fis, clone C | 6.38 |
| 448974 | AI049390 | Hs.22689 | Homo sapiens mRNA; cDNA DKFZp560I318 (f6.28 | |
| 412088 | AI689496 | Hs.108932 | ESTs | 6.04 |
| 417670 | R07785 | | gb:yf15c06.r1 Soares fetal liver spleen | 5.95 |
| 440774 | AI420611 | Hs.127832 | ESTs | 5.91 |
| 426086 | T94907 | Hs.188572 | ESTs | 5.90 |
| 436100 | AA704806 | Hs.143842 | ESTs, Weakly similar to 2004399A chromos | 5.84 |
| 453204 | R10799 | Hs.191990 | ESTs | 5.84 |
| 407289 | AA135159 | Hs.203349 | Homo sapiens cDNA FLJ12149 fis, clone MA | 5.67 |
| 432435 | BE218886 | Hs.282070 | ESTs | 5.61 |
| 434963 | AW974957 | Hs.288719 | Homo sapiens cDNA FLJ12142 fis, clone MA | 5.60 |
| 421221 | AW276914 | Hs.326714 | Homo sapiens clone IMAGE:713177, mRNA se | 5.54 |
| 407328 | AA508857 | Hs.187748 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.51 |
| 440980 | AI042005 | Hs.1117 | tripeptidyl peptidase II | 5.48 |
| 443651 | W22152 | Hs.282929 | ESTs | 5.42 |
| 412668 | AA456195 | Hs.10056 | hypothetical protein FLJ14621 | 5.29 |
| 444838 | AV651680 | Hs.208558 | ESTs | 5.24 |
| 433312 | AI241331 | Hs.131765 | ESTs, Moderately similar to I38937 DNA/R | 5.11 |
| 430665 | BE350122 | Hs.157357 | ESTs, Weakly similar to I78885 serine/th | 5.11 |
| 434966 | AA657494 | | gb:nt66f04.s1 NCI_CGAP_Pr3 Homo sapiens | 5.10 |
| 426897 | AW976570 | Hs.97387 | ESTs | 5.08 |
| 432954 | AI076345 | Hs.214199 | ESTs | 5.07 |
| 431416 | AA532718 | Hs.178604 | ESTs | 5.00 |
| 420717 | AA284447 | Hs.271887 | ESTs | 4.96 |
| 424950 | AA602917 | Hs.156974 | ESTs | 4.94 |
| 438982 | BE046594 | | gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens | 4.92 |
| 419999 | AI760942 | Hs.191754 | ESTs | 4.89 |
| 435812 | AA700439 | Hs.188490 | ESTs | 4.86 |
| 418662 | AI801098 | Hs.151500 | ESTs | 4.79 |
| 428065 | AI634046 | Hs.157313 | ESTs | 4.77 |
| 407618 | AW054922 | Hs.53478 | Homo sapiens cDNA FLJ12366 fis, clone MA | 4.75 |
| 435981 | H74319 | Hs.188620 | ESTs | 4.74 |
| 419145 | N99638 | | gb:za39g11.r1 Soares fetal liver spleen | 4.73 |
| 432340 | AA534222 | | gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens | 4.72 |
| 447982 | H22953 | Hs.137551 | ESTs | 4.72 |

| | | | | |
|--------|----------|------------------------------|--|------|
| 449509 | AA001615 | Hs.84561 | ESTs | 4.72 |
| 407946 | AA226495 | Hs.154292 | ESTs | 4.70 |
| 438607 | AW080237 | Hs.252884 | ESTs | 4.68 |
| 438406 | BE273286 | Hs.254457 | Homo sapiens cDNA FLJ13255 fis, clone OV | 4.62 |
| 426818 | AA554827 | Hs.289115 | DKFZp434A0131 protein | 4.62 |
| 452220 | BE158006 | Hs.212296 | ESTs | 4.60 |
| 436823 | AW749865 | Hs.293645 | ESTs, Weakly similar to I38022 hypothet | 4.60 |
| 433854 | AA610849 | Hs.333239 | ESTs | 4.56 |
| 413816 | AW958181 | Hs.189998 | ESTs | 4.52 |
| 428079 | AA421020 | Hs.208919 | ESTs | 4.52 |
| 421097 | AI280112 | Hs.125232 | Homo sapiens cDNA FLJ13266 fis, clone OV | 4.50 |
| 417035 | AA192455 | Hs.229568 | Homo sapiens clone IMAGE:451939, mRNA se | 4.48 |
| 423974 | AL118754 | gb:DKFZp761P1910_r1 | 761 (synonym: hamy2) | 4.44 |
| 449618 | AI076459 | Hs.15978 | KIAA1272 protein | 4.44 |
| 431615 | AW295859 | Hs.235860 | ESTs | 4.44 |
| 418876 | AA740616 | gb:ny97f11.s1 NCL_CGAP_GCB1 | Homo sapiens | 4.43 |
| 428279 | AA425310 | Hs.155765 | ESTs, Weakly similar to A47582 B-cell gr | 4.42 |
| 430573 | AA744550 | Hs.136345 | ESTs | 4.42 |
| 430929 | AA489166 | Hs.156933 | ESTs | 4.40 |
| 446099 | T93096 | Hs.17126 | hypothetical protein MGC15912 | 4.40 |
| 439362 | AI954880 | Hs.134604 | ESTs | 4.36 |
| 421999 | U50535 | Hs.110630 | Human BRCA2 region, mRNA sequence CG006 | 4.35 |
| 434220 | AI174777 | Hs.283039 | Homo sapiens PRO2492 mRNA, complete cds | 4.33 |
| 432925 | AA878324 | Hs.192734 | ESTs | 4.32 |
| 417819 | AI253112 | Hs.133540 | ESTs | 4.30 |
| 426848 | H72531 | Hs.36190 | ESTs | 4.30 |
| 429831 | AA564489 | Hs.137526 | ESTs | 4.30 |
| 433735 | AA608955 | Hs.109653 | ESTs | 4.30 |
| 418884 | AA230228 | Hs.59197 | ESTs | 4.28 |
| 413243 | AA769266 | Hs.193657 | ESTs | 4.26 |
| 431749 | AI049263 | Hs.306292 | Homo sapiens mRNA; cDNA DKFZp564F133 (fr | 4.23 |
| 428054 | AI946688 | Hs.266619 | ESTs | 4.22 |
| 413967 | AW204431 | Hs.117853 | ESTs, Weakly similar to I38022 hypothet | 4.22 |
| 433230 | AW136134 | Hs.220277 | ESTs | 4.22 |
| 421057 | T58283 | Hs.10450 | Homo sapiens cDNA: FLJ22063 fis, clone H | 4.22 |
| 423578 | AW960454 | Hs.222830 | ESTs | 4.21 |
| 439717 | W94472 | Hs.59529 | ESTs, Moderately similar to ALU1_HUMAN A | 4.20 |
| 443696 | AW607444 | Hs.134622 | ESTs | 4.20 |
| 432722 | AA830532 | Hs.326150 | ESTs | 4.18 |
| 435756 | AI418466 | Hs.33565 | ESTs | 4.14 |
| 428825 | AI084336 | Hs.128783 | ESTs, Weakly similar to I38022 hypothet | 4.14 |
| 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 4.12 |
| 445943 | AW898533 | Hs.181574 | ESTs | 4.12 |
| 450219 | AI826999 | Hs.224624 | ESTs | 4.12 |
| 431379 | AA504264 | Hs.182937 | peptidylprolyl isomerase A (cyclophilin | 4.11 |
| 432451 | AW972771 | Hs.292471 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.10 |
| 443148 | AI034357 | Hs.211194 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 4.08 |
| 450177 | AI698091 | Hs.107845 | ESTs | 4.08 |
| 420911 | U77413 | Hs.102933 | O-linked N-acetylglucosamine (GlcNAc) tr | 4.06 |
| 421114 | AW975051 | Hs.293156 | ESTs, Weakly similar to I78885 serine/th | 4.06 |
| 432731 | R31178 | Hs.287820 | fibronectin 1 | 4.06 |
| 433588 | AI056872 | Hs.133386 | ESTs | 4.06 |
| 434658 | AI624436 | Hs.310286 | ESTs | 4.06 |
| 444040 | AF204231 | Hs.182982 | golgin-67 | 4.06 |
| 429512 | AA453987 | Hs.144802 | ESTs | 4.06 |
| 443349 | AI052572 | Hs.269864 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.04 |
| 439867 | AA847510 | Hs.161292 | ESTs | 4.04 |
| 425955 | T96509 | Hs.248549 | ESTs, Moderately similar to S65657 alpha | 4.02 |
| 431393 | AW971493 | Hs.134269 | ESTs, Highly similar to cytokine recepto | 4.00 |
| 432125 | AW972567 | Hs.287510 | Homo sapiens cDNA FLJ12300 fis, clone MA | 4.00 |
| 435468 | AW362803 | Hs.166271 | ESTs | 3.97 |
| 412059 | AA317952 | Hs.249721 | ESTs, Moderately similar to PC4259 ferr | 3.95 |
| 446682 | AW205632 | Hs.211198 | ESTs | 3.95 |
| 441328 | AI982794 | Hs.159473 | ESTs | 3.92 |
| 455778 | BE088746 | gb:CM2-BT0693-210300-123-d09 | BT0693 Homo | 3.90 |
| 438956 | AW748336 | Hs.168052 | KIAA0421 protein | 3.86 |
| 418303 | AA215701 | Hs.166541 | ESTs, Weakly similar to I38022 hypothet | 3.85 |
| 444816 | Z48633 | Hs.283742 | H.sapiens mRNA for retrotransposon | 3.84 |
| 429355 | AW973253 | Hs.292689 | ESTs | 3.83 |
| 438578 | AA811244 | Hs.164168 | ESTs | 3.83 |
| 432945 | AL043683 | Hs.8173 | hypothetical protein FLJ10803 | 3.83 |
| 435318 | T97301 | Hs.18026 | ESTs | 3.82 |
| 449941 | AW450536 | Hs.209260 | ESTs | 3.80 |
| 424915 | R42755 | Hs.23096 | ESTs | 3.76 |
| 449987 | AW079749 | Hs.184719 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.76 |
| 416265 | AA177088 | Hs.190065 | ESTs | 3.75 |

| | | | | | |
|--------|----------|------------------------------|--|------|------|
| 413497 | BE177661 | gb:RC1-HT0598-020300-011-h02 | HT0598 | Homo | 3.74 |
| 412093 | BE242691 | Hs.14947 | ESTs | | 3.74 |
| 413822 | R08950 | Hs.272044 | ESTs, Weakly similar to ALU1_HUMAN ALU S | | 3.73 |
| 431915 | AK000777 | Hs.272197 | Homo sapiens cDNA FLJ20770 fis, clone CO | | 3.68 |
| 434442 | AA737415 | Hs.152826 | ESTs | | 3.63 |
| 434959 | AW974949 | Hs.186564 | ESTs, Weakly similar to I38022 hypothetl | | 3.63 |
| 427704 | AW971063 | Hs.292882 | ESTs | | 3.62 |
| 426510 | AW861225 | Hs.194637 | BANP homolog, SMAR1 homolog | | 3.60 |
| 435714 | AA699325 | Hs.269880 | ESTs | | 3.60 |
| 432598 | AI341227 | Hs.157106 | ESTs | | 3.57 |
| 438543 | AA810141 | Hs.192182 | ESTs | | 3.55 |
| 422068 | AI807519 | Hs.104520 | Homo sapiens cDNA FLJ13694 fis, clone PL | | 3.54 |
| 418259 | AA215404 | Hs.137289 | ESTs | | 3.54 |
| 428290 | AI932995 | Hs.183475 | Homo sapiens clone 25061 mRNA sequence | | 3.49 |
| 419457 | AA243146 | Hs.209334 | ESTs, Moderately similar to S23A_HUMAN P | | 3.47 |
| 439312 | AA833902 | Hs.270745 | ESTs | | 3.47 |
| 408784 | AW971350 | Hs.63388 | ESTs | | 3.45 |
| 456332 | AA228357 | gb:nc39d05.r1 NCL_CGAP_Pr2 | Homo sapiens | | 3.45 |
| 424762 | AI119442 | Hs.183684 | eukaryotic translation initiation factor | | 3.44 |
| 442884 | AI076570 | Hs.134053 | ESTs | | 3.44 |
| 421023 | AW449855 | Hs.96557 | Homo sapiens cDNA FLJ12727 fis, clone NT | | 3.43 |
| 434575 | AI133446 | Hs.299964 | Homo sapiens clone FLB7723 PRO2055 mRNA, | | 3.42 |
| 430433 | AA478883 | Hs.273766 | ESTs | | 3.39 |
| 419317 | AA236282 | Hs.172318 | ESTs | | 3.38 |
| 448710 | T62926 | Hs.304184 | ESTs | | 3.37 |
| 439322 | H72245 | Hs.188635 | ESTs | | 3.37 |
| 430332 | R51790 | Hs.239483 | Human clone 23933 mRNA sequence | | 3.35 |
| 411755 | BE327036 | Hs.117494 | ESTs | | 3.33 |
| 427882 | AA640987 | Hs.193767 | ESTs | | 3.28 |
| 438899 | AF085833 | Hs.135624 | ESTs | | 3.28 |
| 436535 | AW295687 | Hs.254420 | ESTs | | 3.25 |
| 434936 | AI285970 | Hs.183817 | ESTs | | 3.22 |
| 451730 | AF095687 | Hs.26937 | brain and nasopharyngeal carcinoma susce | | 3.18 |
| 447514 | AI809314 | Hs.208501 | ESTs, Weakly similar to B34087 hypothetl | | 3.18 |
| 413672 | BE156536 | gb:QV0-HT0368-310100-091-h10 | HT0368 Homo | | 3.16 |
| 435073 | AA664078 | gb:ac04a05.s1 | Stratagene lung (937210) H | | 3.13 |
| 450295 | AI766732 | Hs.210628 | ESTs | | 3.13 |
| 419341 | N71463 | Hs.118888 | ESTs, Weakly similar to ALU1_HUMAN ALU S | | 3.13 |
| 434495 | AW352170 | Hs.129086 | Homo sapiens cDNA FLJ12007 fis, clone HE | | 3.12 |
| 408113 | T82427 | Hs.194101 | Homo sapiens cDNA: FLJ20869 fis, clone A | | 3.12 |
| 456437 | AI924228 | Hs.115185 | ESTs, Moderately similar to PC4259 ferr | | 3.12 |
| 421489 | AI922821 | Hs.32433 | ESTs | | 3.12 |
| 436090 | AI640635 | Hs.116468 | EST | | 3.11 |
| 450230 | AW016607 | Hs.201582 | ESTs | | 3.11 |
| 438011 | BE466173 | Hs.145696 | splicing factor (CC1.3) | | 3.09 |
| 418720 | AI381687 | Hs.39526 | ESTs | | 3.09 |
| 433102 | AI343966 | Hs.158528 | ESTs | | 3.08 |
| 436150 | AW510927 | Hs.125243 | ESTs | | 3.05 |
| 440116 | AI798851 | Hs.283108 | hemoglobin, gamma G | | 3.04 |
| 414900 | AW452420 | Hs.248678 | ESTs | | 3.04 |
| 435937 | AA830893 | Hs.119769 | ESTs | | 3.02 |
| 424848 | AI263231 | Hs.327090 | EST | | 3.02 |
| 435354 | AA678267 | Hs.117115 | ESTs | | 3.00 |

TABLE 23A

Table 23A show the accession numbers for those pkeys lacking unigeneID's for tables 1-20A, 21A, 22A, and 23A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

| | |
|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

| Pkey | CAT Number | Accession |
|--------|------------|---|
| 413497 | 1373771_1 | BE177661 H06215 BE144709 BE144829 |
| 413672 | 1382512_1 | BE156536 BE156439 BE156700 BE156449 BE156653 BE156533 BE156524 BE156670 BE156721 BE156723 |
| 417670 | 1692163_1 | R07785 TB5948 TB6972 |
| 418876 | 179960_1 | AA740616 AA654854 AA229923 |
| 419145 | 182217_1 | N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815 |
| 423974 | 233842_1 | AL118754 AA333202 H38001 |
| 432340 | 345248_1 | AA534222 AA632632 T81234 |
| 434966 | 396504_1 | AA657494 AI582663 AI581639 |
| 435073 | 399701_1 | AA664078 AW363313 AA805009 |
| 438962 | 467390_1 | BE046594 BE046667 AA828585 AI207343 |
| 455778 | 1364506_1 | BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952 |
| 456332 | 179104_1 | AA228357 AW841786 AW841716 |

TABLE 24: 34 GENES DOWN-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO COLON CANCER PRIMARY TUMOR SAMPLES CLASSIFIED AS DUKE'S B SURVIVOR

Table 24 shows 34 genes down-regulated in colon cancer derived liver metastases compared to colon cancer primary tumor samples classified as Duke's B stage with a positive survival outcome (Duke's B survivor). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" Duke's B survivor was greater than or equal to 0.25. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" Duke's B survivor level was set to the 50th percentile.

| | |
|----------------|---|
| Pkey: | Unique Eos probeset identifier number |
| ExAccn: | Exemplar Accession number, Genbank accession number |
| UnigeneID: | Unigene number |
| Unigene Title: | Unigene gene title |
| R1: | Genes down liver metastases vs Duke's B survivors |

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
|--------|-----------|-----------|---|------|
| 414522 | AW518944 | Hs.76325 | step II splicing factor SLU7 | 0.05 |
| 416768 | AA363733 | Hs.1032 | regenerating islet-derived 1 alpha (pancreas) | 0.07 |
| 409153 | W03754 | Hs.50813 | hypothetical protein FLJ20022 | 0.07 |
| 414555 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, brain) | 0.11 |
| 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial fluid) | 0.11 |
| 424326 | NM_014479 | Hs.145296 | disintegrin protease | 0.11 |
| 428934 | AF039401 | Hs.194659 | chloride channel, calcium activated, family 1 | 0.12 |
| 417233 | W25005 | Hs.24395 | small inducible cytokine subfamily B (Cytokine) | 0.12 |
| 422260 | AA315993 | Hs.105484 | regenerating gene type IV | 0.12 |
| 425196 | AL037915 | Hs.155097 | carbonic anhydrase II | 0.13 |
| 433356 | AF017986 | Hs.31386 | secreted frizzled-related protein 2 | 0.13 |
| 450685 | L15533 | Hs.423 | pancreatitis-associated protein | 0.14 |
| 407811 | AW190902 | Hs.40098 | cysteine knot superfamily 1, BMP antagonist | 0.15 |
| 414798 | AI286323 | Hs.97411 | hypothetical protein MGC12335 | 0.16 |
| 452852 | AK001972 | Hs.30822 | hypothetical protein FLJ11110 | 0.17 |
| 447513 | AW955776 | Hs.313500 | ESTs, Moderately similar to ALU7_HUMAN A | 0.17 |
| 423541 | AA296922 | Hs.129778 | gastrointestinal peptide | 0.17 |
| 425071 | NM_013989 | Hs.154424 | deiodinase, iodothyronine, type II | 0.18 |
| 406636 | L12064 | | gb:Homo sapiens (clone WR4.12VL) anti-thyroid hormone receptor beta | 0.18 |
| 421515 | Y11339 | Hs.105352 | GalNAc alpha-2, 6-sialyltransferase I, I | 0.18 |
| 428368 | BE440402 | Hs.83326 | matrix metalloproteinase 3 (stromelysin) | 0.19 |
| 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 0.20 |
| 452594 | AU076405 | Hs.29981 | solute carrier family 26 (sulfate transporter) | 0.20 |
| 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cytokine) | 0.21 |
| 408741 | M73720 | Hs.646 | carboxypeptidase A3 (mast cell) | 0.21 |
| 453064 | R40334 | Hs.89463 | potassium large conductance calcium-activated potassium channel | 0.21 |
| 431727 | AW293464 | Hs.162031 | ESTs | 0.22 |
| 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant domain | 0.22 |
| 442064 | AI422867 | Hs.88594 | ESTs | 0.22 |
| 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule) | 0.22 |
| 430280 | AA361258 | Hs.237868 | interleukin 7 receptor | 0.23 |
| 452877 | AI250789 | Hs.32478 | ESTs | 0.23 |
| 410310 | J02931 | Hs.62192 | coagulation factor III (thromboplastin) | 0.24 |
| 402408 | | | | 0.24 |

TABLE 24B

| Pkey: | Unique number corresponding to an Eos probeset | | |
|--------------|--|--------|---------------|
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495. | | |
| Strand: | Indicates DNA strand from which exons were predicted. | | |
| Nt_position: | Indicates nucleotide positions of predicted exons. | | |
| Pkey | Ref | Strand | Nt_position |
| 402408 | 9796239 | Minus | 110326-110491 |

TABLE 25:

Table 25 depicts Seq ID No., UnigeneID, UnigeneTitle, Pkey, and ExAccn for all of the sequences in Table 26. Seq ID No links the nucleic acid and protein sequence information in Table 26 to Table 25.

| Pkey: | Unique Eos probeset identifier number | | | |
|----------------|---|-----------|--|------------|
| ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| UnigeneID: | Unigene number | | | |
| Unigene Title: | Unigene gene title | | | |
| Seq.ID.No.: | Sequence Identification Number found in Table 26 | | | |
| Pkey | ExAccn | UnigeneID | Unigene Title | Seq ID No. |
| 426101 | AL049987 | | Homo sapiens mRNA; cDNA DKFZp564F112 (fr 1-4 | |
| 419145 | N99638 | | gb | 5 & 6 |
| 426818 | AA554827 | Hs.340046 | DKFZp434A0131 protein | 7 & 8 |
| 421057 | T58283 | | Homo sapiens cDNA | 9 |
| 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 10 & 11 |
| 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 12 & 13 |
| 409041 | AB033025 | Hs.50081 | Hypothetical protein, XP_051860 (KIAA119 | 14 & 15 |
| 443162 | T49951 | Hs.9029 | DKFZp434G032 protein | 16 & 17 |
| 436385 | BE551618 | Hs.144097 | ESTs | 18-20 |
| 447033 | AI357412 | Hs.157601 | ESTs | 21 & 22 |
| 439608 | AW884696 | Hs.301732 | hypothetical protein MGC5306 | 23-27 |
| 449032 | AA045573 | Hs.22900 | nuclear factor (erythroid-derived 2)-lk | 28 & 29 |
| 442577 | AA292998 | Hs.163900 | ESTs | 30 & 31 |
| 429970 | AK000072 | Hs.227059 | chloride channel, calcium activated, fam | 32 & 33 |
| 424566 | M16801 | Hs.1790 | nuclear receptor subfamily 3, group C, m | 34 & 35 |
| 457407 | AA505035 | Hs.345911 | ESTs | 36 |
| 430378 | Z29572 | Hs.2556 | tumor necrosis factor receptor superfamily | 37 & 38 |
| 417332 | AW972717 | Hs.288462 | hypothetical protein FLJ21511 | 39 & 40 |

TABLE 25A

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|---|
| 409041 | 10962_2 | AB033025 AL359061 AL045836 A1751521 A1752804 A1752650 AA853580 A1752290 AA853460 A1752769 AA852309 AA853785 AA853219 AW068503 A1752069 AL049389 AW068368 BE439518 W52813 BE141833 A1940574 A1750606 AL109718 AA242845 AA315795 AA307741 AW954603 A1752070 AA350794 A1752649 AA307755 AW951677 AA298896 BE439692 AA852453 AW068826 AW853984 AA418236 AA639417 AW290917 A1750592 A1752768 AL045837 A1926513 AW262903 BE439819 AI459360 AW339074 AW295181 AW029483 A1750945 A1750653 A1752525 A147588 BE440122 A1751522 A1473816 A1752291 AI694639 AI925816 AA539947 AA242752 AW021892 A1755098 AW469299 AW769363 AA853579 A1784082 AA852454 AI925501 AA976657 AW150473 AW166734 |
| 417332 | 166755_1 | AW972717 AA523805 AI962905 A173245 AW235545 A1812045 AW589434 A1826824 AW572339 A1377551 AA195718 A1868470 |
| 419145 | 182217_1 | N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815 |
| 421057 | 198849_1 | T58283 AA765038 AA283052 H99396 AA814751 A1032674 N81016 N81017 BE222349 AA830545 |
| 424566 | 2408_1 | M16801 NN_000801 D57171 AL041328 AF058623 A1201179 AA151766 AA558349 A1698649 A1692765 BE327401 AA744953 AA744951 AW361986 AV651840 AW28984 AW945145 W24096 AA183925 A1458972 AW190993 A1765359 A1634663 A1741201 AI418944 A1767551 A6779687 AW772342 AW629508 BE504300 A1251790 A1522294 AA724341 AW615402 A1537570 AA470665 AI458375 AW768901 AA447079 T23537 A1783744 R44301 D56621 N91919 AA149749 |
| 426101 | 26088_1 | AL049987 AW3622842 T78981 AA247541 A1217018 AW961515 AA632986 AA663108 BE326465 AW872412 A1024689 AA453725 BE150456 AA229448 AA442638 AA442648 AI916737 AA460220 AA68553 A1827987 A1050467 R31132 A1742087 AA442379 N56349 AW769479 AI860142 AI917507 AA813604 AI860141 A1459289 AA522837 A1354470 A1921333 BE466760 AW971193 AW103830 AW277065 AW020895 AI187977 AW82268 A1084517 R95914 AA833517 AA563934 AA437299 AA436880 AA447794 AA812876 AA663178 P31089 AI472712 R64648 A1600372 A1229164 AA703066 AW270324 A191725 AA551512 AA493776 AA554827 A10701001 AW972954 A1039129 AA385540 AA911663 |
| 426818 | 272427_1 | AK000072 AW840683 AW843764 AW844444 AW844515 AW603469 AW882395 A1860838 AW511708 AF127035 NM_012128 AK000138 |
| 429970 | 31134_1 | Z29572 AW976377 AA286871 AA633372 AA987627 AA743176 A1865358 AJ006884 AF031845 Z14955 X63629 NM_001793 BE175433 BE153425 AW364593 BE315317 AW950190 AA314252 BE142943 AW365220 AW368405 BE04269 AW368568 A1040600 A182973 A1591168 BE146183 A1631060 A1830793 W78081 W82295 A1927422 BE009913 A1371793 AW993031 A1204659 AA535113 AW993030 A190281 A155159 A1265637 AW993146 A149268 AA425217 AW473194 AI890930 AA551993 A1952106 W92308 A1827275 W45400 A1952328 AW609233 AA774611 AA551779 AI913967 AI798658 AI537658 AW517535 AA632236 AW339148 AW589522 AA836945 AA961263 AW015821 AW272946 C00249 W430334 BE143121 |
| 430378 | 3170_1 | B5551618 AI207338 BE220568 A1261568 AW841737 AA714722 AA946891 AI033239 |
| 431958 | 3394_1 | AW864696 AW338889 A142866 A1084522 A1244150 A1610339 AA425635 AA764930 AA976965 AW805766 AA057765 AW805845 AW802595 AA262971 A1869620 N75323 BE549060 AW805725 AA025809 N80776 N64595 AW073372 AA025493 AI819475 AW028879 AW189496 AA442907 AW410368 A1911629 N71276 AW316922 AW805838 AA043880 AW189184 AA449756 AA748153 AA105608 A1910643 A1279492 BE160119 AW805761 A1026262 AA782207 AW057652 AW805768 H21998 AW194254 AW275178 A1449040 A1279582 N76314 N54348 |
| 436385 | 418907_1 | AA292998 AW230350 A1676059 AW074092 BE566458 AW078677 AW514801 AW073701 AW170620 A1523736 A1580870 |
| 439608 | 47438_3 | A1923975 AI393326 A170229 AW450814 AW628452 A1671457 AA937534 A1889694 AW339423 AW291875 AA551874 AI682314 AI926227 AA397375 |
| 442577 | 54549_1 | AA292998 AW230350 A1676059 AW074092 BE566458 AW078677 AW514801 AW073701 AW170620 A1523736 A1580870 A1923975 AI393326 A170229 AW450814 AW628452 A1671457 AA937534 A1889694 AW339423 AW291875 AA551874 |
| 443162 | 5613_1 | T49951 AA025326 H04839 AA393303 R63101 W57657 W25628 A1961431 R71165 N39940 H01548 H01759 AA641624 A1634930 AA595296 AW994770 AW994747 BE047247 W38159 AA858133 A170194 AW386273 AA676625 R24676 R79410 AA922863 A151319 H01013 A024482 W2674 H01456 A150588 AW135972 AW631167 A1270332 H04750 T49522 AA004543 R63061 A1093066 A1247539 H01225 H03388 AW472933 A382448 A1219287 N27194 AW389613 A649738 AW994764 AW389614 R25176 AA897262 R71626 A1909471 R71240 AW811917 R76109 A1202312 A1856010 R76162 AL117538 R79411 T586566 AW994674 |
| 446619 | 685_1 | AU076643 AA594604 AA346866 R18197 AA345192 AA337773 AA089791 R84435 AA337838 AW392167 AA075190 D55416 AW150360 AW362257 AA579816 H030489 AW385689 AW385697 A1816216 AW581197 A1037509 A1019562 AA232625 R87905 AW368019 AA242891 AW888502 A1798331 AW385635 AW581221 T96947 A186988 AA369511 AA075191 R80742 AA366406 W92752 H45586 A1664016 AW888497 BE04992 A1384110 A1624256 A1627593 W92728 A1682719 A1948208 A1171734 N40517 J04765 AA379957 AA362403 NM_000582 A1052124 A1300290 AA333447 AA343721 AW889543 BE565767 R76601 R18015 A100531 AA489963 A101266 AA363513 AA344088 A1336750 N75705 D56440 AL110351 AL110331 F12195 R20175 AA336664 H17765 AA363533 AA363590 D28760 AW578517 AA363531 A1814687 A1846899 AA366253 AW951285 A1297992 AA327756 AW361609 AW815455 AW815427 D54182 AW852200 A171630 W27018 AW815864 AW379955 AW378222 AW3622610 BE566022 AW021023 C17352 D58435 AA345409 A1623991 AW020867 A1924770 A1799443 AW946393 AA991239 A1571617 A1935181 A1923998 A1826895 A1860319 AW189873 AW270353 AW023584 A1813811 R99929 AW339056 AA913152 A1636352 A1829394 AW151077 AW192580 A1570119 A1086391 AW021764 AW519154 A1375193 AW268678 BE465690 AW019983 AW28654 A1573138 A1914809 A1954553 A1559242 AA568945 AA886417 AW338527 A1635881 BE465666 A1921239 AA968537 A1856027 A1911981 A1827661 AW511046 BE619780 A1922227 A1811870 AW190131 AW129220 AW512906 A1280757 A1819088 A1623771 A1775616 BE349419 A1126375 H88773 A1241758 AW275157 A1337848 A1613425 A1631387 AA522631 A1273483 A1982898 AW168957 A1464841 BE051588 BE048264 A1499822 AW023812 BE220523 AW973846 BE349276 A141091 A1976060 AW973845 A101270 A1582472 AW813675 A139350 A1282627 A1276044 N22345 A1261875 A1634136 A1824468 AW887693 N27107 R21504 A1042223 N22057 AW198871 A1581019 BE04973 A1252035 N22087 A1570717 H11250 A1804026 AA368098 AA021512 H08842 N26275 A176368 A1758758 AA570371 AA232574 BE221177 AW190221 AW471386 M78225 A1422140 A1624521 AA719775 AA300291 AA568657 A1871430 BE465630 N71862 T2587 W92721 H88774 D54383 AW103693 AW089986 A1832689 R42363 R44962 T98770 AA357374 AW022074 A1356207 T29241 AW089431 A1933875 N66267 N67352 AA121786 AA363910 P09824 T95618 N66888 R80550 A1280657 AW19679 |

R59299 AW021049 H73469 A1954311 BE439454 AW079450 AW973850 AA348338 AW896006 AW268145 AA853631 H17650
R39537 N66873 N67240 H06298 A1784199 R44260 AA904118 AA911756 F04544 AA807809 AA665210 A1696448 T29719
AA837240 T64844 H08926
447033 704603_1 A1357412 A1870708 A1590539 W07459
449032 7945_1 AA045573 AA279920 R20139 AA372783 AW983629 H21473 R78318 W74359 AA022505 AA369091 AW084075 AA503638
AV660815 A1216262 AA779843 BE219825 AF125534 AW972129 A1919099 A1621283 A1300590 A1953701 AA331415 AW610546
AW793050 A1953679 AW793047 AW610543 A1671103 AW292105 AW024112 R77947 W76339 AA305111 AA132523 AA227467
H21401 AW366572 AW024129 A1701886 A1654744 BE042803 A1347173 AW866053 AW662710 R36639 A1469777 AA962733
A1865366 AA501998 AW866054 BE178974
457407 333252_1 AA505035 AW235098 A1634028

Table 26

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #:

see Table 25 & 25A for complete list

| | 1 | 11 | 21 | 31 | 41 | 51 |
|---|------|----|----|----|----|----|
| CAATATAGTA CAATAACTAT TTGATGACA TTTACATGG ATATTATGAG TGATCTAGAG | 60 | | | | | |
| TTGATATGAA GTATATGGGA GGATGTGCAA AGGTGATGTC CAAATACTAT GTCATTTTAT | 120 | | | | | |
| AGGGGGACT TGAGTATCCT TTGTTACCT CAGGAGATCC TGAAACCAGT CCCCCATGGA | 180 | | | | | |
| TACTGAGGC TGACTGTATA GTCTTATCCT CACCGAACCT TCATCTTAAT GGGGAAAGAC | 240 | | | | | |
| TGACTATAAA CAAAAATAT GTAATAGGTG GTGGTAAGTA CGGTGGAGAA GTAACAAATG | 300 | | | | | |
| GGGCAAGTG AGTTATACAG CTCCATTCT AGAAACCTTG GAGTACTTT CTAGTTTAT | 360 | | | | | |
| ACTCTGGTG GTTCTCTTT GTCTCCCTTA TTACATGGGA CTCTGACATG TGCCCATAGC | 420 | | | | | |
| TAGGTGACA GTAGGATCTA CCCGATAGTA GGGTGGCAGT AGGATCTACC CAAAAAAGCGT | 480 | | | | | |
| CCTGCTGATA CAGGGGCTTA GCATCTGTG GTTCTCGAGC CTATAAAAAG AGCTAATGGT | 540 | | | | | |
| GTTCCTCTC TTAACTGTGG CCTCTTACAC TGTTGTTGG ATGATGGTG ATGCTTGGGA | 600 | | | | | |
| TATTGTTT CTTGGAAACT TTGAATATAC AACACTTAC TAGGGAATT GCAATGGAAG | 660 | | | | | |
| CAGAGCAAAG ATGTACAGAG GAAACATGC GTAACTCTG TGGAATTGAA GTCATGAGGC | 720 | | | | | |
| AGCAGAGAGC TAAATACCA GCTTTAAAAA TTTTATTAT TTAGAGGGAA TTACTCTGGG | 780 | | | | | |
| AGTAACAGCA GTAATAGTTA ACGGAGCCAG AATGCTGAG TCATAATT GCAAAAGCAGA | 840 | | | | | |
| GTGGGAGCA ACAGATGTC AAGAGTAGTT GCTGTAGTTC CTCCTGGGT CGTAGGGAGCA | 900 | | | | | |
| GTTCATAT TACTATATAG CTACTGATG AAGAAGAGTT CTAGTGGAGG CCTGGGGTGA | 960 | | | | | |
| CAGCTCTCT TAQTATCTG TGTAACCCCA TTGACCTT TAACAAATCC CTAAGTAAT | 1020 | | | | | |
| AAATGGGCA TCAGGAAAC TAAGTTTCTC TCTGCTGTTT TTGCTTGA GAGAGCTATA | 1080 | | | | | |
| ACTGTAAAG ATCTTATTT CTGACATT TAGTGTGCA CAATATTGG TAATATTAT | 1140 | | | | | |
| GTTCTATA TTGTAATGA ACATTCCTC TCCGGTACAT TTTTGTAA ATTATGTTT | 1200 | | | | | |
| GATGATAAA AGTICACCTT TTATTGATA AAATTGACTG AGATTAATT ATACACATTG | 1260 | | | | | |
| ACAATGGGTA AATAGATT TTCAAGATT TAAAGCTGAA AGGATGACCA CGTAAGCACAA | 1320 | | | | | |
| AAAAAAAGA AAAAACCAA CAAAAATAAA CCCAACCC CTCACAAATT TCGAACACGA | 1380 | | | | | |
| AACATCTTC TGATGCCGG ATCCCTGCT CGACGGTGTGA AGGGGGCAGG AACAGCGAG | 1440 | | | | | |
| GTGTCCTGGG CTGATCCCC GGGGAAGAAAT ATGAT | | | | | | |

Seq ID NO: 2 DNA sequence

Nucleic Acid Accession #: X83301.1

| | 1 | 11 | 21 | 31 | 41 | 51 |
|--|------|----|----|----|----|----|
| GCAAAGCCAG CTGGGCTCT GAGTCGGGTG GGTACTTGGA GAACITACTA CGTCTAGCTG | 60 | | | | | |
| GAGGTTGTA AATGCAACCA TCAGCATGCT GTGCTCTAGCT CAAGATTTC TCCATCCCCT | 120 | | | | | |
| TATTTGGC CAGTGGCTGT CATTACATAT GAGATGTC TCTGAAAGAC TACAGATGAA | 180 | | | | | |
| CTCAAGCTCC ATGAGGGAGT GTTCACTGTG CGAGAGCAGT CATGATGGCC TGCACTCCAC | 240 | | | | | |
| ACAATGCAAC AGAGTGGAAAG AGCAGGTCTC GCTCTTTGG TGATGCTCTG AAAGCTTCTA | 300 | | | | | |
| AGAAAATCA CATCAGGTGA TGGATAGGAG CAACCCCTGA AAACCAAGCT TAGACTATT | 360 | | | | | |
| TTCAAACAGG CTGGTGAATT ACCAGATCTC CGTCAAGTGC AGTAAACCGAT TCAAGTTGGA | 420 | | | | | |
| AGTGTGCTT TTGAATGAG AGAACAAAGT CGTGCACAAAC CAGGGTGGGA CCCAGGGCCA | 480 | | | | | |
| GCTGAAGGGT CTGGGTGCCA ACCTCTGGT GCCGTACCTG ATGCCAACAC ACCCCGCCCTA | 540 | | | | | |
| CTGTACTCC TGGGAGGATG GTGATGCTC ACACCAAAGC CTGGACCCCC TOCCAGCTG | 600 | | | | | |
| TGACTCTTGG GACCAACTC ACCTACGCG CAGACCAAGGG GGCTCTGTAT GTGGATGTGA | 660 | | | | | |
| TCCGTGTGAA CAGCTACTAC TCTGTGATC GCAACTACGG GCACCTGGAG TTGATCGGC | 720 | | | | | |
| TGCACTGTC CGCCCACTT GAGAATTGGT GTGAGACATC ACAACCCAT TATICAGAGC | 780 | | | | | |
| CGCTATGGG TGGAACAGCT TGATGGTTT CACCAAGGGCT GTGTGAATTAC CAGATCTCCG | 840 | | | | | |
| TCAAGTGCAG TAACCACTTC AAGTGGAAAG TATGCTTTT GAATGCGAA AACAAGTCG | 900 | | | | | |
| TGGACACCA GGCTGGGACC CAGGGCCAGC TGAAGGGCT GTGCGAACCC TCTGGTGGCC | 960 | | | | | |
| GTGATGATG CACGACACCC CGCCTTACCT GTACTCTGG GAGGATGGTG ATTGCTACAA | 1020 | | | | | |
| CCAAAGCTT GGACCCCTC CAGCCTGTA CCTTGGGAC CAACTCCACC TAGCAGCAG | 1080 | | | | | |
| ACAAGGGGCC TCTGTATGTG GATGTGATCC GTGTAACAG CTACTACTCT TGGTATGCA | 1140 | | | | | |
| ACTAAGGGCA CCTGGAGTTT ATTGGCTGC AGGCCCTGCA GTGGCCGCC CAGTTTGTA | 1200 | | | | | |
| ATTGGTGTAA GACATCACAA TCCCATT CAGAGCGGT ATGGAGTGGAA AACGCTTGTAA | 1260 | | | | | |
| GGGTTTACCC AGTCTTCCC AGGAACTC GATGAAGTGT TCCACAAAAA TGAGCGACTG | 1320 | | | | | |
| AACCAAGAAG AGGATGACAT TAGATCCAGG AGATACAAACAGGAGATAA TCTCCAGGAT | 1380 | | | | | |
| GCTGTGAA AAAGATCTCTC GGATCCCGAG ATGATATAG GACAAGTTG TCATAATCCA | 1440 | | | | | |
| GCAGGCCAGA AGACTCTTCCAG GGAACACTCAT TTCAAGATGA AAATGGACCA GCGCGACTGG | 1500 | | | | | |
| CTCAAGCTG TAATACACGC ACTTTGGAG GTCTGGGGCG GCGGATCACT TGAGGTCAAG | 1560 | | | | | |
| AGTTGAAAC TAGCTGGCA AACCTGGCAA AACCTCCATCT CTATTAAGA TACAAAAAATT | 1620 | | | | | |
| AGCCAGGAT AGTGTGTCAT GCTCTGAGTC CCAGCTACTT GGATGCTGTA GGCAGGAGA | 1680 | | | | | |
| ATTGCTGAA CCTGGGAGGC AGAGTCTGGG GTGACCGAGA TCATGCCACT GCACCTCCAGC | 1740 | | | | | |
| CTGGGTGACA GAGCCAGACT CGCTCTCTAC TAAAAAAA AAAAAGAAT AAA | | | | | | |

Seq ID NO: 3 Protein sequence:

Protein Accession #: CAA58280.1

| | 1 | 11 | 21 | 31 | 41 | 51 |
|---|-----|----|----|----|----|----|
| MDRSNPVKPA LDYFSNRVLV YQISVKCSNQ FKLEVCLNA ENKVVDNQAG TQQQLKVLGA | 60 | | | | | |
| NLWWPYLMHE HPAYLYSWED GDCSHQSLGP LPACDLWDQL HLRSRQGGSV CGCDPCEQLL | 120 | | | | | |
| LLVSQLRAPG VDSAAAGRPV | | | | | | |

Seq ID NO: 4 DNA sequence

Nucleic Acid Accession #: BC002622.1

| | 1 | 11 | 21 | 31 | 41 | 51 |
|--|----|----|----|----|----|----|
| GGCACAGGGC TCCGCOOCGCG GOOGGGATGC ACTAGGCAA GCCAGCTGGG CTCTGAGTC | 60 | | | | | |

CGGTGGGTAC TTGGAGAACT TACTACGTCT AGCTGGAGGA TTGTAATGC ACCAATCAGC 120
 ATGCTGTGTC TAGCTCAAGA TTTCCTCCAT CCCCTATTG TGGGCCAGTG GCTGTCATTA 180
 CATATGAGAA CTCAAGCTCC ATGAGGAGAT GTTTCATTGT CGAGAGCAGT CATGATGGCC 240
 TGCACTCCAC ACAATGCAAC AGAGTAAAG AGCAGGTCT GCTCTTTGG TGAGTCCTG 300
 AAGCTCTTA AGAAACTTCA CATCAGGTGA TGGATAGGAG CAACCCCTGTA AAACCAAGCT 360
 TAGACTATT TTCAAACAGG CTGGTGAATT ACCAGATCTC CGTCAAGTGC AGTAACCACT 420
 TCAAGTTGGA AGTGTGTCTT TTGAATGCAG AAAACAAAGT CGTGGACAAC CAGGCTGGGA 480
 CCCAGGGCCA GCTGAAGGTG CTGGGTGCCA ACCTCTGGT GCGGTACCTG ATGACGAAC 540
 ACCCGCCCTA CCTGTACTCG TGGGAGGATG GTGATGGCTC ACACCAAAGC CTGGACCCCC 600
 TCCCAAGCTG TGACCTTGT GACCAACTCC ACCTACCGAG CAGACAAGGG GGCTCTGTAT 660
 GTGAGATGTGA TCCGGTGTGAA CAGCTACTAC TCTTGGTATC GCAACTACGG GCACCTGGAG 720
 TTGATTCAAGG TGCACTGGC GCGCCAGTTT GAGAATTGGT GTAGACATC ACAATCCCAT 780
 TATTCAAGAGC GCGTATGGAG TGGAAACGCT TGTAAGGGTTT CACCAAGTCTT TCCCAGGGAA 840
 CTCCGATGAA GTGTTCCAAAC AAAATGAGCG AGTGAACCAA GAAGAGGATG ACATTAGATC 900
 CAGGAGATC AACAGAGGG ATAATCTCCA GGATGCGCTGT GAAGAAAGAT CCCTGGATCC 960
 CAGGATGATT ATAGGACAAGG TTGTCATAA TCCACCCAGGC CAGAACACTT CCAGGGAAAC 1020
 TCATTCAGG AGGTGAAAAT GATGAGTGCAC TCTCTCAAGA TGAAAATGGA CCAGCCCGAG 1080
 TGGCTACGCC CTGTAATACC AGCACCTTGG GAGGCTGAGG CAGGGGGATC ACTTGAGGTC 1140
 AGGAGTTGA AACTAGCTG GCCAACGTG AAAAATCTCA TCTCTTAA AAATACAAAAA 1200
 ATTACCCAAG CATACTGGTG CATGCTGTGA GTCCCAAGCTA CTGGGATGC TGAGGCAGGA 1260
 AGAATGCTT GAACCTGGGA GGCAAGAGTCT ACAGTGAGCTG GAGATCATGC CACTGCACTC 1320
 CAGCTGGGC AACACAGTGA GACTCCATCT CAAAAAAA AAAAAAAA AA

Seq ID NO: 5 Protein sequence:
 Protein Accession #: AAH02622.1

1 11 21 31 41 51

MDRSPVKPA LDYFSNRLVN YQISVKCSNQ FKLBVCLLNA BNKVDNQAG TQQLKVLGA 60
 NLWPSVLMHE HPAYLYSWD GDCHSQSLGP LPACDLCDQL HLRSRQGGSV CGCDPCEQLL 120
 LLVSQLRAPG VDSAAAGRPV

Seq ID NO: 6 DNA sequence
 Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51

ACCTGAGATC AGGAAGTTCTGA GATCAGCTG ACCAATAGGG TGAAACCCCG TCTCTACTAA 60
 AAATACAAAAA AATTAGCTGG ACACGATGGT GGGTGCCTGT GTTCCCGGCT ACTCGGGAGG 120
 CTGAGACAGG AGAACTAGTT GACCTGGAG TTGGTGGTTC CAGTGAGCTG AGATCACACCC 180
 ATTGATCTTCA AAGCCTGGGC AACAAGAGTG AAACCTCCAT GCAAAAAAAAA AAAAGAAAGGG 240
 GCATAATTG TGATGATAAA GGTAAGGAT GGGACATTCT TGGACTTACA 300
 GATGGTGTGA TTGCTTGCT AGAAGAAGAA TTCCCGGTCA AAAAGAAACC ATCAGCTTC 360
 CAAGTGTAA AGAGAGATAA ATCTGTGAAG ATTATAGGG CTACAGGAAA CTTAATCTTT 420
 TCTCTTAAAGAACATTG AGCAAAAATTG AGAACATTG TTCTACGTC TCTAAATTTG 480
 ACATGGACAT TTAGTGGAC TAGAAATTG GGGCATAATT TCTCCAGTG ATTTTTAATT 540
 TTAGCATGTT GATTAACCC TTCTAAATTG GCCAGAACIT AAATAAATAT TGCTTTCTAT 600
 TATTAGTATG CCATCAAAATT TAGAGCTGT TTCAAGCTTTT AATGTTGTCAA GCCTAAATC 660
 CAGATTITG AGGATCTCT CCCCCTTAA AGATATTCA GTAACTGCC GTAGAAATAC 720
 ACATGATAC AAGGGCACTG TATACATCG TCTAAAAAAAT AAAAATATGT ATACCTCTG 780
 GTGAGCTAG CACAGCTTCCCCTAGAA ATACCAATGG AGGTCAACAAA TGTGGCCCAT 840
 ATAGGTTAAT TTGTTAAATT TCTNATAGNC ACC

Seq ID NO: 7 DNA sequence
 Nucleic Acid Accession #: AK000942
 Coding sequence: 1204-1503

1 11 21 31 41 51

GTAAAGGAAT GTCTTTTAA TTTCAGCTTT CTTCCTCCA TGCTAGTGTGTT ATCAGGTTT 60
 GGTATTTT TACTTACAGC ATATGTTATG AAGCTGTTT GAAAATTTGGT TTAGATATA 120
 TCTGCAAGTT TACTACTTGG ACTGTTAAA AAAAATGAA AAAAGTAGT GACATCTGTC 180
 CTCAAGAGAA GTTTCAGGT TGCAATTG TGTTAAATAA CACAGGCTAA AAGGTAATT 240
 ATGTTCTTG GGAATTGAAA TTGTCAGTGG CCCGTACAG AAACCTATCA GTCATATATC 300
 AGCACCAGGT CATTCTTTG CACCTTAGGG ACCATCTGTC CCCTGAGGTG ACCTGAGAAA 360
 CAACCAAGTGG CCCACAGACT GTTATTTCTT CAAGTGGCC AGGATTGAT TTCACTGCCT 420
 TATATCTAT TTGTTGTTGA CAGTGGCTTGG ATTTTTGG AAAACTAAAT TTAAACATA 480
 TTGAAAAAT GTTATAAGAC TTGGACATTA AGTCTGTGA TAGCCAAGG CAGTTTACCA 540
 AAGTAAACAA AATAAAATCT ATGCTCTTC ATGTCAAAG AGCAGTCTGC CATCATGTGG 600
 ATATAATGG ACTATGTTAA GTGACATGGT GTCTACTCTC TACCTAATAA TAGCCTCCCT 660
 CCTGTTCCA CAAGATACCC AACAGGTATA TTAAATTCTAC CAGTTAATAT GTTTGGATA 720
 ATTCGCTGCC TTGAAATGCT ATATGTTTTA TAGTACATCA TAGCTTGTGTTCTCA 780
 AGGAATATC AGTTACATCC TTGGCTAACAT GTGTAAACCTC CATCTACT AAAAATACAA 840
 AAAATAGCC GGCGCTGGTG GGCGGCACCT GTAGTCCAG CTACTCGGGG GGCTGAGGCA 900
 GGAGAATGGC GTGAACCCAG GAGGGGGAGG TTGCAAGTGAG CGGAGATCGT GCCACTGTAC 960
 TCTGGCTGG GAGACAGAGC GAGACTCCAT CTAAAAAAA AAAAAGAAA AAAAAGAAA 1020
 GAGAGAGAGA CCTGGAGTAG AGATCTGTC AAAGAACCTT TTCTCTTG AGAAAGCATCT 1080
 GAAATGGAAAT CTGTTGCTC TTGAAATAT GTACTGCTGT AACAGTGGAA CAACCTCAG 1140
 AGTATGCCCTI CGTGTGGCT ACTCGTGTG GTTTGAACCT GTCTGTGTTT 1200
 GGGTCAGAAATGCTGCACTG GCTGGGCACA TTGGCTCAAG CCTGTAATCC CAGCAATTG 1260
 GGAGGCTGAG GCAGGGGGAT CACCTGGAGT CAGGGCTTCA AGACAGACT GGCAACATG 1320
 GTGAAACCCC GTCTCTACTG AAAATACAAA AATTAGCTGG GCATGGTGGC AGGTGGCTGT 1380
 AATCCCAAGCT ACCTGGGGAGG CTGAGCTGAG AGAATCGCTT GAACCCGGGA GTTGGAGGTT 1440
 GCAGTGGCC GAGATTCGAC CATTGCACTC CAGCTGGGC AACAAAGAGTG AAACCTTTGT 1500

CTCAG

Seq ID NO: 8 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

| 1 | 11 | 21 | 31 | 41 | 51 |
|----|------------|------------|-------------|------------|------------|
| GA | ACTAGGCTG | GGCAACATAG | TGAGACCTCA | TCTCTAAAAT | AAAAAAATA |
| AA | AAAAAAAC | AAAAAACG | CCAATGACA | TCACTCTTG | ATGAAAATGG |
| TT | GTGATGCC | GGGGGGGT | GGGAAATGCT | ATTCAAGCA | CAGCAGAAGA |
| CC | ACACCATG | GCTGGGCACO | GTGGTCACA | CCTGTAATCC | CAGCACTTG |
| GG | GCAGGTYG | GCCTTGAGCT | TAGGAATTG | AGACTAGCCT | GGGCAATAAG |
| AT | CATCTAAA | AAAAAA | AAAAGGTC | ATGAAACATA | TGAAGCAAAA |
| CG | CCCATICTT | TCTTTT | TCAGAGGTATT | TTGGGCCA | ATCTGGTT |
| AC | AGACATTCT | CTAGG | ATGCGGCTCT | ATTCACATAT | AAACAAATA |
| TC | AGAGCTTCT | CTAA | ATGATATCT | ICACTCTTT | TTTCACCA |
| CC | AATACCTAA | AAGCTAAC | TGGGCTTGGT | GGGGTGGCTC | ATACCTGAA |
| GG | TTGGGAGGCC | AAGTGGGAG | GATCACTGA | GCTCAGGAGT | TCCAGACCAT |
| AG | AAACAAAGG | ATTTGAGAT | CAGTGTGGC | ACTTAGCA | ACACCATCT |
| GG | AAAAAA | AAAAAA | AAAAAA | AAAAAA | 720 |

Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: BC010433.1
Coding sequence: 3-335

| 1 | 11 | 21 | 31 | 41 | 51 |
|----|-------------|-------------|-------------|-------------|--------------|
| GG | GTCCCCCTC | CGTCGTGGTC | TGGCGTGTAT | TCCGAGCCTT | GGTGTCTGGC |
| TT | CGTGGTGT | TGGGGTTTC | CGAGCGTTG | TGTCCTGGCG | TTCCGACCG |
| CC | CGGGTTCCG | ACCGTGGTG | TCTGGCACGC | GCCACCCCT | CTGCTTGG |
| GG | CCGATGTA | CC AGA | ACAAGAAAG | ACAAGAAAAT | GATTGAGGA |
| AT | GGAGAAAGC | AGCAAAACG | CCACTGAAA | CAACGCCG | CAGCTTAAT |
| CT | GGTCCAAGC | GGTACATCGT | CATAGCCGG | AAACAGTCAGA | GCCACCAAGC |
| CC | TCAATGCTG | CGAAAGCTG | TCAGGCA | TCAGGCA | AATGATCTT |
| GG | TGAAGGCTCT | GGAAAGGCTG | TACGGTAACC | GGGACCTGAC | CGCACGCTG |
| AT | CTGGCGCTT | CAAGGACTGG | ATGGTTCCA | TGATCATGGA | CAGAGAGTAC |
| CG | TGGAGGCGT | CAGACTTACG | ATACCTATCC | TTAAGAACAT | GGAAAGGGTG |
| AC | TGGACTGTGA | GAGCCTCTAC | CCCCATGTTG | AGGCCCTAA | TTGAGGCTG |
| TC | TGGGTGAATT | TC | TCGTA | TCG | CGAGATAAGA |
| GT | GAAGAGAGCA | ACGGCAGAGC | CCAGGTGCC | AGAGGACTTT | CTTCACGCTT |
| AG | TCTTGTGGA | GAGCAAGCTC | CACCGACACG | CTGCTTACTT | AGTAGACAAC |
| GG | GTGCAAGGGAC | TCAGCTGAG | GACTGGGAGG | GTCAGCAAG | CTCTCTGCTG |
| AT | AGAGACGCTC | CCACCTGGAG | CCAGGGCCAG | GGACCTTCCA | CTCTCTAGGG |
| TC | AGAGACGCTC | ATC | ATC | TTAATTCA | TTAAGAACCTTG |
| CC | CTTGTGATC | ACCTCTGCCT | ATC | ATC | 1020 |
| CA | GGAGTGGAA | TTTGTGAA | TTTGTGAA | TTTGTGAA | TTTGTGAA |
| GA | GGGTGATG | TGAGGAGAGCA | CACTGATAGA | AACTCTTGTG | TCCAGTGC |
| GT | GGGTCAGCTC | CGGGGACAGT | GCCTGGGGGG | GGCGGGACTC | CCACATGCC |
| TC | GGCTCAGCT | CCCGAGCAGC | TGGGACTACA | GGGCCGCGCC | ACCACGCTG |
| GG | GGCTCAGCT | CTCTCCCTC | CTCTCTCT | CTCTCTCT | GCTAACTTT |
| AT | TTGTTTTT | AGTAGAGAC | GGTTTTCACC | GTGTTGGCCA | GGATGGCTT |
| TC | CTCTGTCATC | ACCTCCAA | AGTGTCTGGG | TTACAGGGT | GAGCCACTGC |
| CT | GGCCAGCATG | TTAGACAA | TTAATTCA | CTCTCTGTG | CTGTTTTT |
| CC | AAAGGAATAT | TCTGTGGGG | ACAAAGGTTAC | AGAGGCTCT | ACGACATGAA |
| AA | GGTACTGGCC | TTGGCACAGT | GCCTGGGGGG | GGCGGGACTC | CCACATGCC |
| GG | CA | CTGCTTCTC | CTCTCTCT | CTCTCTCT | TGTGATGTCA |
| GT | CA | CTCTCTCT | CTCTCTCT | CTCTCTCT | 1560 |
| TC | CT | CTCTCTCT | CTCTCTCT | CTCTCTCT | 1620 |
| CC | CA | CA | CA | CA | 1680 |
| AC | AC | AC | AC | AC | 1740 |
| CA | TAACGCTCG | AGTGTCCATT | GGAAAGCCCG | TGTGCTCAT | TTAGACCTTC |
| CG | GGCCTTTCG | ACTCTCTGG | GTCTCTCTC | TTAGACCTTC | ATGGGTATA |
| AC | GGGCGTGGTG | GCACATGCC | GTAAATCCAG | CACCTGGCC | TCCCAAAGTG |
| CT | AGGAGTGA | GACCATGCC | AGCCTCCGTT | GTCTCATTT | AGCTTCA |
| GG | GGGCGTGGTG | CTTCTGGGGT | CTTCTGGGGT | CTTCTGGGGT | GGGTTATAGG |
| AT | CACTTTGAC | TTCTGGGGT | CTTCTGGGGT | CTTCTGGGGT | 1920 |
| TC | TTAA | TTAA | TTAA | TTAA | TTAA |

Seq ID NO: 10 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

| 1 | 11 | 21 | 31 | 41 | 51 |
|----|----------|------------|------------|------------|------------|
| AG | TGGNTCCC | CCGGNCTGCA | GGAAATCGGC | ACGAGATCAT | GATGGCTAAT |
| TC | GGCTTCTC | CGGGGACAGT | GGCTTCTC | GGCTTCTC | ATTTCTGAG |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| CC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| AT | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
| TC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
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| GG | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC | GGCTTCTC |
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Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: NM_000582.1
 Coding sequence: 88-990

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| AACGCCGACC | AAGGAAA | ACT CACTACATG | AGAATTCAG | TGATTTCGTT | TTGCCCTCTA |
| GGCATCACCT | GTG | CATACCA | AGTTAACAG | GCTGATTCG | GAAGTTCTGA |
| CTTCAACAA | CACCA | AGCTTGCC | ACATGGCTAA | ACCC | GTGACCC ATCTCAGAAG |
| CTTCAACAA | CTCC | TAGCCCCACA | GACCC | CTCA | AGAAGCAGCAG |
| CAGAACTCC | TAG | CCCCACA | AGTAA | GTC | ACGAAAGCCA |
| GATGATATGG | ATGATGAA | AGA | TGATGATGAC | CAT | GTGACCA |
| AACGACTCTG | ATGATG | TGA | GACACTGAT | GATT | CTCACC |
| TCTGATGAT | ATGATGAA | ACT | GGTCACTGAT | TTT | CCCACCGG |
| TTC | ACTCCAG | TG | TCACCG | AC | CTGCCAGC |
| GGACTGAGGT | CAA | AACTCTAA | GAAGT | TCG | AAACCGAAGT |
| GACGAGGACA | TCAC | CTACA | CATG | GGAAAGC | GAGGAGTTGA |
| CCCGTTGCCC | AGG | ACCTGAA | CCG | CCCTCT | GAT |
| GAAAGGAGTC | AGC | TGATG | GA | CCAG | GGACAGTTAT |
| TATAAGCGGA | AAGC | AACTGA | TGAG | GA | CCAGAAGC |
| CTTCAAAAG | TCAG | CCGTG | AT | TCAC | GGTCA |
| GTGTA | AGAC | AACT | AGA | ATTC | ACAGCCATG |
| TTAGATAG | CTC | CTG | GGTCA | ATT | TGATGTCACA |
| ATTAGTC | AA | GGTCA | TTAGG | AA | ATACAAATT |
| CTCAGTTTAT | TG | TGATG | TCTATT | TG | AGTCTGGA |
| ATTAGTTAG | TG | TG | GCT | AA | ATAACTAAT |
| CTATGTTAC | T | TG | GTG | AA | AGGTTATGT |
| TCATGAA | T | TG | GTG | AA | CTCAGGAA |
| ATAAC | TTT | TG | GTG | AA | ATTCAGTGA |
| TATCTTTTG | TG | TG | GTG | AA | ATTCAGTGA |
| AATIGCTTAT | TG | TG | GTG | AA | ATTCAGTGA |
| GCCTAAAAAA | AA | AA | AA | AA | AA |

Seq ID NO: 12 Protein sequence:
 Protein Accession #: NP_000573.1

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| PSKSNEHDH | MDDMDDEDD | DHVSDQSID | SNDSDVDDT | DDSHQD | SHSDEDELVT |
| DFPTLPDT | VFTP | VFTV | TDYGRGD | SVV | RPRDIQYPA |
| SEELNGAYKA | IPVAQDNLAP | SDWDSRKGKDS | YETSQLDDQ | S AETHSHKQR | LYKRKANDES |
| NEHSDVIDSQ | ELSKV | SREFH | SHEFHSHEDM | LVVDP | KFRISH EDLSASSEVN |

Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: NM_001793
 Coding sequence: 71-2560

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| CTCTGAGC | ATGGGCTCT | CTCTGAGC | CTCTGCTCT | TCCTCC | TCAGGTTG |
| CTGGCTCAG | TGCGCGGCT | CGAGCGGTG | CGGGCGGTG | TCAGGGAGG | CTGAAGTGAC |
| CTTGGAGGCG | GGAGGCGGG | AGCAGGAGCC | CGGCCAGGC | CTGGGAAAG | TATTGATGGG |
| CTGCCCTGGG | CAAGGAGCCG | CTCTGTTAG | CACTGATAAT | GATGACTTC | CTGTGCGGAA |
| TGGCGAGACA | GTGCA | GGAGGACT | GAAGGA | AGG | ATTCATTGA |
| ATCCAAACGT | ATCT | ACGAA | GACACAA | GAG | ATCTGCCC |
| TGAAATAGTC | AA | GGCTCCT | CAAGGAG | CTCAAGTCTA | ATAAAAGATAG |
| AGACACAAAG | ATTTT | TACA | GCAT | ACGGG | GGCGGGGCA |
| CTTCGCTGTA | GAGA | AGGAGAGA | CAGG | CTGTTG | AA |
| GATTGCGGA | TATG | GCGCT | TG | TG | CAAGGAGGA |
| CCCATGAAAC | ATCT | CCAT | TC | TC | ACGAGCTGG |
| GGACACCTTC | CGAGG | AGGT | TCT | TG | AGGTGAGG |
| GACAGGAC | GTG | AGG | TCT | TG | AGGTGAGG |
| CCATAGCAA | GAAC | AAAG | ACAC | AC | ACACACTGAC |
| CACCATCAGC | GT | CA | TCT | CA | ACACACTGAC |
| CATCCAGGCC | ACAG | ACAT | GG | GG | ACGAGCTGG |
| GATCCTTGAT | GCC | AA | TG | TG | AGTGTGAGG |
| GCC | TG | AA | ATG | CT | GTGAGG |
| CAACTACCA | GG | GTG | GG | GG | GGGGACATT |
| TACCATCACC | AC | CC | AC | AC | ACACACTGAC |
| TTTTGAGGCC | AAA | AA | AC | CC | ACACACTGAC |
| GCTGAAGCTC | CC | AA | AC | CC | ACACACTGAC |
| ACCTGTGTT | GT | CC | AC | CC | ACACACTGAC |
| GCTCTGCTG | GT | CT | AC | CT | ACACACTGAC |
| CATCTGAGA | GA | CC | AC | CC | ACACACTGAC |
| TGTGGGACCC | GTG | GG | GG | GG | ACGAGCTGG |
| GGTCTTGCC | GTG | GG | GG | GG | ACGAGCTGG |
| GGTCTTGCC | GTG | GG | GG | GG | ACGAGCTGG |

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 GCACCTTCT CTGTCAGGCT ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGCCCACTGT 1980
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Seq ID NO: 14 Protein sequence:
 Protein Accession #: NP_001784.2

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 YELEFHGVSE NGASVEDPMN ISIIVTQND HKPKFTQDTB RGSVLEGVLP GTSMQMVTAT 240
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIRHSTGTIS VISSGLDREK VPEYTLTIQ 300
 TDMDGDGTT TAVAAVEILD ANDNAPMFDPD QKYEAHVPEN AVGHEVQRRLT VTLDLAPNSP 360
 AWRATYLMG GDDGDEFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVBV TNEAPPVLKL 420
 PTSTATIVH VEDVNAPVP VPPSKVVEVQ EGIPTGEPCV VYTAEDPDKE NQKISYRILR 480
 DPAGFLAMDP DSQQVLTGVT LDREEQFVNR NNIVBVMVLA MDNGSPPTG TGILLLTID 540
 VNDHGPVPEP RQITCINQSP VRQVLNITDLSLSPHTSPQ AQLTDDSDIV WTAEVNNEEGD 600
 TVVLSKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDH GHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLVLLVRKK RIKEPLL EDDETRDNVVF YGREGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTTP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
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Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: XM_051860.2
 Coding sequence: 261-4346

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| 1 | 11 | 21 | 31 | 41 | 51 |
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GAGCTAGCGC TCAACGAGAG CCCAGCGCGG TGCTATCGGA CAGAGCTGG CGAGCGCAAG 60
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CTTAAGAAA TCTTACTCTC TGTAAGCAAG AGCCAACTTC ACAGGATTAG GAGCTGGGGT 4860
AGAACTGGTCT ATCCCTGGGG AAGAGGCAAG CCCTGCTCTC GGCGTGTCC ACCTTCTAGG 4920
AGACTTTGAG TGGCAGTTGG GGACTTGGAC TAGATGACTC TCAAAGGGCC TTGTTCTCT 4980
GAGATTTCAAG ATATCTGTC CATTTCACAT GGTCACCTGGA ACCAACAGT CTATGGTAT 5040
CCACTGATAT CCATGATGCT GGGTGGCCCA GGCACACAGG GATGGAGGAG TTGAGAACTTA 5100
TGCCTAGCTT GAGGGGCTCAG CTGGCAGTAGA GGGCAGGGC TGAGCTCCAT GTGCACTGCA 5160
ATGGCAGTGG AGAAATCTAC AGAGAGTTAA ATAGGGAGGC AGTGGCATTT CAGAGGGGG 5220
GCTCAGGAAG GTCTCTGTC TACAGGAATG AAGGCTGGGG GCATTTGCT GGGGGGGAGAT 5280
GAGGGCAGCTT CTGGGAATGGC TGAGGGATTG ACCCTCCCTG GCGCTGCTC GTCGAAGCTG 5340
FTGACTACGGG FTGCGGCTCT TGCTCACGTC TCTCTGGCC ACATCATGATG GAGAAGCTG 5400
GTCAGAGGGG AGCAATGGGC TTGCTGCTT ATGAGCACAG AGGAATTCAG TCCCCAGGC 5460
TCTCTGCTCC TGACTTCAAGA TGAGGAGAAGT CCACAGAAGT GAGCTCTGC CTAGGGCT 5520
CATTTGCTCT TCACTCAGGG AACTGAGACCG AGGGGGCCCTC CAGGAGACCC TAGATGCTG 5580
CGTACTCCCT CGGCGCTGGGTTTACAGAGCTT GGAAATATAG AAAATATCTA GCCCAAGGCC 5640
TTCATTTAAAG CAGATGGGGG AAGTGGAGCC CCAAGATGGGG AAAAGAACCC ACAGCTAACG 5700
GAGGGCTCTGG GAGGGCCAC CTCAGGCTCTT GCTGCGCACAC CACATGCTC CAACAAACGGG 5760
CCCCAGAGTG CCCAGGCACT CTGAGGATG CTTCAGGAAA TGGGGACAAG TCCCCCTGAA 5820
GGAAAGGAGGA TGACTAGATG AGAATGACAG TGACAGATC TCTTCCCTCC TGCTCCAGC 5880
GCACAAACCG CGCCCTCTCCCTTCTGGTGTG CGGGCTCTCTG TGCCCTCTAC TTGTTCTACT 5940
ACCTGTCTGC CGACGCTGGG TGACAGTAG CTGCAACTCC CCATGGTGC TACCTGGCTC 6000
TCTCTGCTCTCT GCAGCTCTAC AGGTGGAGGG CAGCAGAGGG AGTAGGGCTC GGCATGTTCTC 6060
TTGGTGGCCA ATTTGGCTGA TTGGGGTTG CTGACAGCTT ATGGGGTCCA CCCCAGTCCC 6120
TTTCACTGTC TGCTTAATGC CCTGCTCTC CCTGGGCCA CCTTATAGAG AGCCCAAAAGA 6180
GCTCTGTTAAGA GAGGGAGAGCTCCTAATGCTG GTTATAATC TTGCAAGGGG CACAGAGTC 6240
TCTCTGGCTC TTGTTGATCAA CTACATTAT CCTCCCTCTC GCCCAACCA CAAACTCTT 6300
CTCTCAAAAGA GGGCCCTGCC CTGGCTCCCTC ACCAAACTGC ACCCATGAGA CTGGTCTCAA 6360
GAGTCATCTC CCCAGGGTGG AGCCAACTGT CAGGGAGGGT TTGGGGCCCAA AACATCTTCTC 6420
AGCTCTGGG AGGTGGACCAT AAGGGCTCTG TTAAAGAGAT ATGGCTGCTT CAAAGGGCAG 6480
AGTCACAGGA AGGACATCTT CCAGGGAGAT TAGTGGTGTAG GGAGAGGAGA GTTAAATG 6540
OCTCTGTCCTCTCTGCTCA CGGGTTGTTGAGT GAGTGTCTAC TCTCTCTAATG CAAGGGCTC 6600
ACACTGTGAA CCACCTAGGA TTGTTGACTCT TCTAGGGC CAGGAATGTTA GAATGCTCTT 6660
GGCTCAGTTC ATTTAAAAAA GATATCTATT TGAAAGCTTCT CAGAGTTGA CATACTGTT 6720
ACAGTACAGG ATCTGTCATC AAAAGTTCTTCTCCTAAACCTCAGCAAGG AGCCAAATATC 6780
TAGGCTATTCTTCTGAGCA CAAATTTCT TATGTTGCTT AAAATGCTC TTGTTGTT 6840
TTCTGTTGTTAAGACTTAAG TGAGTTAGGT CTTTAAGGAA AGCAACGCTC CTCTGAAATG 6900
CTTGTGTTTCTTCTGCTC GAAATAGCTG CTCTCTTCTC GGGAGTTGA TGATAGAGT 6960
GTTGTTAGTAAACATCTCTGAGCAACCTGACATGAA CAAATGATATT TCTTCTTCT 7020

TTATTATATG TGCACCTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTTAAATGTC

Seq ID NO: 16 Protein sequence:

Protein Accession #: XP_051860.2

1 11 21 31 41 51

MGAAGRQDFL FKAMILTISWL TLTCPPGATS TVAAGCPDQS PELQPWNPGH DQDHVVHIGQ 60
 GKTLLTSSA TVYSHISEG GKLVKIDHDE PIVLRTRHIL IDNGGELHAG SALCPFQGNF 120
 TILYGRADE GIOPDPYVGL KYIVGVGGGA LELHGQKQLS WTLNKTILHP GGMAEGGYFF 180
 ERSWHRGKV VHVIDPKSGT VIHSDRFDTY RSKKESERLV QYLNAPVDPGR ILSVAVNDEG 240
 SRNLDDDMARK AMTKLKSCKHF LHLGRHRPWS FLTVKGPNSS SVEDHIEYHG HRGSAARVF 300
 KLFOTHEGEY FNVSLSEEWV QDVEWTEWFD HDKVSQTKEGG EKISDLWKAH PGKICNRPID 360
 IQATTMVGDN LSTEVVYKKG QDVEWTEWFD HDKVSQTKEGG EKISDLWKAH PGKICNRPID 420
 STINLLEDNV OSWKPCDTLV IASTDYSMYQ AEEFQVLPCK SCAPNQVKVA GKPMYLHIGE 480
 EIDGVDMRAE VGILLSRNIV MGEMEDKCYC YRNHCNFPD FDFTGGHHKF ALGFKAALBL 540
 GTELKHMGQQ LVGQYPIFH LAGDVDERGG YDPPTYIRDL SIIHTFSRCV TVHGSNGLI 600
 KDVVGVNSLG HCFITTEDGP ERNTFDHCLG LLVKSGTLLP SDRDSKMKCM ITEDSYPGVI 660
 PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWFIPH HVPTGPSVM YSPGYSEHHP 720
 LGKQYNNRRAA SNYRQAMII NGVKTEASA KDKRPLSII SARVSPHQDA DPLKPREPAI 780
 IRHFIAYKNDQ DHGAWLRRGD VWLSDCRFAD NGIGLTLASG GTFPYDDGSK QEIKNSLFVG 840
 ESGNVGTEMM DNRWGPGLG DHSGRTLPIG QNFPIRGQL YDGPINIQC TFRKFVALEG 900
 RHTSALAFNLSQVSCPHN NVTGIVFVFGF PGPWFNQLDM DGDKTSVHD 960
 VDGVSVEPG SYLTKNNDNL VRHPDCINVP DWRGACCSGC YAQMYYQAYK TSNLRMKIIK 1020
 NDFFPSHPLYL EGALTRSTHY QQYQPVVTLQ KGTYTHWDQT APAELAIWLI NFNKGDWIRV 1080
 GLCYPRGTTT STFWMANPNN NLINCAAAGS EETGFWFIPH HVPTGPSVM YSPGYSEHHP 1140
 KLAQNEEREK FAFCSMKGCE RIKIKALPK NAGVSDCTAT AYPKTERAV VDVPMPKKLF 1200
 GSQQLKTDHF LEVKMESSKQ HFFHLWNDFA YIEVDGKYP SSEDGIQVVV IDGNQGRVVS 1260
 HTSFRNLSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRLKLKE 1320
 QMAFVGFKGS FRPIWVTLDT EDHKAKIFQV VPPIPVKKKK L

Seq ID NO: 17 DNA sequence:

Nucleic Acid Accession #: NM_015515.1

Coding sequence: 61-1329

1 11 21 31 41 51

AGTTCTGGGG TGCCAGGGAG TGGAGCAGAG CTCAGCCCCG TCCCAAACAC AGATGGGACC 60
 ATGAACTCGG GACACAGCTT CAGCCAGACCC CCCCCTGGCT CCTTCATGG CGCCGGAGGT 120
 GGCCTGGGCC GGCCCAGGAG CTTCCTCAGG GCTCCACCG TCCATGGCG TGCGGGGGGA 180
 GCCCTGGCATCT CCCTGTCTT CACCCGGCG AGCTGCCCCAC CCCTCTGGGG GTCTTGGGGT 240
 TCTGGAAGAA GCAGGGCCCT ACTAGGCGGA ATATGGGAAGG CCACCATGCA GAATCTCAAC 300
 GACCGCTGG CCTCTTACCT GGAGAAGGTT CGCGCCCTGG AGGAGGCCAA CATGAAGCTG 360
 GAAAGCCGCA TCTCTGAATG GCACCAAGCAG AGAGATCTCG GCAGTAAGAA AGATTTTCC 420
 CAGTATGAGG AAAAACATCAC ACACCTGCGAG GAGCAGATAG TGATGTTAA GATGACCAAT 480
 GCTCAGATTA TTCTCTCAT TGACAATGCC AGGATGGCAG TGGATGACTT CAACTCTAAG 540
 TATGAAAATG AACACTCCTT TAAGAACAGC TTGAAATTTG AAGTCGAGGG CCTCCGAAGG 600
 ACCTTAGACA ACCTGACCAT CCATGCAACA GACCTAGAAC AGGAGGTGGA AGGAATGAGG 660
 AAAGAGCTCA TTCTCATGAA GGAGCACCAT GAGCAGGAAA TGAGGGAGCA TCATGTGCCA 720
 ATGACTTCA ATGTCATGTA GAAGTGGAT ACAGTCCCA GGGAAAGATCT GATTAAGGTC 780
 CTGGAGGATA TGAGAACAGA ATATGAGCTT ATAATAAGA AGAACATCG AGACTTGGAC 840
 ACTTGGATA AAGAACAGTC TGCAAGCATG TCCCAAGGAGG CAGCCAGTC AGCCACTGTG 900
 CAGAGCAGAC AAGGTGACAT CCACGAAACTG AAGCCGACAT TCCAGGCCCT GGAGATTTGAC 960
 CTGCAAGCAC AGTACAGCAC GAAATCTGCT TTGAAAACAA TGTTATCCGA GACCCAGTCT 1020
 CGGTAACCTCT GCAAGCTCC GGACATGCAA GAGATCATCT CCCACATGAA GGAGGAACCTG 1080
 ACGCAAGCTC GCAAGCAACT GGAGGGCAG ACAATAAGAT ACCAAGTGCT GCTGGGCATC 1140
 AAAACCCACCG TGGAGAACAGA ATTCACCCAGG TACCGAGCGG TCTGGAGGG AGAGAGTGAA 1200
 GGGACACGGG AAGAATCAAA GTCGAGCATG AAAGTGTCTG CAACTCTAAA GATCAAGGCC 1260
 ATAACCCAGG AGACCATCA CGGAAGATTA GTTCTTGTG AAGTGAATGA AATCCAAAAG 1320
 CACGCATGAG ACCAATGAAA GTTTCGCGCT GTTGTAAGT CTATTTCCC CCAAGGAAAG 1380
 TCCCTGACAC GACACACTG AGTGAATTC AAAAGATACC CTTGGATATIA TCAGACTCAG 1440
 AAACCTTTAT TTTTTTTT CTGTAACAGT CTCACCAAGAC TTCTCATAT GCTCTTAATA 1500
 TATTCGACTT TTCTAACTCAA AGTGGCAGTT TATGAGGGTA AAGCTCTACT TTCCCTACTGC 1560
 AGCCTTCAGA TTCTCATCAT TTTCATCTA TTTCATGACCA AATAAAACTC CGCACTAGC

Seq ID NO: 18 Protein sequence:

Protein Accession #: NP_056330.1

1 11 21 31 41 51

MNSGHFSQQT PSASFHGFAGG GWGRPRSFFR APTVHGGAGG ARISLSFTTR SCPPPGGSWG 60
 SGRRSPPLGG NGKATMQLN DRALASYLEKV RALEBANMKL ESRILKWHQQ RDPGSKKDYS 120
 QEENINTHLQ EQIVDGKMTN AQILLIDNA RMAVDDFNLK YENEHSFKKD LEIIVEGLRR 180
 TLDDNLIVTT DLEQVEGMR KELLMEHH EQEMEEHIVP SDFNVNVKVD TGPREDLIKV 240
 LEDMRQEYEL IJKKKHRDLD TWYKEQSAAM SOEAASPATV QRQGDHIEL KRTFQALEID 300
 LQAQYSTKSA LENMLSETQS RYSCKLQDMQ EISHYEEEL TQLRHELQ NNEYQVLLGI 360
 KTHLEKEITT YRRLLEGES GE TREESKSSM KVSATPKA ITQETINGRL VLCQVNEIQK 420
 HA

Seq ID NO: 19 DNA sequence:

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51

TTTTTTTT TAAAAAAA GAGCTTGGT AAGTTTGA TACTTAGTG ACCTTAGCA 60
 TTATCCAGA TTGTATTAA GAACAGTG GAACTGTAAT TTTCTTTC CTTTCAGAAA 120
 GACTCAGG GAACATAAA ATGTTCTA TTTTNNNNNN NNNNNNNNNN NNNNNNNNNN 180
 NNNNACCAT CGTGCATGA TCNNNNNNN NNNNNNNNNN NNNNNTGGG ATCCAGTTTC 240
 AAATAAGGT A TGGAAAAAC AGATGTTTC ATTATGCCA CITAATCCCT ACTCCGATT 300
 ATAATTAC ATGTTGGCT GTAAACTA TACTAACAGA TGCTTGAA AGATGACTTC 360
 TACAAGACA GAAAACCCAC AACACAACAG ATCGCATCAG AAAGCACAGG CATTATCATT 420
 CTTAATTAA CTCTCTTAG ACCGGGACA TGTTGGACAA ATACTTTGT CCTCATGGAT 480
 GGCTTGATAA TTATTTAA TGTTCTAGG TGCTGAGGATT TTCTTTCAGT GGCAGACAC 540
 AAAGGATGTT ACAATTACT CTTAAATAAT ACAATCATGG TTAAATTTC AGTGTAAATC 600
 CATACTATT TTATAGAGAT CGATTATCAT ACATGGGATT TAAAAAATAA CTTACCCATA 660
 TGCTTGCAAA ATAGACTTT CCTATGGGA GGAACATCTT TTAACTAAA ACGGATTAT 720
 TTACATGAGA TTAGACAGTA CATTTCAGC GAGAACCCAGC TTACTGGAT GATCTTTGT 780
 CAGGTGTTGG GCCTCTTCTT TGCTCTGC AACCATAAACC CCTTTTCAGC TGAAGACAC 840
 TGGCTTCAA CCCAACGCCAG GAGTTGGCT CAAATGA

Seq ID NO: 20 DNA sequence
Nucleic Acid Accession #: D32051.1
Coding sequence: 72-1373

GAATTGCAAC CAGGTGGCCA CCCGGTGTCTG GTTTCATTT CCTTGGAAAT TTCTGCTTA 60
 CAGACAGAAC AATGGCACCC CGAGTACTTA TAATTGGCAAG TGAGGAGGAAGG GAACATAACGCC 120
 TGGCTCTGGAA ACTTGGCACCG TCTCTCATCTG TCCTAACAAAGT GTTGGTTGCCTG CCAGGAACACG 180
 CAGGCACTGC CGCTCTGAA AGAATTCTAA ATACCCCTAT CTCAATCAGT GACCACACTG 240
 CCTCTGCTCA ATTCTGCAAAGAAGAAAAA TTGAATTGTG ATTTGTTGGA CCAGAACGAC 300
 CTCTGGCTCG TGGGATTGTTT GGGAACTCTGA GTTCTGCAGG AGTGCATGC TTGGCCCAA 360
 CAGCAGAACG GCCTCAGTTA GAGTCCAGCA AAAGGTTTGCT CAAAGAGTITG ATGGACAGAC 420
 ATGGAAATCCC AACCACAAAC TGGAGGGCTT TCACCAAAAC TGAAGAACGGC TGCGCTTC 480
 TTGGTAGTGC AGACTCTCTG GTCTTGGTGTG TGAAAGGCCAG TTGTTCTGCA GTCTGAAAAG 540
 GGGTAGTTGT TGCAAAGAGC AAAAGAAGAGC CCGTCAGAACG TGTCACAAAGC ATCTAGCAGG 600
 AAAGAACCTT TGGGGCAGCTT GGAGAACCAA TTGTCATTTGA AGAACATCTT GACGGAGAACG 660
 AGGTGTCGTG TCTGTGTTTC ACTGTGGCA AGACTGTGGC COCCATGCC CAGCACAGG 720
 ACCATAAGGCCTT ATTACTGGAG GGAGATGTTG GCCTAACAC AGGGGGAATGG AGGCCTTATG 780
 TTGCGACCCCCC TCAGGTTCTT ATGATCTAT TACTAAAGAT TAAAGACT TGTCTTCAGA 840
 GGACAGTGGGAGGGCTT TGCGATCGAG CAAGAGGGTA CTCCATATAC AGGTATTCCT TATGCTGGAA 900
 TAATGCTGCAAGAACATGGC CCAAAGTTCTC TAGAGTTAA TTGGCTCTTGTGATGCCAG 960
 AGTGCAGGTT AATCTCTCCA CTCTTTAAA GTGTATCTTA TTGAAGTGTATT GCTTCACCT 1020
 TAGATGGACT GCTCTGCACA TCTCTGCCCTG TTGGCTAGA AAACCACACC GCCTAACTG 1080
 TTGTCATGGCC AAGTAAAGGT TATCTGGAGG ACTACCTAACAGG GTGTAGAGTAAACAGGTT 1140
 TTCTCTGGCC TCAAGCTCTA GGACTGGAGG TTGCCCCATGC AGGCATGCGC CTCAAATAG 1200
 GCAAAGTAGT AACTCATGGG GGTAGAGTTIC TTGCACTCAC AGCCATCGGG GAAAATCTCA 1260
 TATCGCCCTT TGAGGAGAGC AAGAAAGGGAC TAGCTGTATTA AAAGTTTGAG GGAGCAATT 1320
 ATAGGAAGAATCCTGGCTT CTGCCCCATAG CTTCTCTCCA GCAGGCCAGG TAAAATCTA 1380
 AGCAAGTTAG CTGTAAGTGCCTT ATTTCGAAAGA CTGGCTAAAGG TTGGCTATGTA GAACATCTCA 1440
 TTAACCTATTA AAGTCATTCGA GTATCTTTTCTCTCTGTGG GAGTGTATACA GTCTGGTTT 1500
 GTATTTGTT TGAATCAAACTGGTTATAG CAATCTAACAA ATGGAAAAAACTTCTCATGATA 1560
 GCGTAAGTTT GGGAAATCTCAGAACATCAC AGTGGTACTG ATTTTATT GTTCTCTTATT 1620
 TTTTTTATTATATTTTTA ATTTTTTAA CAAGGGTCTTC CTCTCTGCC CAAGTCTCA 1680
 TGCTCTGGCC TCCCAAATAG CTGGGACTAC AGGCACAGGCC CACCACACCTG GGCTAATT 1740
 TTGTATTTT TTGTGGAGAT GGGGGTCACTCCTGACAGT TTGTGGCAAC CCGGCTCTG AAACGGCTGG 1800
 CTCAAGTGAT CCTCTCTGCTT TGGCCCTCCA AAAATGCTGGG ACTATAGGCA TGAGGGCTG 1860
 CACTTGGCTC GATACTGATT TTATCTCTGCTGTTTACATAGTGTGTGTTTATGAAACAA 1920
 TATGTCATGGGTTTATCAAA GAAGCTAGAAGA TTGAGAAACTC GGTCTATCAA CTCTGTTAATT 1980
 TGATTTGATT ATACTGTTAA GTTGTGACAGT CCCATTTAA CCTGCGTTTG TATCTTAC 2040
 TAAATGTTGTTTATGACTCTTACATGGTGTGG ATGTACAAACT GTTGTGACTG 2100
 TAAATCAATTAAGCTCTGAGT TTGG

Seq ID NO: 21 Protein sequence:
Protein Accession #: BAA06809.1

1 11 21 31 41 51
MAARVLIIGS GGREHTLAWK LAQSHHVQV LVAPGNAGTA CSEKISNTAI SISDHTALAQ 60
FCKEKKIEFV VVGPEAPLAA GIVGNLRSAG VQCFGPTAEA AQLESSKRFA KEFMDRHGP 120
TAQWKAFTKF BEACCSFILSA DFPALVVKAS GLAAGKGVIV AKSEEACKA VQEIMQKCAF 180
GAAGETTIVB LLDEEGVSC LTCDTGKTV APMPPAQDHKR LLEGDDGPT GGGMAYCPAP 240
QVSNDLLKI KDTVLQRTVD GMQQGPYPT YLIGAYIMLT KNGPKVLFN CRFGDPCEVC 300
IPLKLKSDLV EVIOSTLDGL LCTSLPVWLE NHITALTVVMA SKGYPGDYTK GVEITGFPEA 360
QALGLEVSHA GTALKNGKV THGGRVLAVT AIRENLISAL BEAKKGLAAI KFEGAIYRKD 420
IGFRAlAFLQ QPR

Seq ID NO: 22 DNA sequence
Nucleic Acid Accession #: EOS cloned
Coding sequence: 1-2424

1 11 21 31 41 51
 ATGCCCTT TCCGTGCT GGAGGCCGTC TGTTTCCAG AGTGCCCCA 60
 TCTCTCCTC TCCAGGAATG CCATGTAAGC AAAAGAACCA TCGGAGAT TCTAGCTGCC 120
 AGCACATAGA TGTGGCTC GGCTGAGT GAGCATCTGT TTCTGTAGA TGGGCTAAC 180

AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTG CCATCACAGT CTGTGACGGT 240
 CTGGACATCA GCCCCGAGAG GGTCAGATG TGAGGATTC AGTTCAGTT CACTCTCAT 300
 CTGGAATTCC CCTTGATTG ATTTCAACC CAACAGGAAG TGAAGGCAGG AATCAAGAGG 360
 ATGGTTTCA AAGGAGGGCG CACGGAGACG GAACCTGCTC TGAAATACCT TCTGCACAGA 420
 GGCTTGCTG GAGGAGAGAAA TGCTCTGTG CCCAGATCC TCATCATCGT CACTGATGGG 480
 AAGTCCCCAGG GGGATGTGCG ACTGCCATCC AAGCACTGA AGGAAAGGGG TGTCAGTGTG 540
 TTGCTGTGG GGGTCAGGT TCCCAAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
 AGAGGGCAGC ACGTCCTGTG GTGTCAGGAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
 ACCCTCAGCA GCTGGCCAT CTGCTCAGC GCACCGAGC ACTGCAGGGT CGAGGCTCAC 720
 CCCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTCG CTGGCAATGC CCCATGCTGG 780
 AGAGGATCGC GGCGGACCC TTGGCTGTG CTGTCACACT GTCCCTTCTA CAGCTGGAG 840
 AGAGTGTGCC TAACCACCC TGCCACCTGC TACAGGACCA CCTGCCAGG COCCCTGTGAC 900
 TCGCAGCCCT GCGAGAACATGG AGGCACATGT GTTCCAGAAG GACTGAGCG CTACCACTG 960
 CTCTGCCGC TGICCTTTGAG AGGGAGGAGCT AACCTGTCAG TGAAAGCTGAG CCTGGAAATGC 1020
 AGGGTCAGCC TCCCTCTCT GCTGGACAGC TCTGGGGCA CCACCTGGGA CGGCTTCCG 1080
 CGGGCAAG TCTTGTGAA GCGGTTGTG CGGGCCGTGC TGAGCAGGA CTCTCGGGCC 1140
 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCTCTGT GGGGGAGTAC 1200
 CAGGATGTGCT CTGCTCTGGT CTGGAGCCTC GATGGCATTCT CTTCTGGTGG TGGCCCGC 1260
 CTGACGGCCA GTGCTCTGGC GCAGCGGCCA GAGCGTGGCT TGCGGAGCG CACCAAGGACA 1320
 GGGCAGGACC GGCGCACTGAG AGTGTGGTT TTGCTCAGTG AGTCACACTC CGAGGATGAG 1380
 GTTGGGGAGC CAGCGCTCA CGCAAGGGCG CGAGAGCTGC TCTCTGCTGGG TGTAGGGCAGT 1440
 GAGGCCGTGC GGCGAGAGCT GGAGGAGATC ACAGGAGCCTA CAAAGCATGT ATGGTGTAC 1500
 TCGGATCTCC AGGATCTGTG CAAACAAATC CTCAGCTGC AGGGGAAGCT GTGCAAGCGG 1560
 CAGCGGCCAG GGTGCGGCCA AAACGCCCTG GACCTCGTCT TCACTGTTGGA CACCTCTGCC 1620
 TCACTAGGGC CCGAGAAATT TGTCAGATG CAGACCTTG TGAAAGCTG TGCCCTCCAG 1680
 TTGAGGTGA ACCTCTGAGT GACACAGTC GGCGTGGTGG TGATGGCAG CGAGGTGAG 1740
 ACTGCCTCG AGGCTGGACAC CAAACACCC CGGGCTGCAG TGCTGGGGC CATTAGCCAG 1800
 GCCCCCTAC TAGTGGGGT GGGCTCAGCC GGCAACGCC TGTCGACAT CTATGACAAA 1860
 GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCCA AAGCTGTGTT GGTGCTACA 1920
 GCGGGAGAG GCGCAGAGGA TGCGAGCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC 1980
 TCTGCTTGG TGCTGGGGT GGGCGCTGTC CTAACTGAGG GTCTGGGGAG GCTTGAGGT 2040
 CCCCGGGATT CCCTGATCCA CTGCGCAGCT TACGCCGACC TGCGGTACCA CCAGGAGCTG 2100
 CTCACTGAGT GGCTGTGTTG AGAACCGCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCG 2160
 TCGATGATG AGGGCAGCTG CGTCTCAGG AATGGAGCT ACCCTGCAA GTTCTGGGAT 2220
 GGCTGGAGG GCCCCACTG CGAGAACCGT GAGTGGAGCT CTGCTCTGT ATGTGTGAGC 2280
 CAGGGATGGA TTCTTGAGAC GCCCGTGGG CACATGGCTC CGCTGCAGGA GGGCAGCAGC 2340
 CGTACCCCTC CCAGCAACTA CAGAGAACG CTGGGACTG AAATGGTGCC TACCTCTGG 2400
 AATGTGTG TGCCAGGTCC TTAG

Seq ID NO: 23 Protein sequence:

Protein Accession #: EOS cloned

| | | | | | |
|---|----|----|----|----|----|
| 1 | 11 | 21 | 31 | 41 | 51 |
|---|----|----|----|----|----|

MPPFLLBEAV CVFLPSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVKGFSFERS KHFATVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFT QEVVKARIKR 120
 MVFKGRTEEL ELALKYLLH GLPGRNRASV PQIIVITDG KSQGDVALPS KQLKERGVTV 180
 FAVGVFRPRW EELHALAEQ RQHQVLLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCDFYSWK RVFLTHPATC YRITCPGPCD 300
 SQPCNGGTC AGGCTGGYQC CLPLAFGGEA NCALKLSEEC RVDLFLLDS SAGTLLDGF 360
 RAKFVFRV RAVLSEDSRA RVGVATYSRE LLVAVPVQEY QDVPDLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERFGFSATR QDQRPRVVV LLTESHSEDE VAGPARHARA REILLLGVGS 480
 EAVERAELI TGSPKHMVYV SDPODLFNQI PELOGKLCSR QRPGCRTOAL DLVFMLDTSA 540
 SVGPNENFAQM QSFPVRSCLAQ FEVNPDVTVQ GLVYVGSQVQ TAFGLDTKPT RAAMLRaisQ 600
 APYLGVGSA GTALLHHYDK VMTVQRGARP GVPKAUVVLT GGRGAEDA AV PAQKLRRNGI 660
 SVLVVGVPV LSEGQLRLAG PRDSLHIVAA YADLRYHODV LIEWLGEAK QPVNLCKPSP 720
 CMNEGSCVVLQ NGSYRKCRD GWEGIPHCENR EWSSCSVVCQS QGWILETPLR HMAPVQEGRS 780
 RTPPSNYREG LGTEMVPTFW NVCAVPG

Seq ID NO: 24 DNA sequence:

Nucleic Acid Accession #: see Table 25 & 25A for complete list

| | | | | | |
|---|----|----|----|----|----|
| 1 | 11 | 21 | 31 | 41 | 51 |
|---|----|----|----|----|----|

AGGTGGCTG GTTATCGGGC GTTGGAGGGC TGAGGTGGGG AGGGTGGGT GTACAGAGCT 60
 CTAGGACTCA CGCACAGGC CAGTCGGGG TTTGGCCCG AGGCTGGGT TACAAGCAGC 120
 AAGTGGCGG TTGGGGCAC TGCGAGGGCG TTTAGAAAAA CTGTTAAAAA CAAAGAGCAA 180
 TTGATGATA AATCAGGAAT AGATCTCTT GACCATGTGA CATCTGATGC TGTTGAAACTT 240
 GCAATCTGAA GTGATAACTC TTCTGATAGC AGCTTATTA AAACCTAGTG TATCCCTTAC 300
 TCACCTAAAG GGAGGAAAGG AAAACCCATT CGAAATTTG TTGTCACCC TGAAAGTGT 360
 CACGCAAGTA TTCACTAAGT GACTCATCTT TTGAACCCAGT ACCATTGACT ATAAAAGCTA 420
 TTTTGAAG ATTCAAGAAC AGGAAAGGAG GATATAAAA AAGAAAAAG AGGAGGGTAC 480
 AGCCCAACGG AAGACCCAGG GGAAGACCCAG AAGGAAGGG AAACTCTATA TACTCTAA 540
 TAGATAAGAA GAAACCAATTG AGAACGAGAG GATCTGGCTT CCCATTTTA GAATCAGAGA 600
 ATGAAAAAAA CGCACCTGG AGAAAATTG TAACGTTGA GCAAGCTGT GCAAGAGGAT 660
 TTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACTT GAAAGAATCA TTGAACCAA 720
 TGAATGTGG TGAAGATTTA GAAAATGAAG ATTTTGACAG TGCTAGATAC AAATTTTTGG 780
 ATGATGATGG ATCCATTCT CCTATTGAGG AGTCACAGCT TTATCTTGA GGACATGGTG 840
 TCTGGAGTTA AAGGTATTGG CATACTCCAC ACATCTGAC CATCTTGTAG TGATCGCTA 900
 GGAATGAATG TGATTTGAC TCATTCTATGT ATGAGAGTAA GCAATGCTTT TTTTCAGG 960
 GTGTCAAATT GAGAACCGG TAGATCCCCA CCACCTACAG TAAAAGGAC CCTAAAGTAA 1020
 ATGGTGAAGAATAGT CCCAAAGATT CTGGTGAAT TTGAAAGCTC TCATCACTG 1080
 ATCCATATTA AAACGAGATG ACAGAAGCCA AAGTAATTAT GGGCTGACAG GACAACCTGGA 1140
 TCAGTTCTAT TAAAAGGGC AACATGAAAG ATAATCTT TGACTCCAGC TCTTTAGAGG 1200
 ATCTAAAGTGC ACCTTGATGC AGCTGGAAG AAATCACAC AC TGAAATTC TCGAATAACAA 1260

ATTTATGAC TTTAAAATAAT TTTGTCTAAT GCTACATATA CACAATTAAA AAACCTTAC 1320
 ACTATTCCTA GAAAGTCAGC ATGTATTTT GGCTCGAAGT TCTCTAGTG TTTCTGTGG 1380
 AAGGAATAAA AATTGAGGT TTCAATACAA AAACAAAACA AACAAACAGA AACACGAAA 1440
 ACAACTCTGTT GTGCGGCCGC CCTGGGCCCT TGAGAGAAA ACITTTAGA ACCCCTTTG 1500
 CGTGTGGCG GCCCGGGGGC CCCACAGTG GGTTAGGTG GGCAACCTTG TGTCTACAAG 1560
 TGGTGTCTCC CAACAGAGA GAACACCTCC GGGGTCAAGC GGACAACAAG AGTGGCTCGT 1620
 GAGGACTCTT CACCAAAGT ATATAAAACC CGCCCCGCG GGGACCACC GGCGCTTT 1680
 CTGTAGACAC AACCCCCACA GTGGGAACCT CTGAGGGCGC ACACACAGGG CGAGCCTAT 1740
 CAACAAGGG TGCCAACAG AAACCCGAG TTAAAAATCG

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: BC001972.1
Coding sequence: 183-1019

| 1 | 11 | 21 | 31 | 41 | 51 |
|--|----|----|----|----|----|
| GGTGGCTGG TTATCGGGAG TTGGAGGGCT GAGGTGGGA GGGTGGTGTG TACAGAGCTC 60 | | | | | |
| TAGGACTCAC GCACCAAGGCC AGTCGCGGT TTGGGCCGA GGCGTGGTT ACAAGCAGCA 120 | | | | | |
| AGTGGCGGT TGGGGCCCT GCGGAGGGCT TTAGAAAAC TGTTAAACAC AAAGAGCAAT 180 | | | | | |
| TGATGGATAA ATCAGGATAA GATTCTTG ACCATGTGAC ATCTGATGCT GTGGAACTTG 240 | | | | | |
| CAAATCAGA TGATAACTCT TGATAGCA GCTTATTAA AACTCACTGT ATCCCTACT 300 | | | | | |
| CACCTAAAGG GGAGAAAAGA AACCCCATTC GAAAATTGTG TCGTACACCT GAAAGTGTTC 360 | | | | | |
| ACGCAAGTGA TTTCATCAAGT GACTCATCTT TTGAACCAAT ACCATGACT ATAAAAGCTA 420 | | | | | |
| TTTTGAAAG ATTCAAGAAC AGGAAAAGA GATAAAAAAA AAAGAAAAG AGGGAGTAC 480 | | | | | |
| AGCCAACAGG AAGAACACCG GGAAGACCCAG AAGGAGGAG AAATCTATA TACTCACTAA 540 | | | | | |
| TAGATAAGA GAAACAATTG AGAACGAG GATCTGGCTT CCATTTTA GAATCAGAGA 600 | | | | | |
| ATGAAAAAAA CGCACCTTG AGAAAATTG TAACCTTGA GCAAGCTGTT GCAAGAGGAT 660 | | | | | |
| TTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACT GAAAGAATCA TTGAAGCAAA 720 | | | | | |
| TGAATGTGG TGAAGATTTA GAAAATGAG ATTTGACAGC TCGTAGATAC AAATTTTGG 780 | | | | | |
| ATGATGATGG ATCCATTCTC CCTATGAGG AGTCACAGC AGGAGTAG GATGCAACAC 840 | | | | | |
| ATCTTGAAGA TAACGAATGT GATATCAAAT TGCCAGGGGA TAGTTCTATA GTAAAGTCTG 900 | | | | | |
| AATCCCTGT AAGACTGATG TGTACTCTG AAGAAGAGGA TATTACTGAA GAAGCTGCTT 960 | | | | | |
| TGTCTAAAAA GAGACTACA AAAGCCAAA ATACTGACA GAGAGGCTG AAAATGTGAC 1020 | | | | | |
| AGGATCATGA ATGTCAAAGG CTTATCTT GAGAACATGG TGTCTGGAGT TAAAGGACTA 1080 | | | | | |
| TGTTAGATC TGTTGGAGA AATTCAAGA CAGTGTGCTAA AAGTTGAAA AAGACGGTTG 1140 | | | | | |
| CTAACCTTA TGAAAACCA GATAATCTAC TTTTTACCT TAGGTATTTG CATACTCCAC 1200 | | | | | |
| ACATCTGTAC CATTCTTGAG TGATCGCTTA GGAATGAATG TGATITGAAC TCATTCTATG 1260 | | | | | |
| TGAGGGGTG AACCCAGTAG AACCCAGTAG CCTACACCA CCTACAGTA AAAGGACCC 1320 | | | | | |
| AAAGTAAATTG GTTGAAGAA ATTAGATCCC AAAGAATTCTT GGTAATTGTT GAAGTCTCA 1380 | | | | | |
| TCAGTATATC CATATTTAAA CGAGATGACA GAAGCCAAG TAATTATGGG CTGACAGGAC 1440 | | | | | |
| AACTGGATCA TTTCATCAAATG CTTGAAGATA AATCTTGTG CTCCAGCTT 1500 | | | | | |
| TTAGAGGATC TAAAGTGACC TTGATGACA GTGGAAGAAA TCACACATG GAATTCTCG 1560 | | | | | |
| AATAACAATT TATTGACTTT AAATAATTG GTCTAATGCT ACATATACAC AATTAAAAAA 1620 | | | | | |
| CCTTACACT AAAAAAAA AAAAAA 1680 | | | | | |

Seq ID NO: 26 Protein sequence:
Protein Accession #: AAH01972.1

| 1 | 11 | 21 | 31 | 41 | 51 |
|---|----|----|----|----|----|
| MDKSGIDSLS HVTSDA VELA NRSDNNSDSS LFKTQCPVS PKGEKRNPIR KFVRTPESVH 60 | | | | | |
| ASDSSDSSF EPIPLTIKAI FERFKNRKRR YKKKKRKYQ PTGRPRGRPE GRRNPIYSLI 120 | | | | | |
| DKKKQFRSRG SGFPFLESEN EKNAPWRKIL TFEQAVARGF PNYIEKLKYE HHLKESLKQM 180 | | | | | |
| NVGEDILENED FDSRKYKFLD DDDSIPIEE STAEBEDATH LEDNECDIKL AGDSFIVSSE 240 | | | | | |
| FPVRLSVYLE EEDITEEAAL SKKRATKAKN TGQRGLKM | | | | | |

Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: AK027016
Coding sequence: 207-1043

| 1 | 11 | 21 | 31 | 41 | 51 |
|--|----|----|----|----|----|
| CTTTCTTCC GCACGGTTGG AGGAGGTGG CTGGTTATCG GGAGTTGGAG GGCTGAGGTC 60 | | | | | |
| GGGAGGGTGG TTGTACAGA GCTCTAGAC TCACCCACCA GGCCAGTCGC GGATTITGGG 120 | | | | | |
| CCGAGGCTG GGTACAAAGC AGCAAGTGG CGGTGGGGC CACTGCGAGG CGGTITTTAGA 180 | | | | | |
| AAACTGTTA AAACAAAGAG CAATTGATGG ATAATCAGG AATAGATTCT CTGACCATG 240 | | | | | |
| TGACATCTGA TGCTGTGGAA CTTGCAACAT GAAAGTGATAA CTCTCTGAT AGCAGCTTAT 300 | | | | | |
| TTAAAATCTA GTGTATCTCT TACTCACCA AAGGGAGAA AAGAAACCC ATTGAAAT 360 | | | | | |
| TTGTCTGAC ACCTGAAAGT GTTCACGCAA GTGATTCATC AAGTGAATCA TCTTTGAC 420 | | | | | |
| CAATACATTG GACTTATTTA GCTTATTTG AAAGATTCACAA GAAACAGGAAA AAGAGATATA 480 | | | | | |
| AAAAAAAGAA AAGAGGAGG TACCAAGCAA CAGGAAGACC ACGGGGAAAGA CCAGAAGGAA 540 | | | | | |
| GGAGAAATCC TATATATCTA CTAATAGATA AGAAAGAACCA ATTAGAAGC AGGAGATCTG 600 | | | | | |
| GCTTCCCTT TTAGAATCTA GAGAATGAAA AAAACGACC TTGGAGAAAA ATTAAACGT 660 | | | | | |
| TTGAGCAAGC TTGTCGAAGA GGATTTTTA ACTATATGA AAAGCTGAAG TATGAACACC 720 | | | | | |
| ACCTGAAGA ATCATTGAAG CAAATGAATG TTGGTGAAGA TTAGAAAAT GAAGATTTG 780 | | | | | |
| ACAGTCGTAG ATACAAATTG TTGGATGATG ATGGATCCAT TTCTCTTATT GAGGAGTCAA 840 | | | | | |
| CAGCAGAGGA TGAGGATGCA ACACATCTG AAAGATAACG ATGTGATATC AAATGGCAG 900 | | | | | |
| GGGGATGTTT CATAGTAAGT CTGTAATCTC CTGTAAGACT GAGGTGATAC TTGAGAAAG 960 | | | | | |
| AGGATATTAC TGAAGAAGCT GCTTTGCTA AAAAGAGAGC TACAAAAGCC AAAAATACTG 1020 | | | | | |
| GACAGAGG CCTGAAAATG TGACAGGATC ATGAATGTC AAGGCTTTA TCTTGAGAAC 1080 | | | | | |
| ATGGTGTCTG GAGTTAAAGG TATTGGCATA CTCCACACAT CTGACCATC TTGAGTGT 1140 | | | | | |
| CGCTTAGGAA TGAATGTGAT TTGAAACTCAT TCTATGTTGAG AGGGGTGTCAG ATTGAGAAC 1200 | | | | | |
| AGGTAGATCC CACCAACCTA CAGTAAAAG GACCCCAAAG TAAATGGTT GAAGAAATTA 1260 | | | | | |
| GATCCCAAG ATTCTGGTG AATTGGAG TCTTCATCAG TATATCCATA TTTAAACGAG 1320 | | | | | |

ATGACAGAAG CCAAAGTAAT TATGGCAAGT AATGGTTTT ATCTTAAC TAAGTTATT 1380
 GCTCAAGGGT GTAAATGGCA TTACCAAGGC TTITAGAATG CAGTTCTCA TTGCTGTGG 1440
 ACATGACCAT AAAAAAAT TTCCCAAGTAG GTTTCATC TGCTACGTTG CTAGCAATCA 1500
 GCTTATGGG AACAGTTGAT TAACTGTAAT AGAAATGCAA TACAATAAA ATGTGAACCA 1560
 CATGTGATT TCTTTAAAAA TCAGTGAGAT TTGAAAATTC TCCTAGATCT CTTGAATCAT 1620
 GCAAAATTGC TTGCGCTTA TATTGTAACC CTTGCGGGT GCTAATAACC AAGCAGTTG 1680
 TAGTAGAGTT AACTCAGGCT CGTCTCAGGG ACTCATCAT GTTCACTCAC TGTCACACTCA 1740
 TCTCTGGAA TGTTAAAATC ACTTTTACAC TATTGTTATG TAGGGCTGAC AGGACAATG 1800
 GATCAGITTC ATTAAAAGG TATGTATGCA TTAGAAAAGA CATTGTTATG GGTCACTTCA 1860
 AAGAGGGCTT ATGAGGCTGT GAAACCCAGA GCTCTAACG CTGTGACCAA AGATGGAAGT 1920
 TCTCTATAGG AAAGCATAGC ACTCTTAATG TTGGTGTCA TGTTTCTG AGGAGATATA 1980
 AAACGATAATA ATCCATGATT GTGCGCATG GAGAGTTTA AAGGTTAATC AAAATTCTC 2040
 TCTCTAGGG CAAACTGAA GATAAATCTT TTGACTCCAG CTCCTTAAAGT GATCTAAAGT 2100
 GACCTGTGATG GACAGTGGAA GAAATCACAA CATGGAATCT CTGGAATAAC AATTATTTGA 2160
 CTTTAATAAA TTTTGCTCTAA TGCTACATAT ACACAAATAA AAAACCTTAA CACTATTTCT 2220
 AGAAAGTCAG CATGTATTT TGCTCGAAG TTCTCTAGT GTTTCTGTG GAAGGAATAA 2280
 AAATTGAGT TTCAAAAAAA AAAAAGAAAAA AAAAAGAAAAA AAAAAGAAAAA AAAAAGAAAAA

Seq ID NO: 28 Protein sequence:
 Protein Accession #: BAB15628.1

1 11 21 31 41 51

MDKSGIDSLL HVTSDAELA NRSDNNSDSS LFKTQCIPYS PKGEKRNPJR KFVRTPESVH 60
 ASDSSDSSF EPIPLTIKAI FERFKNRKRR YKKKKKKRYY PTGRPRGRPE GRRNPYIISLI 120
 DKKKQFRSRG SGFPFLESEN EKNAPWRKIL TFEQAVARGF FNYIEKLKYE HHLKESLKQM 180
 NVGEDLENEED FDSRKYFLD DDDSIISPIE STAEDEDATH LEDNECDIKL AGDSFIVSSE 240
 FPVRLSVYLE EEDITEEAAL SKKRATKAEN TGQRGLKM

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_004289.3
 Coding sequence: 493-1695

1 11 21 31 41 51

GGCGCCGCT CGTCCACCGG AGGAGCCGGC GCCAGCGTGG ACGGGGGCAG CCAGGCTGTG 60
 CAGGGGGCG GCGGGGACCC CCGAGCGGCT CGGAGTGGCC CCTTGGACGC CGGGGAAGAG 120
 GAGAAAGGCAC CGCGGAAGC GACGGCTCAG GTGCCGGACG CTGGGGATG TGCAGGGAG 180
 GAGAAATGGG TACTAAGAGA AAAGCACGAA GCTGTGATC ATAGTTCCA GCATAGAGGA 240
 AATGAAGAAA GGGTGTGAGC CCAGAAGGG AACTCACTTC AGCAGAATGA TGATGATGAA 300
 AACAAATATC CAGAGAAAGG TGAGTGGAG CGAGAAAAGA CCACTGAATC TAGAAATGAG 360
 AGACATCTGA ATGGAGAGA TACTCTTC TCTCTGGAG ACTTATC CA GTTGTTC 420
 TCACAGCTG AAAATTCACT GGAGGGCATC TCATTTGGAG ATATTCCTC TCCAGGAGT 480
 ATCAGTGTG AGCATGAACTT TTGACGACAT TATCAAGTAA ACITCAGCCA GGCTATAAGT 540
 CAGGATGTA ATCTTCATGA GGCCATCTG CTTTGTCCA ACAATACATT TAGAAGAGAT 600
 CCAACAGCAA GGACTTACA GTCACAGAA CCATTTCAGC AGTAAATTC TCATACCAAC 660
 AATCTTGAGC AAACCCCTTCA TTGAAACTAT TTGACAGGAT TTCTTTCACC GGTTGACAA 720
 CATATGGAGA ATCTACAAG CCAAGACCTA CTGTATGACC TTGACATAAA TATATTGAT 780
 GAGATAAACT TAATGTATT GGCCACAGAA GACAACTTG ATCCAATCGA TGTTTCTAG 840
 CTTTTGATG AACCAAGATTG TGATCTGGC CTTTCTTATG ATTCAGTICA CAATAATACC 900
 TCTGTCATCA AGCTAATTC CTCTCAGT GTGTTGATG AAGGTGCTAT AGTTTATTC 960
 ACTGACCATO AATCTAGTC CCATCATGAC TTAGAAGGTC CTGTAAGGTG CTACTACCCA 1020
 GAACCAAGTA AGCTTTGTCA CTGGATCAAG AGTGTATCTG ATTCATGAG AGATCTTACA 1080
 TTCAACACG TATTTCATAA CCACACTTAC CACTTACAGC CAACTGCACC AGAATCTACT 1140
 TCTGAACTT TTCCCTGGG TGGGAAGTC CAGAAGATAA GGAGTAGATA CTTTGAAGAC 1200
 ACAGATAGAA ACTTGAGCCG TGATGAAAGC CGTGTCAAG CTTTGCATAT CCCTTTCT 1260
 GTAGATGAAA TTGTCGGCAT GCTCTGTAT CTTTCAATA GCATGTTAG TAGATATTAT 1320
 CTGACGACCC TACAAGTCTC ACTTACCGT GACATCAGAC GAAGAGGGAA AAATAAAGTT 1380
 GCTGCGCAGA ACTGTCGTAAC AGCCAAATTG GACATAATTG TGAATTAGA AGATGATGTA 1440
 TGTAACCTGC AAGCAAGAGA GGGAAACTCTT AAGAGAGAGC AAGCACAATG TAACAAAGCT 1500
 ATTAACATAA TGAAACAGAA ACTGCATGAC CTTTACATG ATATTTTATG TAGATTAAGA 1560
 GATGACCAAG GTAGGGCACTG CAACTCCAAAC CACTATGTC TCCAGTGTAC CCATGATGGA 1620
 AGATCTGAA TAGTACCCAA AGAAGCTGTC GCCTCAGGCC ACAAAGAGA AACCACAAAG 1680
 GGAAGAGAA AGTGAGAAGA AACTGAGAT GGACTCTATT ATGTGAAGTA GTAATGTTCA 1740
 GAAACTGATT ATTTGATCA GAAACCATGG AAACGCTTC AAGAATTTGA TCTTTAAGTA 1800
 CTGCTACTTG AATAACTCTG TTAACCGTGT TTGAAAGCTT ACATGGACAA ATGTTTAGGA 1860
 CTTCAAGATC ACACCTGTGG GCAATCTGGG GGAGCACAAC CTTTCAATG AGTGCATTG 1920
 ATACAAATT CATATGTTATG TCCAAAAGAAT AGGTTAACAT GAAAACCCAG TAAGACTTTC 1980
 CATCTGGCA GCAATCTTIT TTAAAGAGAA GTTGGTACT TCAAAAAGAG CAAACACTGG 2040
 GGATCAATT ATTTAAGAG AGTATTCTAGT TTAAATGCA AAATGGCTT ATTTCTATT 2100
 AGTTGTGATG CACTATAGTG AGCTTTCAA ACACATTTT AATCTTATAA TTAACTTAT 2160
 AAATTCTGCT TCT

Seq ID NO: 30 Protein sequence:
 Protein Accession #: NP_004280

1 11 21 31 41 51

MNSSAHYHVNFSQLISQDVNLHAEILLCPNNTFRRDPATAR TSQSQEPPFLQLNSHTTNPEQ 60
 TLPGNLTGFLSPVDNMHRNLTSQDLLYDL DINIFDEINL MSLATEDNFD PIDVSQLFDE 120
 PDSOSGLSLD SSHNNTSVIDK SNSSHSVCDDE GAIGYCTDHE SSSHHDLEGAA VGGYYPPEPSK 180
 LCHLDQSDSD FHGDLTFQHV FHNHTHYLQP TAPESTSEPF PWPGKSQKIR SRYLEDTDRN 240
 LSRDEQRKA LHIPFSVDEI VGMPVDSFNS MLSRYYLTDL QVSLIRDIRR RGKKNKVAQDN 300
 CRKRKLIDIL NLEDDDVCNLQ AKKETLKREQ AQCNKANIM KQKLHDLYHD IFSRLRDDQG 360

RPVNPNTYAL QCTHDGSILV PKELVASGH KKTQKGKRK

Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: NM_033260.1
 Coding sequence: 1-1208

| 1 | 11 | 21 | 31 | 41 | 51 |
|---|------|----|----|----|----|
| ATGAAATTGG AGGTGTTCGT CCCTCGCGCG GCCCAGGGG ACAACGAGGG CAGTGACCTG | 60 | | | | |
| GAGGGCGCG GGGCAGCGA CGGCCGCTOC CGCGCTGCG CGGCCGGGAGA CGACTCCCTG | 120 | | | | |
| GGCTCAGATG GGGACTGCG GGCCAGCG TCCGCGGCC CGGCCGCCAG AGATACGCAG | 180 | | | | |
| GGCAGCGCG AACAGAGTC GGGAGCGGG CGGCCGCCGG AGGAAGGCGAT CCCCGCAGCA | 240 | | | | |
| GCTGCTGAG CGGTGGTGGC GGAGGGCGCG GAGGGCGGG CGGGGGGCC AGGGCGGGC | 300 | | | | |
| GGCGCGGGGA CGCGAGGG TGCAAGCAGC AAGCCATA CGCGCGGCC CAAGCCCCCCC | 360 | | | | |
| TACTCGTACA CGCGCTCAT CGCCATGGCC ATCCGGACT CGCGGGCGG CGCGTGTGACG | 420 | | | | |
| CTGGCGAGA TCAACAGAGTA CCTCATGGGC AAGTCCCCCT TTTCCCGGG CAGCTAACCG | 480 | | | | |
| GGCTCGCGCA ACTCGCTGCG CCACAAACCTT TCCTCAACAGC ACTGCTTCTG CAAGGTGCTG | 540 | | | | |
| CGCGACCCCT CGCGGCCCTG GGGCAAGGAC AAACATCTGA TGCTCAACCC CAACAGCGAG | 600 | | | | |
| TACACCTTCG CGCACGGGGT CTTCGGCGCG CGCGCGAAGC GCCTCAGCCA CGCGCGCGCG | 660 | | | | |
| GTCCCGCGCG CGCGCGCTGG GCGGAGGGAG GCGCGGGCGC TCCCGCGCC CGCGCGCGCG | 720 | | | | |
| CGCGCGCGCG CGCGCGCGCG CGCGCGCATG CGCTCGCCCG CGCGCGAGGA GGAGGGCGCG | 780 | | | | |
| AGCCCCGGG GCAAGTTCTC CAGCTCTTC GCCATCGACA GCATCTCGC CAAGCCCTC | 840 | | | | |
| CGCAGCGCGC GCCTCAGGGGA CACGGGCCCGG GGGACACGC TTCACTGGG CGCGCGCGCG | 900 | | | | |
| TGCGCGCGCG TGCGCGCGTT CGCCCGCGTC CTCCCGCGG CGCCCTCGAG GGCCCTGCTG | 960 | | | | |
| CGCGCTCGCG CGTACCGGGCG GGGCGAGCGC GCGCGCGCTGG GCGCGCGCGA GGCGAGGTG | 1020 | | | | |
| CCCGAGCGC CGCGCGCCCG CCTCTTGCA CCTCTCCCGG CGCGGCCCG CGCGAGGCC | 1080 | | | | |
| CTCGAGGGCG CGCGCGCGCG CGCGCGCGAC CTGTACTGCG CGCTCGGGCT CGCGCGAGCC | 1140 | | | | |
| CTGAGGGCG CGCTAGTCGG NCCTCTGGC CGCGACCTGT CGTACCCGGT GGAGACGCTC | 1200 | | | | |
| CTAGCTGAA | | | | | |

Seq ID NO: 32 Protein sequence:
 Protein Accession #: NP_150285.1

| 1 | 11 | 21 | 31 | 41 | 51 |
|---|-----|----|----|----|----|
| MKLEVVFTRA AHGDQKQSDL EGAGGSDAPS PLSAAGDDSL GSDGDCAAAP SAGGGARDTQ | 60 | | | | |
| GDGEQSAGGG PGABEEAIPIAA AAAAVVAEGA EAGAAAGPGAG GAGSGEGARS KPYTRPKPP | 120 | | | | |
| YSVIALAMA IRDSAGGLRT LAEINLYLMG KFPFRGSYI GWRNSVRIHL SLNDCFVKVL | 180 | | | | |
| RDPSPWGKD NYWMLNPSE YTFADGVFRR RRKRLSHRAP VPAPGLRPEE APGLPAAPP | 240 | | | | |
| APAAAPASPRM RSPARQEERA SPAGKFSSF AIDSILRKPF RSRRRLRDTAP GTTLQWGAAP | 300 | | | | |
| CPLPAPFAAL LPAAPCRALL PLCAYGAIEP ARLGAREAEV PPTAPPILLA PLPAAAPAKP | 360 | | | | |
| LRGPAAAGGA LYCPRLPAA LQAALVRRPG PHLSYPVETL LA | | | | | |

Seq ID NO: 33 DNA sequence
 Nucleic Acid Accession #: NM_012128.2
 Coding sequence: 43-2796

| 1 | 11 | 21 | 31 | 41 | 51 |
|--|------|----|----|----|----|
| GAACAAACCA ACATTTGAGC CAGGAAATAAC TAGAGAGGG AAATGGGGT ATTCAAGAGGT | 60 | | | | |
| TTGTTTCC TCTTAGTTCT GTGCCCTGCG CACCACTCAA ATATTCCTT CATTAACTG | 120 | | | | |
| AATAATAATG GCTTGAAGA TATTGTCATT GTTATAGATC CTAGTGTGCC AGAAGATGAA | 180 | | | | |
| AAAAAATATG AACAAATAGA GGATATGGTG ACTACAGCTT CTACCTACCT GTTIGAAGCC | 240 | | | | |
| ACAGAAAAAA GATTTTTT CAAAATATGA TCTATATTAA TTCTCGAGAA TTGGAAGGAA | 300 | | | | |
| AATCTCAGT ACAAAAGGCC AACACATGAA AACCTAAAC ATGCTATGT TATAGTTGCA | 360 | | | | |
| CCACCTCAC TCCCAAGGTAG AGATGAACCA TACACCAAGC AGTTCACAGA ATGTTGAGAG | 420 | | | | |
| AAAGGOGAAAT ACATTCACCT CACCCCTGAC CTTCCTACTTG GAAAAAAACAA AAATGAATAT | 480 | | | | |
| GGACCCACCG GCAAACTGTT TGTCATGAG TGGGCTCACCG TCCGGTGGGG AGTGTGAT | 540 | | | | |
| GAGTACAATG AAGATCAGCC TTTCCTACCGT GCTAAGTCAA AAAAATCGA AGCAACAAGG | 600 | | | | |
| TGTTCCCGTAGT CTCTCTGG TAGAAATAGA GTTTATAAGT GTCAAGGAGG CAGCTGCTT | 660 | | | | |
| AGTAGAGCAT CGCAAGATTGA TTCTACAACAA AACACTGTATG GAAAAGATTG CTCATCTT | 720 | | | | |
| CTGTATAAG TACAAACAGA AAAAGCATCC ATAATGTTA TGCAAAAGTAT TGATTCCTGTT | 780 | | | | |
| GTGAAATTG TTAACAGAAA AACCCATAAT CAAGAAAGCTC CAAGCCCTACA AAACATAAAAG | 840 | | | | |
| TGCAATTAA GAAGTACATG GGAGGTGATT AGCAATCTG AGGATTTTAA AAAACACCTAA | 900 | | | | |
| CCCATGGTGA CACCAACCTCC TCCACCTGTC TTCTCATTCG TGAAGATCCG TCAAAAGAATT | 960 | | | | |
| GTGTCCTTAG TCTCTGATAA GTCCTGAAAGC ATGGGGGGTA AGGACCGCCCT AAATCGAATG | 1020 | | | | |
| AATCAAGCAG CAAACACATTCTT CCTCTGCGAG CACTGTGAAATGATGCTCG GGTGGGGATG | 1080 | | | | |
| GTTCACITTG ATAGTACITGC CACTATGTAA ATAAGCTAA TCCAAATAAA AAGCACTGAT | 1140 | | | | |
| GAAAGAAAACA CACTCATGGC AGGATTACCT ACATATCTTC TGGGGAGGAAC TTCCATCTG | 1200 | | | | |
| TCTGGGAAATTAA ATATGTCATT CTAGGTGATT GGAGAGGTAC ATTCACCACT CGATGGATCC | 1260 | | | | |
| GAAGTACTGC TGCTGACTGA TGGGGAGGAT AACACTGCAA GTTCTGTAT TGATGAAAGTG | 1320 | | | | |
| AAACAAAGTG GGGCCATGTC TCTCTTATTG GTCTGGGAA GAGCTGCTGA TGAAGCAGTA | 1380 | | | | |
| ATAGAGATGA GCAAGAACAC AGGAGGAATG CATTCTTATG TTTCAGATGA AGCTCAGAAC | 1440 | | | | |
| AATGGCCCTCA TTGATGCTTT TGGGGCTCTT ACATCAGGAA ATACTGATCT CTCCTCAGAAC | 1500 | | | | |
| TCCCTCAGC TCAGAAAGTAA GGGAATTAACA CTGAATAGTA ATGCTCTGGT GAACGACACT | 1560 | | | | |
| GTCTATAATTG ATAGTACAGT GGGAAAGGAC ACGTTCTTC TCATCACATG GAACAGTCTG | 1620 | | | | |
| CCTCCAGTA TTCTCTCTG GGATCCAGT GGAACAAATAA TGAAAATT CACAGTGGAT | 1680 | | | | |
| GCAACTCTCA AAAATGGCTTA TCTCTGATT CCAGGAACCTG CAAAGGTGGG CACTTGGGCA | 1740 | | | | |
| TACAATCTTC AAGCCAAAGC GAACCCAGAA ACATTAACTA TTACAGTAACT TCTCTCGAGCA | 1800 | | | | |
| GCAAAATCTT CTGTGCTCC AATCACAGTG AATGCTAAAAA TGAATAAGGA CGTAAACAGT | 1860 | | | | |
| TTCCCGAGCC CAATGATTTG TTAACAGAAA ATTCACAGAAG GATATGACC GTGTCITGGA | 1920 | | | | |
| GCAATGTGA CTGCTTTCAT TGAATCAGACG AATGGACATA CAGAAGTTT GGAACTTTTG | 1980 | | | | |
| GATAATGGTG CAGGGCGCTGA TTCTCTAAG AATGATGGAG TCTACTCCAG GTATTTACA | 2040 | | | | |
| GCATATACAG AAAATGGCAAG ATATACTTA AAAGTTGGGG CTCATGGAGG AGCAAAACACT | 2100 | | | | |
| GCCAGGCTAA ATTACGGCC TCCACTGAAT AGAGCCCGCT ACATACCCAGG CTGGGTAGTG | 2160 | | | | |

AACGGGGAAA TTGAAGCAAA CCCGCAAGA CCTGAAATTG ATGAGGATAC TCAGACCACC 2220
 TTGGAGGATT TCAGCCGAC AGCATCGGA GGTCGATTG TGGTATCAC A GTCCCAAGC 2280
 CTCCCTTGC CTGACCAATA CCCACCAAGT CAAATCACAG ACCTTGATGC CACAGTTCAT 2340
 GAGGATAAGA TTATCTTAC ATGGACAGCA CCAGAGATA ATTTGATGT TGGAAAAGTT 2400
 CAACGTTA TCATAAGAT AAGTCAAGT ATTCTGATC TAAGAGACAG TTTTGATGAT 2460
 GCTCTCAAG TAAATCTAC TGATCTCA CCAAAGGAGG CCAACTCCAA GGAAGCTTT 2520
 GCATTTAAC CAGAAAATCT CAGAGAA AATGCAACCC ACATATTTAT TGCCATTAAA 2580
 AGATAGATA AAAGCAATT GACATAAAAT GATCCAAACA TTGACAAGT AACTTGTGTT 2640
 ATCCCTCAAG CAAATCTGA TGACATTGAT CCTACTCTA CTCCCTACTC TACTCCTGAT 2700
 AAAAGCTATA ATCTGGAGT TAATATTTCT ACCTGGTAT TGCTGTGAT TGGGTCTGTT 2760
 GTAATGTTA ACTTTATTT AAGTACCAAC ATTGAAACCT TAACGAAGAA AAAAATCTTC 2820
 AAGTAGACCT AGAAGAGAGT TTTAAAAAAC AAAACATGT AAGTAAGGA TATTCTGAA 2880
 TCTTAAATT CATCCCTGT GTGATCTAA ACTCTAAAA ATAATTTAA GATGTCGAA 2940
 AAGGAACTT TGATTAATAA AAAACACTCA TGGAATATGTA AAAACTGTCA AGATTAATAA 3000
 TTAATGTTT CATTTTTG TTTTTTATGTT TGTAAGAAAT AGTGATGAAC AAAGATCCCT 3060
 TTTCATCTG ATACCTGGTT GTATTTATT TGATGCAACA GTTTCTGAA ATGATATTC 3120
 AAATTGCACTC AAGAATTAA AATCATCTAT CTGAGTAGTC AAAATACAAG TAAAGGAGAG 3180
 CAAATAACA ACATTTGGAA AAAAAAAA AAAAAAAA.

Seq ID NO: 34 Protein sequence:
 Protein Accession #: NP_036260.1

1 11 21 31 41 51

MGLFRGFVFL LVLCLLHQSN TSFIKLNNG FEDIVIVIDP SVPEDEKIE QIEDMVITAS 60
 TYLFATEKR FFFKNVSLI PENWKENPQY KRPKHENKH ADVIVAPPL PGRDEPYTKQ 120
 FTCEGKEV IFPTPDLLG KKQNEYGPP KLFVHEWAHL RWGVFDEYNE DQPFFYRAKSK 180
 KIRATRCIS QSGRNRYVKC QGGSCLSRAC RIDSTTKLYG KDCQFFPDKV QTKEKASIMFM 240
 QSIDSVVFC NEKTHNQEAP SLQNIKCNF STWEVNSE DFKNTPMVT PPPPPVFSLL 300
 KIRQRIVCLV LDKSQSMGKK DRNLNRNQAA KHFLQTVEN GSWSVGMVHFD STATIVNKLI 360
 QIKSSDERNT LMAQLPTYPL GGTSICSGIK YAFQVIGELH SLDGSEVLL LTDGEDNTAS 420
 SCIDEVKQSG AIHVHFIALGR AADEAVIEMS KITGGSHFYV SDEAQNNGLI DAFGALTSGN 480
 TDLSQKSQL ESKGLTLNSN AWMMNDTVIDT STVGKDITFL ITWNSLPSSI SLWDPSGTM 540
 ENFTVDATSK MAYSLIPGTA KVGTWAYNLQ AKANPETLII TVTSRAANSS VPPITVNAKM 600
 NKDVNSFPSP MIVYABILQG YVPVLGANVTF AFIESONHT EVLELLDNGA GADSFKNQDG 660
 YSRVFTAYTE NGRYSLKVR HGGANTARLK LRPPNLRAYA IPGVVVNGEI EANPPRPEID 720
 EDTQTLEDI SRTASGGAFV VSQVPSLPLP DQYPPSQTD LDATVHEDKI LLTWATPGDN 780
 FDVGKVQRYI IRISASIDL RDSFDDALQV NTIDLSPKEA NSKESFAKFP ENISEENATH 840
 IFIAKSIDK SNLTSKVSNI AQVTLFIPQA NPDDIDPTPT PTPTPDKSHN SGVNISTLVL 900
 SVIGSVVIVN FILSTTI

Seq ID NO: 35 DNA sequence:
 Nucleic Acid Accession #: NM_000901.1
 Coding sequence: 217-3171

1 11 21 31 41 51

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 GAGCCTTGCT GCCTCGGGCT CTCCCGCTGC AGGGGAGCG GCACTCGCTG GCCTGGATGT 120
 GGTGGATT AGGGGGGCTC CGCACCGAGG GTTCTGTCGC GGTGCAAGC GCTGCAACAG 180
 GTAGACGGGG AGAGACGGAC COCGGCCAGG GCAGGGATGG AGACCAAAGG CTACACAGT 240
 CTCCCTGAG GTCTAGAT GAAAAGACCG TGGGGTCAAG TTCTCAGGC TGTTGGAGCGT 300
 TCTCCCTGG GACCTACAGA GAGGACCGAT GAGATAACT ACATGGAGAT TGTCACCGTA 360
 AGCTGTGTTT CCGGTGCTAT TCCAACAAAC AGTACTCAAG GAAGCAGCAA AGAAAACAA 420
 GAACTACTC CTGCGCTTC GCAAGACAAAT AATCGGCGCTG GGATTTAAC ATCTGATATT 480
 AAAACTGAGC TGGAACTCAA GGAACCTTC GCAACTGTAG CTGAGTCCAT GGGTTTATAT 540
 ATGGATCTG TAAGGAGATGC TGACTTATCC TATGAGCAGC AGAACCAACA AGGAAGCATG 600
 AGTCACGTA AGATTTATCA GAATGGTAA CAGCTGGTA AATTTCACAA AGGAATGGC 660
 CATGCTCTT CCACCTAAG TTGTGTGAC ACGCCCTGA GATCATTAT GTCTGACTCT 720
 GGGAGCTCG TGAATGGTGG CGTCATGCGC GCCATGTTA AAAGCCCTAT CATGTGTCT 780
 GAGAAAGGCG CGTCGTGTTG CAGCCCTCTG AACATGACAT CTTCGGTTG CAGCCCTGCT 840
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 ATCACCCAGG GAACCTCTCT GACATGCTCC CCTAATGCTG AAAATCGAGG CTCCAGGTG 960
 CACACCCG CACATGCTG CAATGTTGGGC TCTCCCTCT CAAGTCGGT AAGTAGCATG 1020
 AAATCTCAA TTCCAGCCC TCCAAGTCAC TGCACTGTTAA ATCTCCAGT CTCCAGTCCC 1080
 AATAATGTCA CTCTGAGATC CTCTGTGCT AGCCCTGCAA ATATTAACAA CTCAAGGTGC 1140
 TCTGTTCCA CACTAATACAGATCCACGC TTCCAGTCC GGCAGCCAGT 1200
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 TCTGCTGGAT CCAGTACATT GCGGGATGTG GTTCCAGTC CAGACACGCC GGAGAAAGGT 1320
 GCTCAAGAGG TCCCTTCTC TAAGGACTGAG GAAGTAGAGA GTGCCATCTC AAATGGTGTG 1380
 ACTGCCCCAGC TTAAATGTTG CCACTACATA AAACCAAGAC CAGATGGAGC TTTAGCAGC 1440
 TCATGCTAG GAGGAAATAG CAAAATAAT TC GGATTCTT CATTCTCAGT ACCAATAAG 1500
 CAAGAATCAA CCAACCATTC ATGTCAGGC ACCTCTTTA AAGGGAATCC AACAGTAAAC 1560
 CGGTTTCCAT TTATGGATGG CTGCTGTTT TCTCTTATGG ATGATAAAGA CTATTATTC 1620
 CTATCAGGAA TTITAGGACC ACCTGTGCC GGCCTTGATG GTAATGTGA AGGCAGCGGA 1680
 TTCCCACTG GTATTAACAA AGAACCCAGAT GACGGGAGGCT ATTACCCAGA GGCCAGCAGTC 1740
 CCTCCCTCTG CTATTTGTTGG GTTGAATTCA GTTGGGAGCT CCTCCCACTA CAGGATTGGT 1800
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 TCCCTTCTC CTGTCATAC TTTAGTGGAG TCATGGAAAT CACACGGCGA CCTGTGCTCT 1920
 AGAAGAAGTG ATGGGTATCC GGTCTTAGAA TACATCAGC AAAATGTATC AAGCTCTACT 1980
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 CCACAGCAGC AGCACCCCCC ACCCCCCCCC CCACCCCGCG AAGCCCGAGA GOAAGGGACA 2340

ACGTACATCG CTOCTGCAAAGAACCCCG GTCAACACAG CACTGGTTCC TCAAGCTCTCC 2400
 ACAATCTCAC GAGCGCTCAC ACCTTCCCCC GTTATGGTCC TTGAAAACAT TGAACCTGAA 2460
 ATIGTATATG CAGGCTATGA CAGCTAAAAA CCAGATCAC CGGAAAATCT GCTCTCCACG 2520
 CTCAACCGCT TAGCAGGCAA ACAGATGATC CAAGTCGTGA AGTGGGCAAAGGTTCCA 2580
 GGAGTAAAC ACTGCTCTTGAGGACCAA ATTACCCAA TCCAGTATTCTTGGATGTT 2640
 CTATCATTTGGCTTGTAGTACAAACATA CGAACAGCCA ATTCTCTAT 2700
 TTGCCCCAG ACCTAGTCTTAATGAAGAG AAGATGATC AGTCTGCCAT GTATGAACCA 2760
 TGCCAGGGAA TGCAACCAAT CAGCCTTCAG TTCTGTTGAC TGCAAGCTCAC CTTTGAAGAA 2820
 TACACCATCA TGAAAGTTT GCTGCCTACTA AGCACAATTC CAAAGGATGG CCTCAAAAGC 2880
 CAGGCTCATTTGAAGAAAT GAGGACAAAT TACATCAAAG AACTGAGGAA GATGGTAAC 2940
 AAGTGTCCCA ACAACTCTGGCAGAGCTGG CAGAGCTGG ACCAAGCTGAC CAAAGCTGCTG 3000
 GACTCCATGC ATGACCTGGT GAGCGACTGCTGAGTACACCTCTACAC CTTCGGAGAG 3060
 TCCCATGCC TGAAAGTAGA GTTCCCCGCA ATGCTGGTGG AGATCATCG CGAACAGCTG 3120
 CCCAGGTGG AGTCCGGGAA CGCCAAAGCCG CTCTACTTCC ACCGGAAAGTG ACTGCCCGCT 3180
 GCCAGAAGA ACTTTCCCTTAAAGTTCCTTGTGTGTTCC ACACCCAGAA GGACCCAAGA 3240
 AAACCTGTTTAAACATGTTAGTTGATT CACACTGTTAACAGTCTTCAAGTTAA 3300
 AGTCATGTCAGGGTTTGGCGCCGGAAAGCTGTGTTTCC GTGGATTGCGAGAC 3360
 GCAGCTGAA GGATCCCCA CCTCCAACTCC CGCAGCGCTT AGAACACATGT TCCCTGTCT 3420
 CGGGATGAAA AGCCATATCT AGTCAAAAC TCTGATGTTTATTTCTACAGATGGAAGA 3480
 AGTTTAACT ATGCCGTGTA GTTICIGGTA TGCTGCTGTT GTTTAAAGGGTCAAGGA 3540
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 TAGAATGGTAAAGATGATGTTAAATGCTTGGTTGATTCTAGTATCTA TTGTGTGGC 3840
 TTACACATAATTTCGCA GTCTTGTGTTGCTGTTACATGTTAGTATAAATTAT 3900
 GAAGGAGCTGAAATAAGGTTAGGATCTTGTGAAATGAGACACATACA AAAAAGAT 3960
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 CATGCAATAAGAACCTGTTAAGTGTATTAAAGAAGGGAAAGCTGTGCTCCTTTAGCT 4140
 TCAATCTAA TTACCATTAATTACAGTCTGTTGTTAAATACACCTGCT 4200
 TCGTTGTCTTGAAACCTTCTACTTTCTGTTACTTGTGTTGTCTTGCTCCOG 4260
 CTGGGCGATTTGTGGACTCAGCAGCTCTGCTCATCC TGCTCATCC TGCTCATCG 4320
 GGAATGACA CACTGGGTGCTGGAGCTTCAGGAGGTTGTCATTTGACAACACATGTTGG 4380
 GAGAGGAGGTCTTGGAGTGCTGAGCTTGGAAAGCTGCCTGTTTCCTTCTC 4440
 TAGAAGCAGAACCGCTCA CGAGAGTGAAGACTGGAAACTTGATGGCTCA GAGAGCATCT 4500
 TTCTCTCCATTTAGGAAATTCAGATTTTCAAGGAGGAAAGCTGTGCTCCTTTAGCT 4560
 TCTCTGTGTTAAAGATCAGCTTCCCTCCTGATCTGGAAGAGGTCTGCACCTGG 4620
 AACCGGTACAGGAGCACAGATCATGGCAGGATGGCTGGGACCGCCTGGAC 4680
 GGTTCAGTCTGAATGGCATGGAGACAGGAGGGGGTTTAAAGTTTAAAGGTA 4740
 GGTITTTAAATAAGTTTAAACATAACAGTTTGAGAAAATTACAGATCATATAAG 4800
 CAAGACAGTCACTAAATTTAAATCTAATATCTGTTGTTGGCAC TGATGCAATG 4860
 TATGGCTTTCTCTGGCCAAATACACATGTTACCTTGGGGAACTAAACATAT 4920
 GATTCGACTAAATAAAACTACTTTGAATAGAGCCAAATTAACTTAAATGATGATA 4980
 ATCATCAGTTACTGCTAGTAAATCATATTAAATTATTTCAAAATCTAAAGCTGTAGC 5040
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 TICACCATGCAGGAAACATTACCTGCTTCTAAAGACA CCTGCTTAG TGCAAGGG 5160
 AACCTGTGAGACTGCACTAGAGGGAGGA GTCTTCTTCTAATACTGCAATTCTAGGA 5220
 ATTAAATTATAGGAGATCTTAAATACA GTCAACCTACGGTCACAGTAAATGAAAG 5280
 CCACACTTGAAGGATAATAATACACAGCA TGCAAGCTGGGAGTTGCTGCAAACAAATG 5340
 GCTTCACTTACAAAAGCAGTTAGTCTAGACTTGTGTTTATAAAATGAGAATTCTGAC 5400
 TTACTAACCAGGTTGGGTTGGAGATGGTCTGCTCATCAGCTTGTGTTAAACAAAGGTA 5460
 CTGGCTTTCTGTTGCTCCAGGAACTTGTGATIAACAGCAAAGCATATCTAA 5520
 ATTGCTCTTAAATCTGGTTGGTACAGTTCAATACACCAAAAGTTCATATAATT 5580
 TAAGAAACACTAAATGTTAAATGAA GCAATTTATACTTATGCAAAACATATG 5640
 TCTGTCCTGCAAAGGACTGTAAGCAGATTACAATAACATCTT 5700

Seq ID NO: 36 Protein sequence:

Protein Accession #: NP_000892.1

| | | | | | |
|---|-----|----|----|----|----|
| 1 | 11 | 21 | 31 | 41 | 51 |
| | | | | | |
| METKGYHSILP EQLDMERRWG QVSQAVERSSLPTEERTDEN NYMEIVNVSC VSGAIPNNST | 6 | | | | |
| QGSSEKQEL LPCLQQDNRR PGILTSDEK ELESKELSAT VAESMGLYMD SVRDADSYE | 120 | | | | |
| QQNQQGSMSP AKIYQNVQL VKFYKONGHR PSTLSCVNTP LRSFMSDSGS SVNGVVMRAI | 180 | | | | |
| VSPIMCKH SPVSPCSPLNM TSSVCPSPAGI NSVSSSTASF GSPVSPSPN QTPLTCSFN | 240 | | | | |
| AENRGRSRHS PAHASNVGP LSSPLSSMKSISSPPSHCS VKSPVSPSPN VTLRSSVSP | 300 | | | | |
| ANINNSRCSV SSSPNTNNRSLTSSPAASTV GSICSPVNNA FSYTASGTSAGSSTLRDVVP | 360 | | | | |
| SPDTEKQGAQ EVPFPKTEEV ESAISNGVIG QLNIVQYKPF EPDGFSSC LGGNKINSID | 420 | | | | |
| SSFSVPIKQE STKHSCSGTS FKGNPVTNPPT PFMDGSYFSS MDDDKDYYSLS GILGPPVPGF | 480 | | | | |
| DGNCEBGSQFGV KNLQEPDDG SYYPEASIPS SAIVGVNSGQ QSFHYRIGAQ GTISLRSAR | 540 | | | | |
| DOSFOHLSS PPPVNTLVEWS KSHODLSSR SDGYPVLEVI PENVSSSTL SVSTGSSRPS | 600 | | | | |
| KICLVCGDEA SGCHYGVVTC GSCKVFFKRA VEGOHNLYCA GRNDCIDKIRRKNCPCRL | 660 | | | | |
| QRCLQAGMNL GARKSKKLGK LKGIIHEEQPO QQQPPPPP PQSPEEGTYY IAPAKEPSVN | 720 | | | | |
| TALVPLQSTI SRALTPSPVM VLENIEPEV YAGYDSSKPD TAENLLSTLN RLAGKQMIQV | 780 | | | | |
| VKWAJVLPGF KNLPLEDQT LIQYSWMCLS SFALSWRSYK HTNSOFLYFA PDLVFNEEKW | 840 | | | | |
| HQSAMYELCQ GMHQISLQFV RLQLTFEEYT IMKVLLLST IPKDGLKSQA AFEEMRNTYI | 900 | | | | |
| KELRKMWTKC PNNSGOSWQR FYOLTKLLDS MHDLVSDLLE FCFTYTFRESH ALKVEPAML | 960 | | | | |
| VEIISDQLPK VESGNAKPLY FHRK | | | | | |

Seq ID NO: 37 DNA sequence:

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51

CCTACCGGT TCAAGCAACT CTGCTGCC C AGCTCCAA G TAGCTGGGAT TACAGGTGCA 60
 TGCCACTACA CCTGGCTTT TGATTTA GTAGAGATGG TTTCACAT ATGCCCCAGG 120
 CTGATCTTGA ATTCTGGCC TGAAGTAATC TGCCGCC C AGCTCCAA AGTCTGGGA 180
 TTATAGGAGC CACCAACCT GGCAAATCTG GTATTTTA TATGCTCTT GGGCAACTTA 240
 AAAAATGAT TACTCTGTG TTCTCTCTT TTTCCTT GACCAATTG 300
 TGAGACCAA GTATCTCTA CCTAGAAAAA AAACACACTA AACAGTAAT GATTACCAAC 360
 CTATTTGGAA CAAATCTCAA TAAATTAAACA TATACTCAA GGAGAAGACT TAACAAAATC 420
 TTACTTCA TTCTAATAG CTCTTCCAT AAAATGTC CACAAGTG TCAAATTAGT 480
 CCTAACAACT ACTGTTAAGT GATTAATGAA ACAGGAGTG CAGGAGTGAA TTAAATAA 540
 GCAATAAATCAGATGGAC TACCTAAATG TTGAGGGTCC TGATGCAAA CTCTCTGT 600
 ATTGGATGGC ATCTCAGCTT TCTCATAGAG CTGTTCACT GTGAGGGTCT TTATCTCA 660
 TCAGAGCTT CATTATTTCTT TTCTCTAG CAATCAGTCC AAAGCACAAAT GTCAAGAAAGA 720
 TCACAAACACA TGCAACATA ATGGGCTCTA TTGGTACACC CACAGTTTA TCTTAACAA 780
 TC

Seq ID NO: 38 DNA sequence
 Nucleic Acid Accession #: NM_001192.1
 Coding sequence: 219-773

1 11 21 31 41 51

AAGACTCAA CCTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCGCGAAG 60
 ACACAGACAG CCCCCGTAAG AACCCACGAA GCAGGGCAAG TTCAATTGTC TCAACATCT 120
 AGCTGCTT GCTGCATTTG CTCTGGAACT TTGTAGAGA TATTACCTGT CCTTCAGGC 180
 TGTTCTCTTG TGTAGCTCCCT TGTTCTCTT TTGTGATCAT GTGAGATG GCTGGGCACT 240
 GCTCCAAA TGAATTTTG GACAGTTGT TGATGCTT CATACTCTGT CAACTTCGAT 300
 GTTCTCTAA TACTCTCTT CTAACTATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT 360
 CAGTGAAGG AACGAATGCG ATTCTCTGGA CCTGTTGGG ACTGAGCTTA ATAATTCTT 420
 TGGCAGTTT CGTGTAAATG TTGCTCAA GGAAGATAAG CTCTGAACCA TAAAGGAGC 480
 AGTTAAAAA CACAGATCA GGTCTCTGG GCATGCTAA CATIGACCTG GAAAAGAGCA 540
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 GTGAAAGCTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTT CCACCTCCAG 660
 CTATGGAGGA AGGCGCAACC ATTCTTGCA CCACGAAAC GAATGACTAT TGCAAGAGC 720
 TGCCAGCTGC TTGAGTGCT ACGGAGATAG AGAAATCAAT TCTGCTAGG TAATTAACCA 780
 TTTCGACTCG AGCAGTGCCTT CTTTAAATAT TTGCTGAG AATAGTGTGAT GTGTCAGATC 840
 TCTTGGAT GACTGTATT TTCACTGCC GATACAGCTT TTGTCCTCT AACTGTGAA 900
 ACTCTTATG TTAGATATAT TTCTCTAGT TACTGTTGGG AGCTTAATGG TAGAAACTTC 960
 CTGGTTCA TGATTAAGT TTTCCTT CCTGA

Seq ID NO: 39 Protein sequence
 Protein Accession #: NP_001183.1

1 11 21 31 41 51

MLOMAGQCSQ NEYFDSSLHA CIPCQLRCSS NTPLTCQRY CNASVINSVK GTNAILWTCL 60
 GLSLIISLAV FVLMFLLRKI SSEPLKDERK NTGSGLLGMA NIDLEKSRTG DEILIPRGL 120
 YTVEEETCED CIKSKPKVDS DHCFLPLAME EGATILVTK TDYCKSLPA ALSATEIEKS 180
 ISAR

Seq ID NO: 40 DNA sequence
 Nucleic Acid Accession #: NM_025087.1
 Coding sequence: 183-2282

1 11 21 31 41 51

ACACTGCCTC GGTTGGCAA GTGGGTCACT TGGCTGGGGC TCACTTGCA ACGGGACCGG 60
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 GGCTAGGGCA CGGGGGCGA CCCGCACCGC TTTCCTGGAA AGCCTGCCC CTGGCCCGGG 180
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 CTCTCTACCA TGACCTGGGA CGCATGATCT ATTACTTCC TTGCAAACA CTAGAACCTCA 300
 CTGGCTCTGA AGGTTTACTG ATAGCATTTCTTCTCAAA ATTCTCAACA ATTACTCTT 360
 TCTGAAATT GTTAAACAGA AAGTGGATGC TAACCTCTGCT GAGGATAATC ACTATTGGCA 420
 GCATAGCCCTC TTCCCAAGCT CCAAATGCCA AACITCGACT GATGGTCTT GCGCTGGGG 480
 TGTCCTCTC ACTGATAGTCA CGAGCTGTA CTGGGTGTC AGGAAGCTCAT TTGCAAAGGT 540
 ACCTCAGAAT TTGGGGATTC ATTTCAGGAC AGATGTCT TTGTTCTA CGCATATGGT 600
 ATACTCACT AAACCCAAATC TGAGTTATC AGATGTCCTA CAAAGTGATA CTGACATTA 660
 GTGCGATAGC CACACTTGAT CGTATGCA CAGATGTTGA CTGCGATGAA CCTGAGAAA 720
 AGAAGACTGG TGAGCTGGC ACGGGGATGG CCTCTAGACCC CAACTGGCTG CTGGCAGGGG 780
 CTGCTTCTGG TAGCCCTGGT TTCTCTACCC ACTGGGTTT TGAGAGCTC TCTCTCTGGT 840
 CCAGATGGGC AGTGGAGGG CATCCACATC CAGGGCCAGA TCCCTAACCA TTGGGAGGTG 900
 CAGTACTGCT GTGCTGGCA AGTGGATGTA TGCTTCCATC TTGTTCTGG TTCTGTTGA 960
 CTGGTTGAT CTGGTGGGTT ACAGGAACAG CTTCAGCTG GGGGCTCTT TACCTGCACA 1020
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 AACACCTTGA ACACCTTAACTCAGGGA CAAACCTGG GAAAACCATG ACCATTGCCA 1140
 TGATATTCTA TCTCTCTAGAA ATATTTCTG TGCCCTGGTG CACAGCTTT AAGTTGTC 1200
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 TTGTTGGTGT GGGGATGTTG GGATAGGGAC TACGGCATAA AGOCTATGAG AGAAAATGG 1440
 GCAAAGTGGC ACCAACCAAA GAGGTCTCTG CTGCGCATCTG GCCTTCACTG TTGGATATG 1500
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 ATTCATAAC AATTTGGAG AGTGTGCTT CTAAGCCCTA TATGGGAAAC AATGACTTAA 1620

CCATGGGCT AGGGGAAAG TTGGGTTCT ATACAGACT TGGCCAAGC ACAAGGTATC 1680
 ACAAATGGG GATTATGGCT TTGTCAGAT ACCCAATGT GAAATCTGAG CATCACCTTC 1740
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 TGCAAGCTAT TGCTGTTCA AAACATCTGA AAAGTAGCTC TAATCAAGTG ATATTCCTGG 1920
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 TGAAAGATAT CGACAGCACT GATCATGACA GATGGTGTGA ATACATTATG TATCGAGGGC 2040
 TGATCAGTTT GGGTTATGCA AGAATCTCCC ATGCTGAACT GAGTGATTCA GAAATTCCAGA 2100
 TGGAAAATT TAGGATCCTGATGACCCCC CTAATTATAG AGACAAACAG AAAAGGGTCA 2160
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 GAAACATTTA AAAACAAGAG TTATGGCTG GGAAAATCTA AGAAAAAAAG TATGTAAAGAT 2340
 AAAAGAAGA GATTAATGAA AGTGGGGAAAC TACACATGAA GAACTCAAC TAAAAAAACA 2400
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 ATTTCTCAA AAAAAAAA AAAAAAA

Seq ID NO: 41 Protein sequence:
 Protein Accession #: NP_079363.1

| | | | | | |
|---|----|----|----|----|----|
| 1 | 11 | 21 | 31 | 41 | 51 |
|---|----|----|----|----|----|

MTSLWREILL ESLLGCVWS L YHDLGPMIY YFPLQTLIELT GLEGFSIAFL SPIFLITTPF 60
 WKLVNKKWML TLLRITIGS IASFQAPNAK LRLMVLALGV SSSLIVQAVT WWSGSHLQRVY 120
 LRIWGFILGQ I VLVVLRIWY TSLNPWISYQ MSNKVILTLS AIA TLDRTG DGDCSKPEEK 180
 KTGEVATGMA SRPNWLLAGA AFGSLVFLTH WVFGEVSLVS RWAVSGHHPF GPDPNPFGGA 240
 VLLCLASGLM LPSCLWFRGT GLI WWWVGT A SAAGLILYLT WAAA VSGCVF AIFTASMWPO 300
 TLGHLINSGT NPGKTMIIAM IFYLLEIFFC AWCTAKFKVP GGYYARERSD VLLGTMMLI 360
 GLNMLFGPKK NLDLLLQTKN SSKVLFRKSE KYMKLFLWLL VGVLGLGL RHKAYERKLG 420
 KVAPTEVSA AIWPPRFQYD NEGWSLERS AHLLNETGAD FITILESADAS KPYMGNNDLT 480
 MWLGEKLGFY TDGPSTRYH TWGIMALSRY PIVKSHHILL PSPEGHIAPA ITLTVNISGK 540
 LVDFVVTHFG NHEDDLDRKL QIAAVSKLLK SSSNQVFLG YITSAPGSRD YLQLTEHGNV 600
 KIDSTDHDR WCEYIMYRGL IRLGYARISH AELSDSEIQM AKFRIPDDT NYRDNQKVVI 660
 DHREVSEKIH FNPRFGSYKE GHNYENNBNF HMNTPKYFL

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a metastatic colorectal cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.
- 1 2. The method of claim 1, wherein the biological sample comprises isolated nucleic acids.
- 1 3. The method of claim 1, wherein the polynucleotide is labeled.
- 1 4. The method of claim 1, wherein the polynucleotide is immobilized on a solid surface.
- 1 5. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.
- 1 6. An expression vector comprising the nucleic acid of claim 5.
- 1 7. A host cell comprising the expression vector of claim 6.
- 1 8. An isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.
- 1 9. An antibody that specifically binds a polypeptide of claim 8.
- 1 10. The antibody of claim 10, which is an antibody fragment.
- 1 11. The antibody of claim 10, which is a humanized antibody
- 1 12. A method of detecting a metastatic colorectal cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody of claim 9.
- 1 13. The method of claim 12, wherein the antibody is labeled.
- 1 14. A method of detecting antibodies specific to metastatic colorectal cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-26.

15. A method for identifying a compound that modulates a metastatic colorectal cancer-associated polypeptide, the method comprising the steps of:

(i) contacting the compound with a metastatic colorectal cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.; and

(ii) determining the functional effect of the compound upon the polypeptide.

16. The method of claim 15, wherein the functional effect is determined by measuring ligand binding to the polypeptide.

17. A method of inhibiting proliferation of a metastatic colorectal cancer-associated cell to treat colorectal cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound that modulates a polypeptide encoded by a sequence as shown in Tables 1-26.

18. A drug screening assay comprising the steps of

(i) administering a test compound to a mammal having colorectal cancer or a cell isolated therefrom;

(ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26. in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of colorectal cancer.

19. A pharmaceutical composition for treating a mammal having colorectal cancer, the composition comprising a compound identified by the assay of claim 18 and a physiologically acceptable excipient.

20. A method of detecting a metastatic colorectal cancer-associated polypeptide in a cell from a patient, the method comprising contacting a biological sample from the patient with an antibody that specifically binds a polypeptide encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

21. The method of claim 20, wherein the antibody is labeled.